

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 09:49:30 ; Search time 25 Seconds  
(without alignments)  
3.564 Million cell updates/sec

Title: US-10-633-163-47  
Perfect score: 4267  
Sequence: 1 gggtatctgtgcgcagcag.....tgcaggtgtattaaaaaaa 4267

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 525 seqs, 10440 residues

Total number of hits satisfying chosen parameters: 1050

Minimum DB seq length: 8  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 567 summaries

Database : fetchrnpb47.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description          |
|------------|-------|---------------|--------|----|----------------------|
| 1          | 33    | 0.8           | 33     | 1  | US-09-750-401-29     |
| 2          | 33    | 0.8           | 33     | 1  | US-10-309-788-29     |
| 3          | 33    | 0.8           | 33     | 1  | US-10-238-306B-29    |
| 4          | 33    | 0.8           | 33     | 1  | US-10-629-453-29     |
| 5          | 25    | 0.6           | 25     | 1  | US-09-750-401-31     |
| 6          | 25    | 0.6           | 25     | 1  | US-10-309-788-31     |
| 7          | 25    | 0.6           | 25     | 1  | US-10-238-306B-31    |
| 8          | 25    | 0.6           | 25     | 1  | US-10-189-267-14     |
| 9          | 25    | 0.6           | 25     | 1  | US-10-629-453-31     |
| 10         | 25    | 0.6           | 25     | 1  | US-10-719-900-43634  |
| 11         | 25    | 0.6           | 25     | 1  | US-10-719-900-79674  |
| 12         | 25    | 0.6           | 25     | 1  | US-10-719-900-80968  |
| 13         | 25    | 0.6           | 25     | 1  | US-10-719-900-105991 |
| 14         | 25    | 0.6           | 25     | 1  | US-10-719-900-115675 |
| 15         | 25    | 0.6           | 25     | 1  | US-10-719-900-125985 |
| 16         | 25    | 0.6           | 25     | 1  | US-10-719-900-164292 |
| 17         | 25    | 0.6           | 25     | 1  | US-10-719-900-219322 |
| 18         | 25    | 0.6           | 25     | 1  | US-10-719-900-226895 |
| 19         | 25    | 0.6           | 25     | 1  | US-10-719-900-324991 |
| 20         | 25    | 0.6           | 25     | 1  | US-10-719-900-350767 |
| 21         | 25    | 0.6           | 25     | 1  | US-10-719-900-366993 |
| 22         | 25    | 0.6           | 25     | 1  | US-10-719-900-443782 |
| 23         | 25    | 0.6           | 25     | 1  | US-10-719-900-508233 |
| 24         | 25    | 0.6           | 25     | 1  | US-10-719-900-547596 |
| 25         | 25    | 0.6           | 25     | 1  | US-10-719-900-548689 |
| 26         | 25    | 0.6           | 25     | 1  | US-10-719-900-548829 |
| 27         | 25    | 0.6           | 25     | 1  | US-10-719-900-553274 |
| 28         | 25    | 0.6           | 25     | 1  | US-10-719-900-563977 |
| 29         | 25    | 0.6           | 25     | 1  | US-10-719-900-600913 |
| 30         | 25    | 0.6           | 25     | 1  | US-10-719-900-605442 |
| 31         | 25    | 0.6           | 25     | 1  | US-10-719-900-661249 |
| 32         | 25    | 0.6           | 25     | 1  | US-10-719-900-664806 |
| 33         | 25    | 0.6           | 25     | 1  | US-10-719-900-678709 |
| 34         | 25    | 0.6           | 25     | 1  | US-10-719-900-707594 |
| 35         | 25    | 0.6           | 25     | 1  | US-10-719-900-718938 |
| 36         | 25    | 0.6           | 25     | 1  | US-10-719-900-726398 |
| 37         | 25    | 0.6           | 25     | 1  | US-10-719-900-739550 |
| 38         | 25    | 0.6           | 25     | 1  | US-10-719-900-779378 |
| 39         | 25    | 0.6           | 25     | 1  | US-10-719-900-813289 |
| 40         | 25    | 0.6           | 25     | 1  | US-10-719-900-858151 |
| 41         | 25    | 0.6           | 25     | 1  | US-10-719-900-868129 |
| 42         | 25    | 0.6           | 25     | 1  | US-10-719-900-877801 |
| 43         | 25    | 0.6           | 25     | 1  | US-10-719-900-926328 |
| 44         | 25    | 0.6           | 25     | 1  | US-10-719-900-970882 |
| 45         | 25    | 0.6           | 25     | 1  | US-10-189-267-6      |
| 46         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-43633  |
| 47         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-79673  |
| 48         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-80967  |
| 49         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-105992 |
| 50         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-115676 |
| 51         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-125986 |
| 52         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-164291 |
| 53         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-219321 |
| 54         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-226896 |
| 55         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-324990 |
| 56         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-350766 |
| 57         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-366992 |
| 58         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-443781 |
| 59         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-508232 |
| 60         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-547597 |
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| 62         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-548828 |
| 63         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-553275 |
| 64         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-563976 |
| 65         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-600912 |
| 66         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-605443 |
| 67         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-661248 |
| 68         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-664807 |
| 69         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-678708 |
| 70         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-707595 |
| 71         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-718939 |
| 72         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-726399 |
| 73         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-739552 |
| 74         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-779379 |
| 75         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-813290 |
| 76         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-858152 |
| 77         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-868130 |
| 78         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-877802 |
| 79         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-926327 |
| 80         | 23.4  | 0.5           | 25     | 1  | US-10-719-900-970881 |
| 81         | 22    | 0.5           | 22     | 1  | US-09-750-401-32     |
| 82         | 22    | 0.5           | 22     | 1  | US-10-309-788-32     |
| 83         | 22    | 0.5           | 22     | 1  | US-10-238-306B-32    |
| 84         | 22    | 0.5           | 22     | 1  | US-10-629-453-32     |
| 85         | 20.8  | 0.5           | 25     | 1  | US-10-719-900-522566 |
| 86         | 20    | 0.5           | 20     | 1  | US-09-948-002-48     |
| 87         | 20    | 0.5           | 20     | 1  | US-09-948-002-49     |
| 88         | 20    | 0.5           | 20     | 1  | US-09-948-002-50     |
| 89         | 20    | 0.5           | 20     | 1  | US-09-948-002-51     |
| 90         | 20    | 0.5           | 20     | 1  | US-09-948-002-52     |
| 91         | 20    | 0.5           | 20     | 1  | US-09-948-002-53     |
| 92         | 20    | 0.5           | 20     | 1  | US-09-948-002-54     |
| 93         | 20    | 0.5           | 20     | 1  | US-09-948-002-55     |
| 94         | 20    | 0.5           | 20     | 1  | US-09-948-002-56     |
| 95         | 20    | 0.5           | 20     | 1  | US-09-948-002-57     |
| 96         | 20    | 0.5           | 20     | 1  | US-09-948-002-58     |
| 97         | 20    | 0.5           | 20     | 1  | US-09-948-002-59     |
| 98         | 20    | 0.5           | 20     | 1  | US-09-948-002-60     |
| 99         | 20    | 0.5           | 20     | 1  | US-09-948-002-61     |
| 100        | 20    | 0.5           | 20     | 1  | US-09-948-002-62     |
| 101        | 20    | 0.5           | 20     | 1  | US-09-948-002-63     |
| 102        | 20    | 0.5           | 20     | 1  | US-09-948-002-64     |
| 103        | 20    | 0.5           | 20     | 1  | US-09-948-002-65     |
| 104        | 20    | 0.5           | 20     | 1  | US-09-948-002-66     |
| 105        | 20    | 0.5           | 20     | 1  | US-09-948-002-67     |
| 106        | 20    | 0.5           | 20     | 1  | US-09-948-002-68     |





|       |      |     |    |   |                     |                    |       |      |     |    |   |                      |                   |
|-------|------|-----|----|---|---------------------|--------------------|-------|------|-----|----|---|----------------------|-------------------|
| c 253 | 20   | 0.5 | 20 | 1 | US-10-633-163-63    | Sequence 63, Appl  | c 326 | 16.8 | 0.4 | 20 | 1 | US-10-112-653-742    | Sequence 742, App |
| c 254 | 20   | 0.5 | 20 | 1 | US-10-633-163-64    | Sequence 64, Appl  | 327   | 16.8 | 0.4 | 20 | 1 | US-10-017-995-520    | Sequence 520, App |
| c 255 | 20   | 0.5 | 20 | 1 | US-10-633-163-65    | Sequence 65, Appl  | c 328 | 16.8 | 0.4 | 20 | 1 | US-10-017-995-520    | Sequence 520, App |
| c 256 | 20   | 0.5 | 20 | 1 | US-10-633-163-66    | Sequence 66, Appl  | 329   | 16.8 | 0.4 | 20 | 1 | US-10-017-995-769    | Sequence 769, App |
| c 257 | 20   | 0.5 | 20 | 1 | US-10-633-163-67    | Sequence 67, Appl  | c 330 | 16.8 | 0.4 | 20 | 1 | US-10-017-995-769    | Sequence 769, App |
| c 258 | 20   | 0.5 | 20 | 1 | US-10-633-163-68    | Sequence 68, Appl  | c 331 | 16.8 | 0.4 | 20 | 1 | US-10-209-608-42     | Sequence 42, Appl |
| c 259 | 19.2 | 0.4 | 24 | 1 | US-09-894-799-22    | Sequence 22, Appl  | 332   | 16.8 | 0.4 | 20 | 1 | US-10-367-470-13     | Sequence 13, Appl |
| c 260 | 19.2 | 0.4 | 24 | 1 | US-09-954-556-13    | Sequence 13, Appl  | 333   | 16.8 | 0.4 | 20 | 1 | US-10-367-470-14     | Sequence 14, Appl |
| c 261 | 19.2 | 0.4 | 24 | 1 | US-10-648-984-22    | Sequence 22, Appl  | 334   | 16.8 | 0.4 | 20 | 1 | US-10-314-578-520    | Sequence 520, App |
| c 262 | 19.2 | 0.4 | 19 | 1 | US-10-189-267-13    | Sequence 13, Appl  | 335   | 16.8 | 0.4 | 20 | 1 | US-10-314-578-520    | Sequence 520, App |
| c 263 | 19   | 0.4 | 20 | 1 | US-10-189-267-74    | Sequence 74, Appl  | 336   | 16.8 | 0.4 | 20 | 1 | US-10-314-578-769    | Sequence 769, App |
| c 264 | 19   | 0.4 | 20 | 1 | US-10-189-267-214   | Sequence 214, Appl | c 337 | 16.8 | 0.4 | 20 | 1 | US-10-314-578-769    | Sequence 769, App |
| c 265 | 18.8 | 0.4 | 22 | 1 | US-10-155-407A-18   | Sequence 18, Appl  | 338   | 16.8 | 0.4 | 20 | 1 | US-10-189-267-7      | Sequence 7, Appl  |
| c 266 | 18.8 | 0.4 | 22 | 1 | US-10-155-407A-18   | Sequence 18, Appl  | c 339 | 16.8 | 0.4 | 20 | 1 | US-10-189-267-23     | Sequence 23, Appl |
| c 267 | 18.4 | 0.4 | 20 | 1 | US-09-823-634A-15   | Sequence 15, Appl  | c 340 | 16.8 | 0.4 | 20 | 1 | US-10-189-267-35     | Sequence 35, Appl |
| c 268 | 18.4 | 0.4 | 20 | 1 | US-09-823-647B-15   | Sequence 15, Appl  | c 341 | 16.8 | 0.4 | 20 | 1 | US-10-189-267-41     | Sequence 41, Appl |
| c 269 | 18.4 | 0.4 | 20 | 1 | US-10-367-470-15    | Sequence 15, Appl  | c 342 | 16.8 | 0.4 | 20 | 1 | US-10-189-267-44     | Sequence 44, Appl |
| c 270 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-31    | Sequence 31, Appl  | c 343 | 16.8 | 0.4 | 20 | 1 | US-10-189-267-46     | Sequence 46, Appl |
| c 271 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-39    | Sequence 39, Appl  | c 344 | 16.8 | 0.4 | 20 | 1 | US-10-189-267-71     | Sequence 71, Appl |
| c 272 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-42    | Sequence 42, Appl  | 345   | 16.8 | 0.4 | 20 | 1 | US-10-189-267-174    | Sequence 174, App |
| c 273 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-49    | Sequence 49, Appl  | 346   | 16.8 | 0.4 | 20 | 1 | US-10-189-267-181    | Sequence 181, App |
| c 274 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-50    | Sequence 50, Appl  | 347   | 16.8 | 0.4 | 20 | 1 | US-10-189-267-186    | Sequence 186, App |
| c 275 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-57    | Sequence 57, Appl  | 348   | 16.8 | 0.4 | 20 | 1 | US-10-189-267-188    | Sequence 188, App |
| c 276 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-76    | Sequence 76, Appl  | c 349 | 16.8 | 0.4 | 20 | 1 | US-10-683-386-42     | Sequence 42, Appl |
| c 277 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-78    | Sequence 78, Appl  | c 350 | 16.8 | 0.4 | 20 | 1 | US-10-633-163-69     | Sequence 69, Appl |
| c 278 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-180   | Sequence 180, App  | 351   | 16.8 | 0.4 | 20 | 1 | US-10-831-778-520    | Sequence 520, App |
| c 279 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-192   | Sequence 192, App  | c 352 | 16.8 | 0.4 | 20 | 1 | US-10-831-778-520    | Sequence 520, App |
| c 280 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-193   | Sequence 193, App  | c 353 | 16.8 | 0.4 | 20 | 1 | US-10-831-778-769    | Sequence 769, App |
| c 281 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-200   | Sequence 200, App  | c 354 | 16.8 | 0.4 | 20 | 1 | US-10-831-778-769    | Sequence 769, App |
| c 282 | 18.4 | 0.4 | 20 | 1 | US-10-189-267-216   | Sequence 216, App  | 355   | 16.8 | 0.4 | 20 | 1 | US-10-838-659-22     | Sequence 22, Appl |
| c 283 | 18.4 | 0.4 | 21 | 1 | US-10-792-280-88    | Sequence 88, Appl  | c 356 | 16.8 | 0.4 | 20 | 1 | US-10-838-659-22     | Sequence 22, Appl |
| c 284 | 18   | 0.4 | 18 | 1 | US-10-028-158-9     | Sequence 9, Appl   | 357   | 16.8 | 0.4 | 20 | 1 | US-10-838-659-76     | Sequence 76, Appl |
| c 285 | 18   | 0.4 | 18 | 1 | US-10-146-058-67    | Sequence 67, Appl  | c 358 | 16.8 | 0.4 | 20 | 1 | US-10-838-659-76     | Sequence 76, Appl |
| c 286 | 18   | 0.4 | 18 | 1 | US-10-146-058-104   | Sequence 104, App  | c 359 | 16.4 | 0.4 | 18 | 1 | US-10-146-058-76     | Sequence 76, Appl |
| c 287 | 18   | 0.4 | 18 | 1 | US-10-789-119-2     | Sequence 2, Appl   | c 360 | 16.4 | 0.4 | 18 | 1 | US-10-146-058-133    | Sequence 133, App |
| c 288 | 17.4 | 0.4 | 20 | 1 | US-10-189-267-33    | Sequence 33, Appl  | c 361 | 16.4 | 0.4 | 18 | 1 | US-10-789-119-4      | Sequence 4, Appl  |
| c 289 | 17.4 | 0.4 | 20 | 1 | US-10-189-267-43    | Sequence 43, Appl  | 362   | 16.4 | 0.4 | 19 | 1 | US-09-766-450-48     | Sequence 48, Appl |
| c 290 | 17.4 | 0.4 | 20 | 1 | US-10-189-267-58    | Sequence 58, Appl  | c 363 | 16.4 | 0.4 | 19 | 1 | US-10-683-990-59     | Sequence 59, Appl |
| c 291 | 17.4 | 0.4 | 20 | 1 | US-10-189-267-70    | Sequence 70, Appl  | c 364 | 16.4 | 0.4 | 19 | 1 | US-10-683-990-156    | Sequence 156, App |
| c 292 | 17.4 | 0.4 | 20 | 1 | US-10-189-267-7     | Sequence 187, App  | c 365 | 16.4 | 0.4 | 20 | 1 | US-09-791-943-10     | Sequence 10, Appl |
| c 293 | 17.4 | 0.4 | 20 | 1 | US-10-189-267-201   | Sequence 201, App  | c 366 | 16.4 | 0.4 | 20 | 1 | US-10-189-267-27     | Sequence 27, Appl |
| c 294 | 17.4 | 0.4 | 20 | 1 | US-10-189-267-211   | Sequence 211, App  | 367   | 16.4 | 0.4 | 20 | 1 | US-10-189-267-177    | Sequence 177, App |
| c 295 | 17.4 | 0.4 | 21 | 1 | US-10-786-720-12633 | Sequence 12633, A  | 368   | 16.4 | 0.4 | 20 | 1 | US-10-289-763-2628   | Sequence 2628, Ap |
| c 296 | 17.4 | 0.4 | 21 | 1 | US-10-792-280-85    | Sequence 85, Appl  | c 369 | 16.4 | 0.4 | 20 | 1 | US-10-415-463-10     | Sequence 10, Appl |
| c 297 | 17   | 0.4 | 20 | 1 | US-09-953-047-49    | Sequence 49, Appl  | c 370 | 16.4 | 0.4 | 20 | 1 | US-10-728-399-292    | Sequence 292, App |
| c 298 | 17   | 0.4 | 20 | 1 | US-10-630-401-49    | Sequence 49, Appl  | c 371 | 16.4 | 0.4 | 20 | 1 | US-10-728-399-369    | Sequence 369, App |
| c 299 | 17   | 0.4 | 20 | 1 | US-10-663-189-7     | Sequence 7, Appl   | c 372 | 16.4 | 0.4 | 20 | 1 | US-10-728-399-475    | Sequence 475, App |
| c 300 | 16.8 | 0.4 | 20 | 1 | US-09-725-263-42    | Sequence 42, Appl  | c 373 | 16   | 0.4 | 16 | 1 | US-10-028-158-16     | Sequence 16, Appl |
| c 301 | 16.8 | 0.4 | 20 | 1 | US-09-823-634A-13   | Sequence 13, Appl  | 374   | 16   | 0.4 | 16 | 1 | US-10-028-158-17     | Sequence 17, Appl |
| c 302 | 16.8 | 0.4 | 20 | 1 | US-09-823-634A-14   | Sequence 14, Appl  | c 375 | 16   | 0.4 | 16 | 1 | US-10-146-058-105    | Sequence 105, App |
| c 303 | 16.8 | 0.4 | 20 | 1 | US-09-823-647B-13   | Sequence 13, Appl  | c 376 | 16   | 0.4 | 16 | 1 | US-10-146-058-113    | Sequence 113, App |
| c 304 | 16.8 | 0.4 | 20 | 1 | US-09-823-647B-14   | Sequence 14, Appl  | c 377 | 16   | 0.4 | 17 | 1 | US-10-156-306-524    | Sequence 524, App |
| c 305 | 16.8 | 0.4 | 20 | 1 | US-09-888-326-192   | Sequence 192, App  | c 378 | 16   | 0.4 | 17 | 1 | US-10-156-306-525    | Sequence 525, App |
| c 306 | 16.8 | 0.4 | 20 | 1 | US-09-888-326-192   | Sequence 192, App  | c 379 | 16   | 0.4 | 17 | 1 | US-10-238-700-8      | Sequence 8, Appl  |
| c 307 | 16.8 | 0.4 | 20 | 1 | US-09-888-326-193   | Sequence 193, App  | c 380 | 16   | 0.4 | 18 | 1 | US-09-775-479-9      | Sequence 9, Appl  |
| c 308 | 16.8 | 0.4 | 20 | 1 | US-09-888-326-193   | Sequence 193, App  | c 381 | 16   | 0.4 | 25 | 1 | US-10-719-900-164292 | Sequence 164292,  |
| c 309 | 16.8 | 0.4 | 20 | 1 | US-09-948-002-69    | Sequence 69, Appl  | c 382 | 15.8 | 0.4 | 19 | 1 | US-09-888-326-342    | Sequence 342, App |
| c 310 | 16.8 | 0.4 | 20 | 1 | US-09-776-479-520   | Sequence 520, App  | c 383 | 15.8 | 0.4 | 19 | 1 | US-09-888-326-342    | Sequence 342, App |
| c 311 | 16.8 | 0.4 | 20 | 1 | US-09-776-479-520   | Sequence 520, App  | 384   | 15.8 | 0.4 | 19 | 1 | US-09-776-479-138    | Sequence 138, App |
| c 312 | 16.8 | 0.4 | 20 | 1 | US-09-776-479-520   | Sequence 520, App  | c 385 | 15.8 | 0.4 | 19 | 1 | US-09-776-479-138    | Sequence 138, App |
| c 313 | 16.8 | 0.4 | 20 | 1 | US-09-776-479-520   | Sequence 520, App  | c 386 | 15.8 | 0.4 | 19 | 1 | US-09-776-479-138    | Sequence 138, App |
| c 314 | 16.8 | 0.4 | 20 | 1 | US-09-776-479-769   | Sequence 769, App  | c 387 | 15.8 | 0.4 | 19 | 1 | US-09-776-479-138    | Sequence 138, App |
| c 315 | 16.8 | 0.4 | 20 | 1 | US-09-776-479-769   | Sequence 769, App  | c 388 | 15.8 | 0.4 | 19 | 1 | US-10-112-653-131    | Sequence 131, App |
| c 316 | 16.8 | 0.4 | 20 | 1 | US-09-776-479-769   | Sequence 769, App  | c 389 | 15.8 | 0.4 | 19 | 1 | US-10-112-653-131    | Sequence 131, App |
| c 317 | 16.8 | 0.4 | 20 | 1 | US-09-776-479-769   | Sequence 769, App  | c 390 | 15.8 | 0.4 | 19 | 1 | US-10-017-995-138    | Sequence 138, App |
| c 318 | 16.8 | 0.4 | 20 | 1 | US-09-965-101-22    | Sequence 22, Appl  | c 391 | 15.8 | 0.4 | 19 | 1 | US-10-017-995-138    | Sequence 138, App |
| c 319 | 16.8 | 0.4 | 20 | 1 | US-09-965-101-22    | Sequence 22, Appl  | 392   | 15.8 | 0.4 | 19 | 1 | US-10-314-578-138    | Sequence 138, App |
| c 320 | 16.8 | 0.4 | 20 | 1 | US-09-965-101-76    | Sequence 76, Appl  | c 393 | 15.8 | 0.4 | 19 | 1 | US-10-314-578-138    | Sequence 138, App |
| c 321 | 16.8 | 0.4 | 20 | 1 | US-09-965-101-76    | Sequence 76, Appl  | 394   | 15.8 | 0.4 | 19 | 1 | US-10-683-990-97     | Sequence 97, Appl |
| c 322 | 16.8 | 0.4 | 20 | 1 | US-10-146-058-99    | Sequence 99, Appl  | c 395 | 15.8 | 0.4 | 19 | 1 | US-10-683-990-194    | Sequence 194, App |
| c 323 | 16.8 | 0.4 | 20 | 1 | US-10-112-653-497   | Sequence 497, App  | 396   | 15.8 | 0.4 | 19 | 1 | US-10-831-778-138    | Sequence 138, App |
| c 324 | 16.8 | 0.4 | 20 | 1 | US-10-112-653-497   | Sequence 497, App  | c 397 | 15.8 | 0.4 | 19 | 1 | US-10-831-778-138    | Sequence 138, App |
| c 325 | 16.8 | 0.4 | 20 | 1 | US-10-112-653-742   | Sequence 742, App  | c 398 | 15.6 | 0.4 | 22 | 1 | US-09-750-401-32     | Sequence 32, Appl |

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|-------|------|-----|----|---|---------------------|--------------------|-------|------|-----|----|---|----------------------|--------------------|
| c 399 | 15.6 | 0.4 | 22 | 1 | US-10-309-788-32    | Sequence 32, Appl  | c 472 | 14.4 | 0.3 | 17 | 1 | US-10-287-949A-3612  | Sequence 3612, Ap  |
| c 400 | 15.6 | 0.4 | 22 | 1 | US-10-238-306B-32   | Sequence 32, Appl  | 473   | 14.4 | 0.3 | 17 | 1 | US-10-287-949A-6425  | Sequence 6425, Ap  |
| c 401 | 15.6 | 0.4 | 22 | 1 | US-10-629-453-32    | Sequence 32, Appl  | 474   | 14.4 | 0.3 | 17 | 1 | US-10-287-949A-7146  | Sequence 7146, Ap  |
| c 402 | 15.4 | 0.4 | 17 | 1 | US-10-156-306-526   | Sequence 526, Appl | 475   | 14.4 | 0.3 | 17 | 1 | US-10-287-949A-7538  | Sequence 7538, Ap  |
| c 403 | 15.4 | 0.4 | 17 | 1 | US-10-156-306-527   | Sequence 527, Appl | c 476 | 14.4 | 0.3 | 17 | 1 | US-10-712-672-716    | Sequence 716, App  |
| c 404 | 15.4 | 0.4 | 17 | 1 | US-10-238-700-9     | Sequence 9, Appl   | c 477 | 14.4 | 0.3 | 17 | 1 | US-10-712-672-717    | Sequence 717, App  |
| c 405 | 15.4 | 0.4 | 18 | 1 | US-09-725-265-18    | Sequence 18, Appl  | 478   | 14.4 | 0.3 | 17 | 1 | US-10-713-633-4      | Sequence 4, Appl   |
| c 406 | 15.4 | 0.4 | 18 | 1 | US-09-891-517-18    | Sequence 18, Appl  | 479   | 14.4 | 0.3 | 17 | 1 | US-10-713-633-551    | Sequence 551, App  |
| c 407 | 15.4 | 0.4 | 18 | 1 | US-10-146-058-112   | Sequence 112, App  | 480   | 14.4 | 0.3 | 17 | 1 | US-10-498-462-47     | Sequence 47, Appl  |
| c 408 | 15.4 | 0.4 | 18 | 1 | US-10-209-608-18    | Sequence 18, Appl  | 481   | 14.4 | 0.3 | 17 | 1 | US-10-498-462-48     | Sequence 48, Appl  |
| c 409 | 15.4 | 0.4 | 18 | 1 | US-10-232-881-3     | Sequence 3, Appl   | c 482 | 14.4 | 0.3 | 18 | 1 | US-09-725-265-15     | Sequence 15, Appl  |
| c 410 | 15.4 | 0.4 | 18 | 1 | US-10-232-881-5     | Sequence 5, Appl   | c 483 | 14.4 | 0.3 | 18 | 1 | US-09-725-265-16     | Sequence 16, Appl  |
| c 411 | 15.4 | 0.4 | 18 | 1 | US-10-683-386-18    | Sequence 18, Appl  | c 484 | 14.4 | 0.3 | 18 | 1 | US-09-725-265-17     | Sequence 17, Appl  |
| c 412 | 15.4 | 0.4 | 18 | 1 | US-10-760-940-3     | Sequence 3, Appl   | c 485 | 14.4 | 0.3 | 18 | 1 | US-09-725-265-19     | Sequence 19, Appl  |
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| c 415 | 15.4 | 0.4 | 19 | 1 | US-09-865-044-3     | Sequence 3, Appl   | c 488 | 14.4 | 0.3 | 18 | 1 | US-09-891-517-17     | Sequence 17, Appl  |
| c 416 | 15.4 | 0.4 | 19 | 1 | US-10-057-813-3     | Sequence 3, Appl   | c 489 | 14.4 | 0.3 | 18 | 1 | US-09-891-517-19     | Sequence 19, Appl  |
| c 417 | 15.4 | 0.4 | 19 | 1 | US-10-397-887-3     | Sequence 3, Appl   | c 490 | 14.4 | 0.3 | 18 | 1 | US-09-904-744-2      | Sequence 2, Appl   |
| c 418 | 15.4 | 0.4 | 19 | 1 | US-10-349-143-4619  | Sequence 4619, Ap  | c 491 | 14.4 | 0.3 | 18 | 1 | US-09-961-077-1157   | Sequence 1157, Ap  |
| c 419 | 15.4 | 0.4 | 19 | 1 | US-10-701-550-3     | Sequence 3, Appl   | c 492 | 14.4 | 0.3 | 18 | 1 | US-09-994-311-7      | Sequence 7, Appl   |
| c 420 | 15.4 | 0.4 | 19 | 1 | US-10-670-011-33    | Sequence 33, Appl  | c 493 | 14.4 | 0.3 | 18 | 1 | US-10-077-383-27     | Sequence 27, Appl  |
| c 421 | 15.4 | 0.4 | 19 | 1 | US-10-670-011-129   | Sequence 129, App  | c 494 | 14.4 | 0.3 | 18 | 1 | US-10-209-608-15     | Sequence 15, Appl  |
| c 422 | 15.4 | 0.4 | 20 | 1 | US-10-663-189-7     | Sequence 7, Appl   | c 495 | 14.4 | 0.3 | 18 | 1 | US-10-209-608-16     | Sequence 16, Appl  |
| c 423 | 15   | 0.4 | 17 | 1 | US-10-156-306-523   | Sequence 523, App  | c 496 | 14.4 | 0.3 | 18 | 1 | US-10-209-608-17     | Sequence 17, Appl  |
| c 424 | 15   | 0.4 | 17 | 1 | US-10-735-592-47    | Sequence 47, Appl  | c 497 | 14.4 | 0.3 | 18 | 1 | US-10-209-608-19     | Sequence 19, Appl  |
| c 425 | 15   | 0.4 | 18 | 1 | US-09-775-479-8     | Sequence 8, Appl   | c 498 | 14.4 | 0.3 | 18 | 1 | US-10-145-857-19     | Sequence 19, Appl  |
| c 426 | 14.8 | 0.3 | 18 | 1 | US-09-725-265-20    | Sequence 20, Appl  | c 499 | 14.4 | 0.3 | 18 | 1 | US-10-683-386-15     | Sequence 15, Appl  |
| c 427 | 14.8 | 0.3 | 18 | 1 | US-09-891-517-20    | Sequence 20, Appl  | c 500 | 14.4 | 0.3 | 18 | 1 | US-10-683-386-16     | Sequence 16, Appl  |
| c 428 | 14.8 | 0.3 | 18 | 1 | US-09-969-373-2296  | Sequence 2296, Ap  | c 501 | 14.4 | 0.3 | 18 | 1 | US-10-683-386-17     | Sequence 17, Appl  |
| c 429 | 14.8 | 0.3 | 18 | 1 | US-09-904-744-3     | Sequence 3, Appl   | c 502 | 14.4 | 0.3 | 18 | 1 | US-10-683-386-19     | Sequence 19, Appl  |
| c 430 | 14.8 | 0.3 | 18 | 1 | US-09-949-305B-2    | Sequence 2, Appl   | c 503 | 14.4 | 0.3 | 18 | 1 | US-10-473-126-652    | Sequence 652, App  |
| c 431 | 14.8 | 0.3 | 18 | 1 | US-10-146-058-72    | Sequence 72, Appl  | c 504 | 14.4 | 0.3 | 18 | 1 | US-10-473-126-1066   | Sequence 1066, Ap  |
| c 432 | 14.8 | 0.3 | 18 | 1 | US-10-146-058-79    | Sequence 79, Appl  | c 505 | 14.4 | 0.3 | 18 | 1 | US-10-872-984-7      | Sequence 7, Appl   |
| c 433 | 14.8 | 0.3 | 18 | 1 | US-10-146-058-85    | Sequence 85, Appl  | c 506 | 14.4 | 0.3 | 18 | 1 | US-10-845-667-1432   | Sequence 1432, Ap  |
| c 434 | 14.8 | 0.3 | 18 | 1 | US-10-146-058-96    | Sequence 96, Appl  | c 507 | 14.4 | 0.3 | 25 | 1 | US-10-719-900-164291 | Sequence 164291, A |
| c 435 | 14.8 | 0.3 | 18 | 1 | US-10-146-058-115   | Sequence 115, App  | c 508 | 14.4 | 0.3 | 14 | 1 | US-09-263-959-816    | Sequence 816, App  |
| c 436 | 14.8 | 0.3 | 18 | 1 | US-10-146-058-128   | Sequence 128, App  | c 509 | 14   | 0.3 | 14 | 1 | US-09-263-959-857    | Sequence 57, Appl  |
| c 437 | 14.8 | 0.3 | 18 | 1 | US-10-146-058-132   | Sequence 132, App  | c 510 | 14   | 0.3 | 14 | 1 | US-10-146-058-57     | Sequence 57, Appl  |
| c 438 | 14.8 | 0.3 | 18 | 1 | US-10-085-906-135   | Sequence 135, App  | c 511 | 14   | 0.3 | 14 | 1 | US-10-146-058-63     | Sequence 63, Appl  |
| c 439 | 14.8 | 0.3 | 18 | 1 | US-10-209-608-20    | Sequence 20, Appl  | c 512 | 14   | 0.3 | 14 | 1 | US-10-146-058-71     | Sequence 71, Appl  |
| c 440 | 14.8 | 0.3 | 18 | 1 | US-10-352-704-24    | Sequence 24, Appl  | c 513 | 14   | 0.3 | 14 | 1 | US-10-146-058-74     | Sequence 74, Appl  |
| c 441 | 14.8 | 0.3 | 18 | 1 | US-10-320-033-4     | Sequence 4, Appl   | c 514 | 14   | 0.3 | 14 | 1 | US-10-146-058-91     | Sequence 75, Appl  |
| c 442 | 14.8 | 0.3 | 18 | 1 | US-10-328-578-142   | Sequence 142, App  | c 515 | 14   | 0.3 | 14 | 1 | US-10-146-058-91     | Sequence 91, Appl  |
| c 443 | 14.8 | 0.3 | 18 | 1 | US-10-297-068-282   | Sequence 282, App  | c 516 | 14   | 0.3 | 14 | 1 | US-10-146-058-101    | Sequence 101, App  |
| c 444 | 14.8 | 0.3 | 18 | 1 | US-10-683-386-20    | Sequence 20, Appl  | c 517 | 14   | 0.3 | 14 | 1 | US-10-146-058-103    | Sequence 103, App  |
| c 445 | 14.8 | 0.3 | 18 | 1 | US-10-623-371-142   | Sequence 142, App  | c 518 | 14   | 0.3 | 14 | 1 | US-10-146-058-106    | Sequence 106, App  |
| c 446 | 14.8 | 0.3 | 18 | 1 | US-10-849-072-22    | Sequence 22, Appl  | c 519 | 14   | 0.3 | 14 | 1 | US-10-146-058-122    | Sequence 122, App  |
| c 447 | 14.8 | 0.3 | 18 | 1 | US-10-949-072-24    | Sequence 24, Appl  | c 520 | 14   | 0.3 | 14 | 1 | US-10-146-058-136    | Sequence 136, App  |
| c 448 | 14.8 | 0.3 | 18 | 1 | US-10-701-347-6     | Sequence 6, Appl   | c 521 | 14   | 0.3 | 14 | 1 | US-10-343-710-146    | Sequence 146, App  |
| c 449 | 14.8 | 0.3 | 18 | 1 | US-10-701-347-11    | Sequence 11, Appl  | c 522 | 14   | 0.3 | 14 | 1 | US-10-468-753-45     | Sequence 45, Appl  |
| c 450 | 14.4 | 0.3 | 16 | 1 | US-09-882-945A-280  | Sequence 280, App  | c 523 | 14   | 0.3 | 14 | 1 | US-10-468-753-46     | Sequence 46, Appl  |
| c 451 | 14.4 | 0.3 | 16 | 1 | US-10-146-058-94    | Sequence 94, Appl  | c 524 | 14   | 0.3 | 14 | 1 | US-10-468-753-48     | Sequence 48, Appl  |
| c 452 | 14.4 | 0.3 | 16 | 1 | US-10-146-058-107   | Sequence 107, App  | c 525 | 14   | 0.3 | 14 | 1 | US-10-855-595-17     | Sequence 17, Appl  |
| c 453 | 14.4 | 0.3 | 16 | 1 | US-10-807-114-280   | Sequence 280, App  | c 526 | 14   | 0.3 | 14 | 1 | US-10-855-595-21     | Sequence 21, Appl  |
| c 454 | 14.4 | 0.3 | 17 | 1 | US-10-156-306-526   | Sequence 526, App  | c 527 | 14   | 0.3 | 14 | 1 | US-10-855-532-17     | Sequence 17, Appl  |
| c 455 | 14.4 | 0.3 | 17 | 1 | US-10-156-306-527   | Sequence 527, App  | c 528 | 14   | 0.3 | 14 | 1 | US-10-855-532-21     | Sequence 21, Appl  |
| c 456 | 14.4 | 0.3 | 17 | 1 | US-09-780-533A-233  | Sequence 233, App  | c 529 | 14   | 0.3 | 15 | 1 | US-09-504-231A-321   | Sequence 321, App  |
| c 457 | 14.4 | 0.3 | 17 | 1 | US-09-776-474-942   | Sequence 942, App  | c 530 | 14   | 0.3 | 15 | 1 | US-09-504-231A-322   | Sequence 322, App  |
| c 458 | 14.4 | 0.3 | 17 | 1 | US-09-930-423-998   | Sequence 998, App  | c 531 | 14   | 0.3 | 15 | 1 | US-09-274-553D-321   | Sequence 321, App  |
| c 459 | 14.4 | 0.3 | 17 | 1 | US-09-930-423-1179  | Sequence 1179, Ap  | c 532 | 14   | 0.3 | 15 | 1 | US-09-274-553D-322   | Sequence 322, App  |
| c 460 | 14.4 | 0.3 | 17 | 1 | US-09-745-237A-998  | Sequence 998, App  | c 533 | 14   | 0.3 | 15 | 1 | US-10-027-632-52311  | Sequence 52311, A  |
| c 461 | 14.4 | 0.3 | 17 | 1 | US-09-745-237A-1179 | Sequence 1179, Ap  | c 534 | 14   | 0.3 | 15 | 1 | US-10-027-632-52311  | Sequence 52311, A  |
| c 462 | 14.4 | 0.3 | 17 | 1 | US-10-041-856-35    | Sequence 35, Appl  | c 535 | 14   | 0.3 | 15 | 1 | US-10-230-007B-17    | Sequence 17, Appl  |
| c 463 | 14.4 | 0.3 | 17 | 1 | US-10-156-306-528   | Sequence 528, App  | c 536 | 14   | 0.3 | 15 | 1 | US-10-647-982A-17    | Sequence 17, Appl  |
| c 464 | 14.4 | 0.3 | 17 | 1 | US-10-238-700-7     | Sequence 7, Appl   | c 537 | 14   | 0.3 | 17 | 1 | US-10-041-856-35     | Sequence 35, Appl  |
| c 465 | 14.4 | 0.3 | 17 | 1 | US-10-339-793-439   | Sequence 439, App  | c 538 | 14   | 0.3 | 17 | 1 | US-09-090-672B-105   | Sequence 105, App  |
| c 466 | 14.4 | 0.3 | 17 | 1 | US-10-138-674-1773  | Sequence 1773, Ap  | c 539 | 14   | 0.3 | 17 | 1 | US-09-780-533A-857   | Sequence 857, App  |
| c 467 | 14.4 | 0.3 | 17 | 1 | US-10-138-674-3612  | Sequence 3612, Ap  | c 540 | 14   | 0.3 | 17 | 1 | US-09-780-533A-2399  | Sequence 2399, Ap  |
| c 468 | 14.4 | 0.3 | 17 | 1 | US-10-138-674-6452  | Sequence 6425, Ap  | c 541 | 14   | 0.3 | 17 | 1 | US-09-780-533A-2400  | Sequence 2400, Ap  |
| c 469 | 14.4 | 0.3 | 17 | 1 | US-10-138-674-7146  | Sequence 7146, Ap  | c 542 | 14   | 0.3 | 17 | 1 | US-09-730-559B-107   | Sequence 107, App  |
| c 470 | 14.4 | 0.3 | 17 | 1 | US-10-138-674-7538  | Sequence 7538, Ap  | c 543 | 14   | 0.3 | 17 | 1 | US-10-163-552-948    | Sequence 948, App  |
| c 471 | 14.4 | 0.3 | 17 | 1 | US-10-287-949A-1773 | Sequence 1773, Ap  | c 544 | 14   | 0.3 | 17 | 1 | US-10-156-306-522    | Sequence 522, App  |

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; CURRENT APPLICATION NUMBER: US/10/309,789
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 33
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR consensus sequence of TGF beta 2
US-10-309-788-29

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Best Local Similarity 33.3%; Pred. No. 7.8;
Matches 11; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

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Db       1    UUUUUUUUCUUUUAAUUGAAUGUCUU 33
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### RESULT 3

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; sequence 29, Application US/10/238306B
; Publication No. US20030235830A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA
; TITLE OF INVENTION: complexes
; FILE REFERENCE: RBN-001CN
; CURRENT APPLICATION NUMBER: US/10/238,306B
; CURRENT FILING DATE: 2002-09-10
; PRIORITY APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 33
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-10-238-306B-29

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Query Match      0.8%; Score 33; Length 33;
Best Local Similarity 33.3%; Pred. NO. 7.8;
Matches 11; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY      3264  TTTTTCCTTTTAAATGTAAATGGTCTTT 3296
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RESULT 4
US-10-629-453-29
; Sequence 29, Application US/10629453
; Publication No. US20040096878A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA
; TITLE OF INVENTION: complexes
; FILE REFERENCE: RBN-001DV
; CURRENT APPLICATION NUMBER: US/10/629.453

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, CURRENT FILING DATE: 2003-07-29
, PRIOR APPLICATION NUMBER: US 09/750,401
, PRIOR FILING DATE: 2000-12-28
, PRIOR APPLICATION NUMBER: US 60/173,338
, PRIOR FILING DATE: 1999-12-28
, NUMBER OF SEQ ID NOS: 37
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 29
, LENGTH: 33
, TYPE: RNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: 3 -UTR sequence of
US-10-629-453-29

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Query Match 0.8%; Score 33; DB 1; Length 33;  
Best Local Similarity 33.3%; Pred. No. 7.8;  
Matches 11; Conservative 22; Mismatches 0; Indels

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; Publication No. US20020004211A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for iso
; TITLE OF INVENTION: complexes
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/7
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence
US-09-750-401-31

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Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 36.0%; Pred. No. 42;  
Matches 9; Conservative 16; Mismatches 0; Indels

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Db 1 TTCAATTTTTTTTATATACATCTT 25

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RESULT 6
US-10-309-788-31
; Sequence 31, Application US/10309788
; Publication No. US2003021466A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tensenbaum, Scott A.
; APPLICANT: Tenson, Craig C.
; APPLICANT: Phelps, William C.
; TITLE OF INVENTION: Method for Identifying
; FILE REFERENCE: RBN-001CP
; CURRENT APPLICATION NUMBER: US/10/309788
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/173,441
; PRIOR FILING DATE: 1999-12-28

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; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO: 1
; SEQ ID NO: 2
; SEQ ID NO: 3
; SEQ ID NO: 4
; SEQ ID NO: 5
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; SEQ ID NO: 38
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; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR consensus sequence
; US-10-309-788-31

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Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 36.0%; Pred. No. 42;  
Matches 9; Conservative 16; Mismatches 0; Indels

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Db 1 UTCAAUUUUUUUAUACUAUCUU 25

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RESULT 7
US-10-238-306B-31
; Sequence 31, Application US/10238306B
; Publication No. US20030235890A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; TITLE OF INVENTION: Methods for isol
; TITLE OF INVENTION: complexes
; FILE REFERENCE: RBN-001CN
; CURRENT APPLICATION NUMBER: US/10/23
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 09/750,
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/173,
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence
US-10-238-306B-31

```

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 36.0%; Pred. No. 42;  
Matches 9; Conservative 16; Mismatches 0; Indels

**Qy**            3693 TTCAATTTTATTATATACTATCCT 3717  
               :|||:::||||:|:|:|:  
**pB**            1 UTCAAUUUUUUAUACUAUCUU 25

```

, RESULT 8
, US-10-189-267-14
, Sequence 14, Application US/10189287
, Publication No. US20040006030A1
, GENERAL INFORMATION:
, APPLICANT: Brett P. Monia
, APPLICANT: Susan M. Freier
, APPLICANT: Kennan W. Dobie
, TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
, FILE REFERENCE: PTS-0038
, CURRENT APPLICATION NUMBER: US/10/189,267
, CURRENT FILING DATE: 2002-07-02
, NUMBER OF SEQ ID NOS: 284
, SEQ ID NO 14
, LENGTH: 25
, TYPE: DNA
,

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-189-267-14

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1789 AAACAGAGCGGAGGCTGAATGCT 1813
Db 1 AAACAGAGCGGAGGCTGAATGCT 25

RESULT 9
US-10-629-453-31
; Sequence 31, Application US/10629453
; Publication No. US20040096878A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: RBN-001DV
; CURRENT APPLICATION NUMBER: US/10/629,453
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3 -UTR sequence of TGF beta 2
US-10-629-453-31

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 36.0%; Pred. No. 42;
Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 3693 TTCAATTTTATATATATCTT 3717
Db 1 UUCAUUUUUUUAUAUACUACUU 25

RESULT 10
US-10-719-900-43634
; Sequence 43634, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43634
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-43634

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2115 AAGAAGCGCGCTTTGGATGCTGCT 2139
Db 1 AAGAAGCGCGCTTTGGATGCTGCT 25

RESULT 11
US-10-719-900-79674
; Sequence 79674, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 79674
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-79674

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3748 AATGACATGAGCTACCTGGTCCAT 3772
Db 1 AATGACATGAGCTACCTGGTCCAT 25

RESULT 12
US-10-719-900-80968
; Sequence 80968, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 80968
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-80968

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2452 AATGCAGCTAAAGTCTTGGGAAG 2476
Db 1 AATGCAGCTAAAGTCTTGGGAAG 25

RESULT 13
US-10-719-900-105991
; Sequence 105991, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900

```

; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 105991  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-105991

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2054 ACATCTCTGCTAAATGTTGTTGCC 2078  
|||||  
DB 1 ACATCTCTGCTAAATGTTGTTGCC 25

## RESULT 14

US-10-719-900-115675  
; Sequence 115675, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 115675

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-115675

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3357 ACCGTGAAGTGGCTGTGATCTACA 3381  
|||||  
DB 1 ACCGTGAAGTGGCTGTGATCTACA 25

## RESULT 15

US-10-719-900-125985  
; Sequence 125985, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 125985

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-125985

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3979 ACTCAGAGTCTTAGTACTGGGCTA 4003  
|||||  
DB 1 ACTCAGAGTCTTAGTACTGGGCTA 25

## RESULT 16

US-10-719-900-164292

; Sequence 164292, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 164292

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-164292

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3172 AGCAAAACACGTCGTCTGCGAAGCTT 3196  
|||||  
DB 1 AGCAAAACACGTCGTCTGCGAAGCTT 25

## RESULT 17

US-10-719-900-219322

; Sequence 219322, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,808

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 982914

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 219322

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-719-900-219322

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3849 AGTGTTTCAGCCTTTCTGCGTCAG 3873  
|||||  
DB 1 AGTGTTTCAGCCTTTCTGCGTCAG 25

## RESULT 18

US-10-719-900-226895

; Sequence 226895, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1

; CURRENT APPLICATION NUMBER: US/10/719,900

; CURRENT FILING DATE: 2003-11-20

```
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 226895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-226895

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4189 ATAATTTCATCCATTATTTCCCTGA 4213
      |||||||
Db 1 ATAATTTCATCCATTATTTCCCTGA 25

RESULT 19
US-10-719-900-324991
; Sequence 324991, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-324991

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3787 CAGTTCCTTCTATTTTCCAAAGAT 3811
      |||||||
Db 1 CAGTTCCTTCTATTTTCCAAAGAT 25

RESULT 20
US-10-719-900-350767
; Sequence 350767, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 350767
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-350767

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3312 CCGGTGAATGTTGACCTGTTTGA 3336
```

```
Db 1 CCGGTGAATGTTGACCTGTTTGA 25

RESULT 21
US-10-719-900-366993
; Sequence 366993, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366993
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-366993

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3138 CTAAGCAAGTCTTCTGCGAAAAAT 3162
      |||||||
Db 1 CTAAGCAAGTCTTCTGCGAAAAAT 25

RESULT 22
US-10-719-900-443782
; Sequence 443782, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443782
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-443782

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2514 GACAACGATGACGACCATGATGTTT 2538
      |||||||
Db 1 GACAACGATGACGACCATGATGTTT 25

RESULT 23
US-10-719-900-508233
; Sequence 508233, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
```



```
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508233
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-508233

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2414 GATCGACAGCTTCCAAATATGATT 2438
Db 1 GATCGACAGCTTCCAAATATGATT 25

RESULT 24
US-10-719-900-547596
; Sequence 547596, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 547596
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-547596

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4167 GCCAGCACTCGTCATTTTATTCATA 4191
Db 1 GCCAGCACTCGTCATTTTATTCATA 25

RESULT 25
US-10-719-900-548688
; Sequence 548688, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 548688
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-548688

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3297 GCCAGTTTAAGCAAGCCGGTGAAT 3321
Db 1 GCCAGTTTAAGCAAGCCGGTGAAT 25
```

```
Db 1 GCCAGTTTAAGCAAGCCGGTGAAT 25

RESULT 26
US-10-719-900-548829
; Sequence 548829, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 548829
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-548829

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3204 GCCATATGCCCAAGAGGCGCTGTAA 3228
Db 1 GCCATATGCCCAAGAGGCGCTGTAA 25

RESULT 27
US-10-719-900-553274
; Sequence 553274, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 553274
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-553274

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4044 GCCGTTCAAAGACACACAGTTCAAA 4068
Db 1 GCCGTTCAAAGACACACAGTTCAAA 25

RESULT 28
US-10-719-900-563977
; Sequence 563977, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
```

; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 563977  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-563977

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3959 GCTAGGTTTAAAGTCTCAACTCA 3983  
|||  
Db 1 GCTAGGTTTAAAGTCTCAACTCA 25

RESULT 29  
US-10-719-900-600913  
; Sequence 600913, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 600913  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-600913

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2090 GGAGTCACACAGTCCAGCGGGG 2114  
|||  
Db 1 GGAGTCACACAGTCCAGCGGGG 25

RESULT 30  
US-10-719-900-605442  
; Sequence 605442, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 605442  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-605442

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2129 GGATGCTGCTACTGCTTTAGAAAT 2153  
|||  
Db 1 GGATGCTGCTACTGCTTTAGAAAT 25

RESULT 31  
US-10-719-900-661249  
; Sequence 661249, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 661249  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-661249

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3283 GTAAATGGTCTTGGCAGTTTAAG 3307  
|||  
Db 1 GTAAATGGTCTTGGCAGTTTAAG 25

RESULT 32  
US-10-719-900-664806  
; Sequence 664806, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 664806  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-664806

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2315 GTACAACACCATAATCCGAGCT 2339  
|||  
Db 1 GTACAACACCATAATCCGAGCT 25

RESULT 33  
US-10-719-900-678709  
; Sequence 678709, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914

```

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 678709
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-678709

Query Match
Best Local Similarity 0.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3340 GTATTGTCAGACTTTTGACCGTGA 3364
Db 1 GTATTGTCAGACTTTTGACCGTGA 25

RESULT 34
US-10-719-900-707594
; Sequence 707594, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 707594
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-707594

Query Match
Best Local Similarity 0.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3153 GTGGAAAAATCAAGCCCGAGCAA 3177
Db 1 GTGGAAAAATCAAGCCCGAGCAA 25

RESULT 35
US-10-719-900-718938
; Sequence 718938, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 718938
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-718938

Query Match
Best Local Similarity 0.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2356 GTGTGTCAGGATCTGGACCACT 2380
Db 1 GTGTGTCAGGATCTGGACCACT 25

```

```

RESULT 36
US-10-719-900-726398
; Sequence 726398, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 726398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-726398

Query Match
Best Local Similarity 0.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2281 GTTCAGACACTCAACACACCAAGT 2305
Db 1 GTTCAGACACTCAACACACCAAGT 25

RESULT 37
US-10-719-900-739550
; Sequence 739550, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 739550
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-739550

Query Match
Best Local Similarity 0.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4010 GTTCTTTAACTCCTATATTATGG 4034
Db 1 GTTCTTTAACTCCTATATTATGG 25

RESULT 38
US-10-719-900-779378
; Sequence 779378, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

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; SEQ ID NO 779378
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-779378

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3833 TAGGTTTGAGCTCCACAGTGTTTCA 3857
Db 1 TAGGTTTGAGCTCCACAGTGTTTCA 25

RESULT 39
US-10-719-900-813289
; Sequence 813289, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 813289
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-813289

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4198 TCATTATTTCCTGATTTTCATTGA 4222
Db 1 TCATTATTTCCTGATTTTCATTGA 25

RESULT 40
US-10-719-900-858151
; Sequence 858151, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 858151
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-858151

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3373 TGATCTACAAATACAGGTTTTTCCTT 3397
Db 1 TGATCTACAAATACAGGTTTTTCCTT 25
```

```
RESULT 41
US-10-719-900-868129
; Sequence 868129, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 868129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-868129

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3186 TGCCGAAGCTTCATGAGCGCCATAT 3210
Db 1 TGCCGAAGCTTCATGAGCGCCATAT 25

RESULT 42
US-10-719-900-877801
; Sequence 877801, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 877801
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-877801

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 TGGAAACCACTGACCATTTCTCTATTA 2395
Db 1 TGGAAACCACTGACCATTTCTCTATTA 25

RESULT 43
US-10-719-900-926328
; Sequence 926328, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 926328
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-926328

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4029 TTATGACTCTCTTTCGGGTTCAA 4053
Db 1 TTATGACTCTCTTTCGGGTTCAA 25

RESULT 44
US-10-719-900-970882
; Sequence 970882, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 970882
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-970882

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3862 TTTCGCGTCAGTGTCAGTCATGTG 3886
Db 1 TTTCGCGTCAGTGTCAGTCATGTG 25

RESULT 45
US-10-189-267-6/c
; Sequence 6, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-189-267-6

Query Match          0.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2142 TGCCTTAGAAATGTCAGGATAATT 2166
Db 25 TGCCTTAGAAATGTCAGGATAATT 1

RESULT 46
US-10-719-900-43633
; Sequence 43633, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43633
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-43633

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2115 AAGAAGCGCGCTTTGGATGCTGCCT 2139
Db 1 AAGAAGCGCGCTATGATGCTGCCT 25

RESULT 47
US-10-719-900-79673
; Sequence 79673, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 79673
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-79673

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3748 AATGACATGAGCTACCTGGGTCCAT 3772
Db 1 AATGACATGAGCAACCTGGGTCCAT 25

RESULT 48
US-10-719-900-80967
; Sequence 80967, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 80967
```

```
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-80967

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2452 AATGCAGCTAAAGTCTCTTGGAAG 2476
      |||||
Db 1 AATGCAGCTAAACTCTTGGGAAG 25

RESULT 49
US-10-719-900-105992
/ Sequence 105992, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 105992
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-105992

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2054 ACATCTCTCGCTAAATGTTGTGCC 2078
      |||||
Db 1 ACATCTCTCGCTATATGTTGTGCC 25

RESULT 50
US-10-719-900-115676
/ Sequence 115676, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 115676
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-115676

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3357 ACCGTGAAGTGGTGTGTGATCTACA 3381
      |||||
Db 1 ACCGTGAAGTGGTGTGTGATCTACA 25

RESULT 51
US-10-719-900-125986
/ Sequence 125986, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 125986
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-125986

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3979 ACTCAGAGTCTTAGTGACTGGGCTA 4003
      |||||
Db 1 ACTCAGAGTCTTTGTGACTGGGCTA 25

RESULT 52
US-10-719-900-164291
/ Sequence 164291, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 164291
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-10-719-900-164291

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3172 ACCTAACACGTGTCTGCCGAGCTT 3196
      |||||
Db 1 ACCTAACACGTGTCTGCCGAGCTT 25

RESULT 53
US-10-719-900-219321
/ Sequence 219321, Application US/10719900
/ Publication No. US20050026164A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
/ FILE REFERENCE: 3528.1
/ CURRENT APPLICATION NUMBER: US/10/719,900
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,808
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 982914
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 219321
/ LENGTH: 25
```

```

; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-219321

Query Match
Best Local Similarity 0.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3849 AGTGTTCAGCCTTTCCTCGTCAG 3873
Db 1 AGTGTTCAGCCATTTCCTCGTCAG 25

RESULT 54
US-10-719-900-226896
; Sequence 226896, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 226896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-226896

Query Match
Best Local Similarity 0.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4189 ATAATTTCATCATTTATTTCCCTCGA 4213
Db 1 ATAATTTCATCTTTATTTCCCTCGA 25

RESULT 55
US-10-719-900-324990
; Sequence 324990, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324990
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-324990

Query Match
Best Local Similarity 0.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3787 CAGTTCCTTCTATTTTCCAAAGAT 3811
Db 1 CAGTTCCTTCTATTTTCCAAAGAT 25

RESULT 56
US-10-719-900-350766
; Sequence 350766, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 350766
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-350766

Query Match
Best Local Similarity 0.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3312 CCGGTCAAATGTTGACCTGTTTGA 3336
Db 1 CCGGTCAAATGTTGACCTGTTTGA 25

RESULT 57
US-10-719-900-366992
; Sequence 366992, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366992
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-366992

Query Match
Best Local Similarity 0.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3138 CTAAGCAAGTCTTCTGTGAAAAAT 3162
Db 1 CTAAGCAAGTCTTCTGTGAAAAAT 25

RESULT 58
US-10-719-900-443781
; Sequence 443781, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443781
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-443781

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; ORGANISM: Mus musculus
US-10-719-900-443781

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2514 GACAACGATGACGACCATGATGTTT 2538
      |||||
Db 1 GACAACGATGACGACCATGATGTTT 25

RESULT 59
US-10-719-900-508232
; Sequence 508232, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508232
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-508232

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2414 GATCGAACAGCTTCCAAATGATT 2438
      |||||
Db 1 GATCGAACAGCTTCCAAATGATT 25

RESULT 60
US-10-719-900-547597
; Sequence 547597, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 547597
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-547597

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4167 GCAGCACTCGTCATTTTATTGATA 4191
      |||||
Db 1 GCAGCACTCGTCATTTTATTGATA 25

RESULT 61
US-10-719-900-548689
; Sequence 548689, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 548689
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-548689

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3297 GCCAGTTTAAGCAAGCGGTGAAT 3321
      |||||
Db 1 GCCAGTTTAAGCTAGCCGGTGAAT 25

RESULT 62
US-10-719-900-548828
; Sequence 548828, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 548828
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-548828

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3204 GCCATATGCCACAGAGCCTGTAA 3228
      |||||
Db 1 GCCATATGCCACAGAGCCTGTAA 25

RESULT 63
US-10-719-900-553275
; Sequence 553275, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 553275
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-553275
```

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US-10-719-900-553275
Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4044 GCCGTTCAAAGGAGACAGTTCAAA 4068
      |||||
Db 1 GCCGTTCAAAGGAGACAGTTCAAA 25

RESULT 64
US-10-719-900-563976
; Sequence 563976, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 563976
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-563976

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3959 GCTAGGGTTAAGAAATCTCAACTCA 3983
      |||||
Db 1 GCTAGGGTTAAGAAATCTCAACTCA 25

RESULT 65
US-10-719-900-600912
; Sequence 600912, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 600912
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-600912

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2090 GGAGTCACAACAGTCCAGCGCGGG 2114
      |||||
Db 1 GGAGTCACAACAGTCCAGCGCGGG 25

RESULT 66
US-10-719-900-605443
; Sequence 605443, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 605443
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-605443

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2129 GGATGCTGCTACTGCTTTAGAAAT 2153
      |||||
Db 1 GGATGCTGCTACTGCTTTAGAAAT 25

RESULT 67
US-10-719-900-661248
; Sequence 661248, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 661248
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-661248

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3283 GTAAATGGTTCTTTCAGTTTAAAG 3307
      |||||
Db 1 GTAAATGGTTCTTTCAGTTTAAAG 25

RESULT 68
US-10-719-900-664807
; Sequence 664807, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 664807
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-664807
```

Query Match 0.5%; Score 23.4; DB 1; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 66;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTACACACCAATTAATCCCGAAGCT 2339  
 |||||  
 Db 1 GTACACACCAATTAATCCCGAAGCT 25

RESULT 69  
 US-10-719-900-678708  
 ; Sequence 678708, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 678708  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-719-900-678708

Query Match 0.5%; Score 23.4; DB 1; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 66;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3340 GTATTGTCAGACTTTGACCGTGA 3364  
 |||||  
 Db 1 GTATTGTCAGACTTTGACCGTGA 25

RESULT 70  
 US-10-719-900-707595  
 ; Sequence 707595, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 707595  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-719-900-707595

Query Match 0.5%; Score 23.4; DB 1; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 66;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3153 GTGGAAAAATCAAGCCCGAGCAA 3177  
 |||||  
 Db 1 GTGGAAAAATCATAGCCCGAGCAA 25

RESULT 71  
 US-10-719-900-718939  
 ; Sequence 718939, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 718939  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-719-900-718939

Query Match 0.5%; Score 23.4; DB 1; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 66;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2356 GTGTGTCGCCAGGATCTGGAACCACT 2380  
 |||||  
 Db 1 GTGTGTCGCCAGGTTCTGGAACCACT 25

RESULT 72  
 US-10-719-900-726399  
 ; Sequence 726399, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 726399  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-719-900-726399

Query Match 0.5%; Score 23.4; DB 1; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 66;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2281 GTTCAGACACTCAACACACCAAAAGT 2305  
 |||||  
 Db 1 GTTCAGACACTCTACACACCAAAAGT 25

RESULT 73  
 US-10-719-900-739552  
 ; Sequence 739552, Application US/10719900  
 ; Publication No. US20050026164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xue Mei Zhou  
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 ; FILE REFERENCE: 3528.1  
 ; CURRENT APPLICATION NUMBER: US/10/719,900  
 ; CURRENT FILING DATE: 2003-11-20  
 ; PRIOR APPLICATION NUMBER: 60/427,808  
 ; PRIOR FILING DATE: 2002 11 20  
 ; NUMBER OF SEQ ID NOS: 982914  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 739552  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-10-719-900-739552

```

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4010 GTTCTTTTAACCTCATATTTATGG 4034
Db 1 GTTCTTTTAACCTCATATTTATGG 25

RESULT 74
US-10-719-900-779379
; Sequence 779379, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 779379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-779379

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3833 TAGGTTTGAGCTCCACAGTGTTTCA 3857
Db 1 TAGGTTTGAGCTCCACAGTGTTTCA 25

RESULT 75
US-10-719-900-813290
; Sequence 813290, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 813290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-813290

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4198 TCCATTATTTCCCTGATTTCATTGA 4222
Db 1 TCCATTATTTCCCTGATTTCATTGA 25

RESULT 76
US-10-719-900-858152
; Sequence 858152, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou

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; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 858152
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-858152

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3373 TGATCTACAATACAGGTTTTCCTT 3397
Db 1 TGATCTACAATACAGGTTTTCCTT 25

RESULT 77
US-10-719-900-868130
; Sequence 868130, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 868130
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-868130

Query Match          0.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 66;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3186 TGCCGAAGCTTCATGACGCCATAT 3210
Db 1 TGCCGAAGCTTCATGACGCCATAT 25

RESULT 78
US-10-719-900-877802
; Sequence 877802, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 877802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-877802

Query Match          0.5%; Score 23.4; DB 1; Length 25;

```

Best Local Similarity 96.0%; Pred. No. 66;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2371 TGAACCACTGACCACTCTCTATTA 2395  
Db 1 TGAACCACTGACCACTCTCTATTA 25

RESULT 79

US-10-719-900-926327  
; Sequence 926327, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 926327  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-926327

Query Match 0.5%; Score 23.4; DB 1; Length 25;  
Best Local Similarity 96.0%; Pred. No. 66;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTGGCGTTCAAA 4053  
Db 1 TTATGGACTCTCTTGGCGTTCAAA 25

RESULT 80

US-10-719-900-970881  
; Sequence 970881, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 970881  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-970881

Query Match 0.5%; Score 23.4; DB 1; Length 25;  
Best Local Similarity 96.0%; Pred. No. 66;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3862 TTTCGCGTCAGTGTGAGTCATGTG 3886  
Db 1 TTTCGCGTCAGTGTGAGTCATGTG 25

RESULT 81

US-09-750-401-32  
; Sequence 32, Application US/09750401  
; Publication No. US20020004211A1  
; GENERAL INFORMATION:  
; APPLICANT: Keene, Jack D.  
; APPLICANT: Carson, Craig C.

; APPLICANT: Tenenbaum, Scott A.  
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
; FILE REFERENCE: RBN-001  
; CURRENT APPLICATION NUMBER: US/09/750,401  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,338  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2  
US-09-750-401-32

Query Match 0.5%; Score 22; DB 1; Length 22;  
Best Local Similarity 22.7%; Pred. No. 75;  
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAATGCTTTT 4099  
Db 1 UUUUCUUUAAUGGUUUUU 22

RESULT 82

US-10-309-788-32  
; Sequence 32, Application US/10309788  
; Publication No. US20030211466A1  
; GENERAL INFORMATION:  
; APPLICANT: Keene, Jack D.  
; APPLICANT: Tenenbaum, Scott A.  
; APPLICANT: Carson, Craig C.  
; APPLICANT: Phelps, William C.  
; TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Targets  
; FILE REFERENCE: RBN-001CP  
; CURRENT APPLICATION NUMBER: US/10/309,788  
; CURRENT FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: US 60/173,338  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 09/750,401  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 3'-UTR consensus sequence of TGF beta 2  
US-10-309-788-32

Query Match 0.5%; Score 22; DB 1; Length 22;  
Best Local Similarity 22.7%; Pred. No. 75;  
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAATGCTTTT 4099  
Db 1 UUUUCUUUAAUGGUUUUU 22

RESULT 83

US-10-238-306B-32  
; Sequence 32, Application US/10238306B  
; Publication No. US20030235830A1  
; GENERAL INFORMATION:  
; APPLICANT: Keene, Jack D.  
; APPLICANT: Tenenbaum, Scott A.  
; APPLICANT: Carson, Craig C.  
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
; APPLICANT: complexes

```

; FILE REFERENCE: RBN-001CN
; CURRENT APPLICATION NUMBER: US/10/238,306B
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-10-238-306B-32

Query Match      0.5%; Score 22; DB 1; Length 22;
Best Local Similarity 22.7%; Pred. No. 75;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAATGTTTTTTT 4099
Db 1 UUUUUCUUUAUUGGUUUUUU 22

RESULT 84
US-10-629-453-32
; Sequence 32, Application US/10629453
; Publication No. US20040096878A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; TITLE OF INVENTION: complexes
; FILE REFERENCE: RBN-001DV
; CURRENT APPLICATION NUMBER: US/10/629,453
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-10-629-453-32

Query Match      0.5%; Score 22; DB 1; Length 22;
Best Local Similarity 22.7%; Pred. No. 75;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAATGTTTTTTT 4099
Db 1 UUUUUCUUUAUUGGUUUUUU 22

RESULT 85
US-10-719-900-522566
; Sequence 522566, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
;

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; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 522566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-522566

Query Match      0.5%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3937 AGTTCGCACAAATGTAGGCTTAGC 3960
Db 2 ATTGGCACAAATGTAGGCTTAGC 25

RESULT 86
US-09-948-002-48/c
; Sequence 48, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-48

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAAACTGCCGCGC 53
Db 20 GAGCTGCTGAAACTGCCGCGC 1

RESULT 87
US-09-948-002-49/c
; Sequence 49, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

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```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-49

    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 259 AAGCTAGGGAAGGTCGCGAG 278
    Db 20 AAGCTAGGGAAGGTCGCGAG 1

RESULT 88
US-09-948-002-50/c
; Sequence 50, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-50

    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 362 TGGCCGCTCGAGCAAGAAA 381
    Db 20 TGGCCGCTCGAGCAAGAAA 1

RESULT 89
US-09-948-002-51/c
; Sequence 51, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-51

    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 493 GGGATCCTCGCGCTGCTC 512
    Db 20 GGGATCCTCGCGCTGCTC 1

RESULT 90
US-09-948-002-52/c
; Sequence 52, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-52

    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 671 ACACGTGTGGAAGCAGGCG 690
    Db 20 ACACGTGTGGAAGCAGGCG 1

RESULT 91
US-09-948-002-53/c
; Sequence 53, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-53

    Query Match          0.5%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 830 TCAGATCAGCCACTCCGAC 849
    Db 20 TCAGATCAGCCACTCCGAC 1
```



Db 20 TCAGATCAGCCACTCGGCAC 1

## RESULT 92

US-09-948-002-54/c  
; Sequence 54, Application US/09948002  
; Publication No. US20030050265A1

; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/09/948,002  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 54  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-948-002-54

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1016 TTGGGACGCTTGCAATTTT 1035  
Db 20 TTGGGACGCTTGCAATTTT 1

## RESULT 93

US-09-948-002-55/c  
; Sequence 55, Application US/09948002  
; Publication No. US20030050265A1

; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/09/948,002  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 55  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-948-002-55

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 GCTCCTGCATCTGGTCCCGG 1266  
Db 20 GCTCCTGCATCTGGTCCCGG 1

## RESULT 94

US-09-948-002-56/c

; Sequence 56, Application US/09948002  
; Publication No. US20030050265A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/09/948,002  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 56  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-948-002-56

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 GCAGGAGAGGCAAGCCGGA 1470  
Db 20 GCAGGAGAGGCAAGCCGGA 1

## RESULT 95

US-09-948-002-57/c  
; Sequence 57, Application US/09948002  
; Publication No. US20030050265A1

; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/09/948,002  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 57  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-948-002-57

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 GTCTTCGCTTGCAAAACCC 1687  
Db 20 GTCTTCGCTTGCAAAACCC 1

## RESULT 96

US-09-948-002-58/c  
; Sequence 58, Application US/09948002  
; Publication No. US20030050265A1

; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-58

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1754 TCCACCCAGCGCTACATCG 1773
Db 20 TCCACCCAGCGCTACATCG 1

RESULT 97
US-09-948-002-59/c
; Sequence 59, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-59

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2032 AAAAAACCAAGTGGGAAGACC 2051
Db 20 AAAAAACCAAGTGGGAAGACC 1

RESULT 98
US-09-948-002-60/c
; Sequence 60, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
```

```
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-60

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2321 CACCATAAATCCGGAAGCTT 2340
Db 20 CACCATAAATCCGGAAGCTT 1

RESULT 99
US-09-948-002-61/c
; Sequence 61, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-61

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2478 CAGGACACGAAAATCACGGT 2497
Db 20 CAGGACACGAAAATCACGGT 1

RESULT 100
US-09-948-002-62/c
; Sequence 62, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
```

|   |   |
|---|---|
| <pre>; SEQ ID NO 62 ; LENGTH: 20 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-09-948-002-64</pre>   | <pre>Query Match          0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre> |
| <pre>QY      3297 GCCAGTTTAAAGCAGCCGGT 3316                  DB       20  GCCAGTTTAAAGCAAGCCGGT 1</pre>   | <pre>Query Match          0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre> |
| RESULT 103  |   |
| <pre>US-09-948-002-65/c ; Sequence 65, Application US/09948002 ; Publication No. US20030050265A1 ; GENERAL INFORMATION: ; APPLICANT: Nicholas M. Dean ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH ; FILE REFERENCE: ISPH-0607 ; CURRENT APPLICATION NUMBER: US/09/948,002 ; PRIOR FILING DATE: 2000-09-05 ; PRIOR APPLICATION NUMBER: 09/661,753 ; PRIOR FILING DATE: 2000-09-14 ; PRIOR APPLICATION NUMBER: 60/154,546 ; PRIOR FILING DATE: 1999-09-17 ; NUMBER OF SEQ ID NOS: 71 ; SEQ ID NO 65 ; LENGTH: 20 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-09-948-002-65</pre> | <pre>Query Match          0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre> |
| <pre>QY      3352 TTTTGACCGTGAAGTGGCTG 3371                  DB       20  TTTTGACCGTGAAGTGGCTG 1</pre>  | <pre>Query Match          0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre> |
| RESULT 104  |   |
| <pre>US-09-948-002-66/c ; Sequence 66, Application US/09948002 ; Publication No. US20030050265A1 ; GENERAL INFORMATION: ; APPLICANT: Nicholas M. Dean ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH ; FILE REFERENCE: ISPH-0607 ; CURRENT APPLICATION NUMBER: US/09/948,002 ; PRIOR FILING DATE: 2000-09-05 ; PRIOR APPLICATION NUMBER: 09/661,753 ; PRIOR FILING DATE: 2000-09-14 ; PRIOR APPLICATION NUMBER: 60/154,546 ; PRIOR FILING DATE: 1999-09-17 ; NUMBER OF SEQ ID NOS: 71 ; SEQ ID NO 66 ; LENGTH: 20 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-09-948-002-66</pre> | <pre>Query Match          0.5%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre> |

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3753 CATGAGCTACCTGGGTCCAT 3772  
Db 20 CATGAGCTACCTGGGTCCAT 1

## RESULT 105

US-09-948-002-67/c

; Sequence 67, Application US/09948002  
; Publication No. US20030050265A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; FILE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/09/948,002  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 67  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-948-002-67

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3874 TGTGAGTCATGTGGCGGTG 3893  
Db 20 TGTGAGTCATGTGGCGGTG 1

## RESULT 106

US-09-948-002-68/c

; Sequence 68, Application US/09948002  
; Publication No. US20030050265A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; FILE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/09/948,002  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 68  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-948-002-68

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4097 TTTGGTGTCTCATGGGTGTA 4116  
Db 20 TTTGGTGTCTCATGGGTGTA 1

## RESULT 107

US-10-028-158-8

; Sequence 8, Application US/10028158  
; Publication No. US20020110833A1  
; GENERAL INFORMATION:  
; APPLICANT: Caniggia, Isabella  
; APPLICANT: Post, Martin  
; APPLICANT: Lye, Stephen  
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF  
; TITLE OF INVENTION: TROPICOLAST  
; FILE REFERENCE: 11757.38USWO  
; CURRENT APPLICATION NUMBER: US/10/028,158  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US/09/380,662  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: PCT/CA98/00180  
; PRIOR FILING DATE: 1998-03-05  
; PRIOR APPLICATION NUMBER: US 60/039,919  
; PRIOR FILING DATE: 1997-03-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-028-158-8

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 CATCTGGTCCCGGTGGCGCT 1273  
Db 1 CATCTGGTCCCGGTGGCGCT 20

## RESULT 108

US-10-189-267-12

; Sequence 12, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-10-189-267-12

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1757 CACCCAGCGCTACATCGATA 1776  
Db 1 CACCCAGCGCTACATCGATA 20

## RESULT 109

US-10-189-267-21/c

; Sequence 21, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:

1

```
US-10-189-267-96/c
; Sequence 96, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 96
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-96

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 CCTCTCCCTTCAGGAGAA 933
Db 20 CCTCTCCCTTCAGGAGAA 1

RESULT 115
US-10-189-267-97/c
; Sequence 97, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-97

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 CCTCTCCCTTCAGGAGAA 933
Db 20 CCTCTCCCTTCAGGAGAA 1

RESULT 116
US-10-189-267-98/c
; Sequence 98, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 98

QY 1015 GTTGGGACCGTTCGATT 1034
Db 20 GTTGGGACCGTTCGATT 1

RESULT 117
US-10-189-267-99/c
; Sequence 99, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 99
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-99

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1094 CTTTGCAAAAGTTTCGTATT 1113
Db 20 CTTTGCAAAAGTTTCGTATT 1

RESULT 118
US-10-189-267-100/c
; Sequence 100, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-100

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1133 CCGCTCTGAGAATTACTAGT 1152
Db 20 CCGCTCTGAGAATTACTAGT 1

RESULT 119
US-10-189-267-101/c
; Sequence 101, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 101
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-101

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1138 CTGAGAATTACTAGTTCTT 1157
Db 20 CTGAGAATTACTAGTTCTT 1157
```

```

Db      20 CTGAGATTACTAGTTTCTT 1
RESULT 119
US-10-189-267-101/c
; Sequence 101, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 101
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-101
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1205 TCCTTTTAAAAACATGCACCT 1224
          |||||
Db      20 TCCTTTTAAAAACATGCACCT 1

RESULT 120
US-10-189-267-102/c
; Sequence 102, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 102
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-102
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1209 TTTAAAAACATGCACCTACTG 1228
          |||||
Db      20 TTTAAAAACATGCACCTACTG 1

RESULT 121
US-10-189-267-103/c
; Sequence 103, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 103
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-103
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1218 ATGCACCTACTGTGCTGTGAG 1237
          |||||
Db      20 ATGCACCTACTGTGCTGTGAG 1

RESULT 122
US-10-189-267-104/c
; Sequence 104, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 104
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-104
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1239 ACCTTTTGTCTCTGCACTCT 1258
          |||||
Db      20 ACCTTTTGTCTCTGCACTCT 1

RESULT 123
US-10-189-267-105/c
; Sequence 105, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 105
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-105
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1239 ACCTTTTGTCTCTGCACTCT 1258
          |||||
Db      20 ACCTTTTGTCTCTGCACTCT 1

```



Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1269 GCGCTCAGTCTGTCTACCTG 1288  
|||||  
Db 20 GCGCTCAGTCTGTCTACCTG 1

## RESULT 124

US-10-189-267-106/c  
; Sequence 106, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 106  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-106

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1314 ATCGCAAGAGGATCGAGGC 1333  
|||||  
Db 20 ATCGCAAGAGGATCGAGGC 1

## RESULT 125

US-10-189-267-107/c  
; Sequence 107, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 107  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-107

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1321 AGAGGATCGAGGCATCCGC 1340  
|||||  
Db 20 AGAGGATCGAGGCATCCGC 1

## RESULT 126

US-10-189-267-108/c  
; Sequence 108, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 108  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-108

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1335 ATCGCGGCAGATCTGTAG 1354  
|||||  
Db 20 ATCGCGGCAGATCTGTAG 1

## RESULT 127

US-10-189-267-109/c  
; Sequence 109, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 109  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-109

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1376 CCGGAAGACTATCCGAGC 1395  
|||||  
Db 20 CCGGAAGACTATCCGAGC 1

## RESULT 128

US-10-189-267-110/c  
; Sequence 110, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 110  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide

```
US-10-189-267-110
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CCGGAGGTGATTTCATCT 1428
Db      20 CCGGAGGTGATTTCATCT 1

RESULT 129
US-10-189-267-111/c
; Sequence 111, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 111
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-111

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCATCTACAC 1433
Db      20 AGGTGATTTCATCTACAC 1

RESULT 130
US-10-189-267-112/c
; Sequence 112, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 112
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-112

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1422 TCCATCTACACAGTACCAG 1441
Db      20 TCCATCTACACAGTACCAG 1

RESULT 131
US-10-189-267-113/c
; Sequence 113, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 113
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-113

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAGAGGTT 1526
Db      20 AGTACTACGCCAAGAGGTT 1

RESULT 133
US-10-189-267-115/c
; Sequence 115, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 115
; LENGTH: 20
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-115

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1515 GCCAGGAGGTTTATAAAAT 1534
Db 20 GCCAAGGAGGTTTATAAAAT 1

RESULT 134
US-10-189-267-116/c
; Sequence 116, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-116

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 TTTATAAAATCGACATGCCG 1544
Db 20 TTTATAAAATCGACATGCCG 1

RESULT 135
US-10-189-267-117/c
; Sequence 117, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 117
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-117

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CCTCCGAAAATGCCATCCCG 1574
Db 20 CCTCCGAAAATGCCATCCCG 1
```

```
RESULT 136
US-10-189-267-118/c
; Sequence 118, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-118

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 CCACCTTCTACAGCCCTAC 1595
Db 20 CCACCTTCTACAGCCCTAC 1

RESULT 137
US-10-189-267-119/c
; Sequence 119, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-119

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 TTTCTACAGACCTACTTCA 1599
Db 20 TTTCTACAGACCTACTTCA 1

RESULT 138
US-10-189-267-120/c
; Sequence 120, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
```

```
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 120
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-120

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1584 TACAGACCTTACTTCAGAAAT 1603
Db 20 TACAGACCTTACTTCAGAAAT 1

RESULT 139
US-10-189-267-121/c
; Sequence 121, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 121
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-121

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 TACTTCAGAAATCTCCGCTT 1612
Db 20 TACTTCAGAAATCTCCGCTT 1

RESULT 140
US-10-189-267-122/c
; Sequence 122, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 122
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-122

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1599 TACTTCAGAAATCTCCGCTT 1612
Db 20 TACTTCAGAAATCTCCGCTT 1

RESULT 141
US-10-189-267-123/c
; Sequence 123, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 123
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-123

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1854 CACAAAGACAGGAACCTGGG 1873
Db 20 CACAAAGACAGGAACCTGGG 1

RESULT 142
US-10-189-267-124/c
; Sequence 124, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 124
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-124

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1877 TAAATAAGTTTACACATGCC 1896
Db 20 TAAATAAGTTTACACATGCC 1

RESULT 143
US-10-189-267-125/c
; Sequence 125, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 125
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-125

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1962 AGATTTCAGGTTATTGATGG 1981
Db 20 AGATTTCAGGTTATTGATGG 1

RESULT 144
US-10-189-267-126/c
; Sequence 126, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-126
```

; APPLICANT: Kenneth W. Doble  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 125  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-125

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1967 TGCAGGTATTGATGGACCT 1986  
Db 20 TGCAGGTATTGATGGACCT 1  
|||||

RESULT 144  
US-10-189-267-126/c  
; Sequence 126, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Doble

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 126  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-126

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1996 CCAGTGGTGATCAGAAACT 2015  
Db 20 CCAGTGGTGATCAGAAACT 1  
|||||

RESULT 145  
US-10-189-267-127/c  
; Sequence 127, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Doble

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 127  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-127

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2000 TGGTGATCAGAAACTATAA 2019  
Db 20 TGGTGATCAGAAACTATAA 1  
|||||

RESULT 146  
US-10-189-267-128/c  
; Sequence 128, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Doble

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 128  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-128

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 AAACATATAAGTCCACTAGG 2030  
Db 20 AAACATATAAGTCCACTAGG 1  
|||||

RESULT 147  
US-10-189-267-129/c  
; Sequence 129, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Doble

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 129  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-129

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2051 CCCACATCTCTGCTAATGT 2070  
Db 20 CCCACATCTCTGCTAATGT 1  
|||||

RESULT 148  
US-10-189-267-130/c  
; Sequence 130, Application US/10189267

|   |  |   |  |
|---|--|---|--|
| Publication No. US20040006030A1                                   |  | ORGANISM: Artificial Sequence                               |  |
| GENERAL INFORMATION:  |  | FEATURE:  |  |
| APPLICANT: Brett P. Monia   |  | OTHER INFORMATION: Antisense Oligonucleotide                |  |
| APPLICANT: Susan M. Freier  |  | US-10-189-267-132   |  |
| APPLICANT: Kenneth W. Dobie                                       |  | Query Match   |  |
| TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION |  | 0.5%; Score 20; DB 1; Length 20;                            |  |
| FILE REFERENCE: PTS-0038  |  | Best Local Similarity 100.0%; Pred. No. 1.1e+02;            |  |
| CURRENT APPLICATION NUMBER: US/10/189,267                         |  | Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |
| CURRENT FILING DATE: 2002-07-02                                   |  |   |  |
| NUMBER OF SEQ ID NOS: 284   |  |   |  |
| SEQ ID NO 130   |  | QY 2142 TGCCTTAGAAATGTGCAGGA 2161                           |  |
| LENGTH: 20  |  |   |  |
| TYPE: DNA   |  | Db 20 TGCCTTAGAAATGTGCAGGA 1                                |  |
| ORGANISM: Artificial Sequence                                     |  |   |  |
| FEATURE:  |  |   |  |
| OTHER INFORMATION: Antisense Oligonucleotide                      |  |   |  |
| US-10-189-267-130   |  |   |  |
| Query Match   |  | 0.5%; Score 20; DB 1; Length 20;                            |  |
| Best Local Similarity 100.0%; Pred. No. 1.1e+02;                  |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       |  |   |  |
| QY 2060 CCTGCTAATGTTGTCGCCT 2079                                  |  |   |  |
|   |  |   |  |
| Db 20 CCTGCTAATGTTGTCGCCT 1                                       |  |   |  |
| RESULT 149  |  |   |  |
| US-10-189-267-131/c   |  |   |  |
| Sequence 131, Application US/10189267                             |  |   |  |
| Publication No. US20040006030A1                                   |  |   |  |
| GENERAL INFORMATION:  |  |   |  |
| APPLICANT: Brett P. Monia   |  |   |  |
| APPLICANT: Susan M. Freier  |  |   |  |
| APPLICANT: Kenneth W. Dobie                                       |  |   |  |
| TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION |  |   |  |
| FILE REFERENCE: PTS-0038  |  |   |  |
| CURRENT APPLICATION NUMBER: US/10/189,267                         |  |   |  |
| CURRENT FILING DATE: 2002-07-02                                   |  |   |  |
| NUMBER OF SEQ ID NOS: 284   |  |   |  |
| SEQ ID NO 131   |  |   |  |
| LENGTH: 20  |  |   |  |
| TYPE: DNA   |  |   |  |
| ORGANISM: Artificial Sequence                                     |  |   |  |
| FEATURE:  |  |   |  |
| OTHER INFORMATION: Antisense Oligonucleotide                      |  |   |  |
| US-10-189-267-131   |  |   |  |
| Query Match   |  | 0.5%; Score 20; DB 1; Length 20;                            |  |
| Best Local Similarity 100.0%; Pred. No. 1.1e+02;                  |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       |  |   |  |
| QY 2075 GCCCTCCTACAGACTGCAGT 2094                                 |  |   |  |
|   |  |   |  |
| Db 20 GCCCTCCTACAGACTGCAGT 1                                      |  |   |  |
| RESULT 150  |  |   |  |
| US-10-189-267-132/c   |  |   |  |
| Sequence 132, Application US/10189267                             |  |   |  |
| Publication No. US20040006030A1                                   |  |   |  |
| GENERAL INFORMATION:  |  |   |  |
| APPLICANT: Brett P. Monia   |  |   |  |
| APPLICANT: Susan M. Freier  |  |   |  |
| APPLICANT: Kenneth W. Dobie                                       |  |   |  |
| TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION |  |   |  |
| FILE REFERENCE: PTS-0038  |  |   |  |
| CURRENT APPLICATION NUMBER: US/10/189,267                         |  |   |  |
| CURRENT FILING DATE: 2002-07-02                                   |  |   |  |
| NUMBER OF SEQ ID NOS: 284   |  |   |  |
| SEQ ID NO 132   |  |   |  |
| LENGTH: 20  |  |   |  |
| TYPE: DNA   |  |   |  |
| ORGANISM: Artificial Sequence                                     |  |   |  |
| FEATURE:  |  |   |  |
| OTHER INFORMATION: Antisense Oligonucleotide                      |  |   |  |
| US-10-189-267-131   |  |   |  |
| Query Match   |  | 0.5%; Score 20; DB 1; Length 20;                            |  |
| Best Local Similarity 100.0%; Pred. No. 1.1e+02;                  |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       |  |   |  |
| QY 2075 GCCCTCCTACAGACTGCAGT 2094                                 |  |   |  |
|   |  |   |  |
| Db 20 GCCCTCCTACAGACTGCAGT 1                                      |  |   |  |
| RESULT 151  |  |   |  |
| US-10-189-267-133/c   |  |   |  |
| Sequence 133, Application US/10189267                             |  |   |  |
| Publication No. US20040006030A1                                   |  |   |  |
| GENERAL INFORMATION:  |  |   |  |
| APPLICANT: Brett P. Monia   |  |   |  |
| APPLICANT: Susan M. Freier  |  |   |  |
| APPLICANT: Kenneth W. Dobie                                       |  |   |  |
| TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION |  |   |  |
| FILE REFERENCE: PTS-0038  |  |   |  |
| CURRENT APPLICATION NUMBER: US/10/189,267                         |  |   |  |
| CURRENT FILING DATE: 2002-07-02                                   |  |   |  |
| NUMBER OF SEQ ID NOS: 284   |  |   |  |
| SEQ ID NO 133   |  |   |  |
| LENGTH: 20  |  |   |  |
| TYPE: DNA   |  |   |  |
| ORGANISM: Artificial Sequence                                     |  |   |  |
| FEATURE:  |  |   |  |
| OTHER INFORMATION: Antisense Oligonucleotide                      |  |   |  |
| US-10-189-267-133   |  |   |  |
| Query Match   |  | 0.5%; Score 20; DB 1; Length 20;                            |  |
| Best Local Similarity 100.0%; Pred. No. 1.1e+02;                  |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       |  |   |  |
| QY 2151 AATGTCAGGATAATTGCTG 2170                                  |  |   |  |
|   |  |   |  |
| Db 20 AATGTCAGGATAATTGCTG 1                                       |  |   |  |
| RESULT 152  |  |   |  |
| US-10-189-267-134/c   |  |   |  |
| Sequence 134, Application US/10189267                             |  |   |  |
| Publication No. US20040006030A1                                   |  |   |  |
| GENERAL INFORMATION:  |  |   |  |
| APPLICANT: Brett P. Monia   |  |   |  |
| APPLICANT: Susan M. Freier  |  |   |  |
| APPLICANT: Kenneth W. Dobie                                       |  |   |  |
| TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION |  |   |  |
| FILE REFERENCE: PTS-0038  |  |   |  |
| CURRENT APPLICATION NUMBER: US/10/189,267                         |  |   |  |
| CURRENT FILING DATE: 2002-07-02                                   |  |   |  |
| NUMBER OF SEQ ID NOS: 284   |  |   |  |
| SEQ ID NO 134   |  |   |  |
| LENGTH: 20  |  |   |  |
| TYPE: DNA   |  |   |  |
| ORGANISM: Artificial Sequence                                     |  |   |  |
| FEATURE:  |  |   |  |
| OTHER INFORMATION: Antisense Oligonucleotide                      |  |   |  |
| US-10-189-267-134   |  |   |  |
| Query Match   |  | 0.5%; Score 20; DB 1; Length 20;                            |  |
| Best Local Similarity 100.0%; Pred. No. 1.1e+02;                  |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       |  |   |  |
| QY 2169 TGCCTTCGCCCTCTTTACAT 2188                                 |  |   |  |
|   |  |   |  |
| Db 20 TGCCTTCGCCCTCTTTACAT 1                                      |  |   |  |

```
RESULT 153
US-10-189-267-135/c
; Sequence 135, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-135
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2181 CTTTACATTGATTTTAAGAG 2200
|||||
Db 20 CTTTACATTGATTTTAAGAG 1

RESULT 154
US-10-189-267-136/c
; Sequence 136, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 136
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-136
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 GATTTTAAGAGGATCTTGG 2209
|||||
Db 20 GATTTTAAGAGGATCTTGG 1

RESULT 155
US-10-189-267-137/c
; Sequence 137, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
```

```
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-137
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TGGATCCATGAACCCCAAGG 2236
|||||
Db 20 TGGATCCATGAACCCCAAGG 1

RESULT 156
US-10-189-267-138/c
; Sequence 138, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 138
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-138
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2226 GAACCCAAAGGTTACAATGC 2245
|||||
Db 20 GAACCCAAAGGTTACAATGC 1

RESULT 157
US-10-189-267-139/c
; Sequence 139, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 139
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-139
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2226 GAACCCAAAGGTTACAATGC 2245
|||||
Db 20 GAACCCAAAGGTTACAATGC 1
```

```
RESULT 158
US-10-189-267-140/c
; Sequence 140, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 140
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-140
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2238 TACAATGCTAACTTCTGTGC 2257  
 Db 20 TACAATGCTAACTTCTGTGC 1

RESULT 158  
 US-10-189-267-140/c  
 ; Sequence 140, Application US/10189267  
 ; Publication No. US20040006030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 140  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-189-267-140

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2292 CAACACACCAAGTCTCTAG 2311  
 Db 20 CAACACACCAAGTCTCTAG 1

RESULT 159  
 US-10-189-267-141/c  
 ; Sequence 141, Application US/10189267  
 ; Publication No. US20040006030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 141  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-189-267-141

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2349 CCTTGCTGTGTGCCAGGA 2368  
 Db 20 CCTTGCTGTGTGCCAGGA 1

RESULT 160  
 US-10-189-267-142/c  
 ; Sequence 142, Application US/10189267  
 ; Publication No. US20040006030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 142  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-189-267-142

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 142  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-189-267-142

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2444 GTCTTGTAATGCAGCTAAA 2463  
 Db 20 GTCTTGTAATGCAGCTAAA 1

RESULT 161  
 US-10-189-267-143/c  
 ; Sequence 143, Application US/10189267  
 ; Publication No. US20040006030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 143  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-189-267-143

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2451 AAATGCAGCTAAAGTCCTTG 2470  
 Db 20 AAATGCAGCTAAAGTCCTTG 1

RESULT 162  
 US-10-189-267-144/c  
 ; Sequence 144, Application US/10189267  
 ; Publication No. US20040006030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 144  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-189-267-144



Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2487 AAAATCAGGTGACAAATGAC 2506  
|||||

Db 20 AAAATCAGGTGACAAATGAC 1

## RESULT 163

US-10-189-267-145/c  
; Sequence 145, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 145  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-145

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2635 GTTCTGTTGTTAAACTGG 2654  
|||||

Db 20 GTTCTGTTGTTAAACTGG 1

## RESULT 164

US-10-189-267-146/c  
; Sequence 146, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 146  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-146

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2640 GTTGTAAACTGGCATCT 2659  
|||||

Db 20 GTTGTAAACTGGCATCT 1

## RESULT 165

US-10-189-267-147/c  
; Sequence 147, Application US/10189267  
; Publication No. US20040006030A1

; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 147  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-147

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2970 TGTGTTACTATATGAAC 2989  
|||||

Db 20 TGTGTTACTATATGAAC 1

## RESULT 166

US-10-189-267-148/c  
; Sequence 148, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 148  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-148

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2977 CTATATAATGAACCTTTCAT 2996  
|||||

Db 20 CTATATAATGAACCTTTCAT 1

## RESULT 167

US-10-189-267-149/c  
; Sequence 149, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 149  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
US-10-189-267-149

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-149

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2988 ACCTTTCATACCCCTGGAA 3007
    |||||
Db 20 ACCTTTCATACCCCTGGAA 1

RESULT 168
US-10-189-267-150/c
; Sequence 150, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 150
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-150

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3049 AAACATCATGATGGCTTAAG 3068
    |||||
Db 20 AAACATCATGATGGCTTAAG 1

RESULT 169
US-10-189-267-151/c
; Sequence 151, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 151
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-151

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3073 TTGAACCTCAAAATAGGCAGG 3092
    |||||
Db 20 TTGAACCTCAAAATAGGCAGG 1

RESULT 170
US-10-189-267-152/c
; Sequence 152, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-152

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3122 GTGAGTTGTTATAGGACTAA 3141
    |||||
Db 20 GTGAGTTGTTATAGGACTAA 1

RESULT 171
US-10-189-267-153/c
; Sequence 153, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 153
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-153

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3279 AATTGTAATGTTCTTTGC 3298
    |||||
Db 20 AATTGTAATGTTCTTTGC 1

RESULT 172
US-10-189-267-154/c
; Sequence 154, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
```

```
; SEQ ID NO 154
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-154

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3292 TCTTCCAGTTTAAGCAAG 3311
      |||||
Db 20 TCTTCCAGTTTAAGCAAG 1

RESULT 173
US-10-189-267-155/c
; Sequence 155, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 155
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-155

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3505 ACAGTAACACTTTACATGT 3524
      |||||
Db 20 ACAGTAACACTTTACATGT 1

RESULT 174
US-10-189-267-156/c
; Sequence 156, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-156

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3512 CTACTTTACATGTAATGTGT 3531
      |||||
Db 20 CTACTTTACATGTAATGTGT 1

RESULT 175
US-10-189-267-157/c
; Sequence 157, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 157
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-157

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3520 CATGTAATGTAGATCTTA 3539
      |||||
Db 20 CATGTAATGTAGATCTTA 1

RESULT 176
US-10-189-267-158/c
; Sequence 158, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 158
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-158

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3642 GCTGCCAGTACCTTTGAAT 3661
      |||||
Db 20 GCTGCCAGTACCTTTGAAT 1

RESULT 177
US-10-189-267-159/c
; Sequence 159, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
```

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; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 172  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-189-267-172

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1965 TTTCAGGTATTGATGCAC 1984  
|||||  
Db 1 TTTCAGGTATTGATGCAC 20

RESULT 183  
US-10-189-267-184  
; Sequence 184, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 184  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-189-267-184

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 CCGCGGCAGATCCTGAGCA 1356  
|||||  
Db 1 CCGCGGCAGATCCTGAGCA 20

RESULT 184  
US-10-189-267-190  
; Sequence 190, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 190  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-189-267-190

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1412 GGAGGTGATTTCCATCTACA 1431  
|||||  
Db 1 GGAGGTGATTTCCATCTACA 20

RESULT 185  
US-10-189-267-225  
; Sequence 225, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 225  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-225

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 AACTGAACCTCCATTCTTC 879  
|||||  
Db 1 AACTGAACCTCCATTCTTC 20

RESULT 186  
US-10-189-267-226  
; Sequence 226, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 226  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-226

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 CCTCTCCCTTCAGGAGAAA 933  
|||||  
Db 1 CCTCTCCCTTCAGGAGAAA 20

RESULT 187  
US-10-189-267-227  
; Sequence 227, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia

Query Match 0.5%; Score 20; DB 1; Length 20;

RESULT 192  
US-10-189-267-232  
; Sequence 232, Application US/10189267  
; Publication No. US2004006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 232  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-232

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1269 GCGCTCAGTCTGTCTACCTG 1288  
|||||  
Db 1 GCGCTCAGTCTGTCTACCTG 20

RESULT 193  
US-10-189-267-233  
; Sequence 233, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 233  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-233

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1314 ATCCGCAAGAGGATCGAGGC 1333  
|||||  
Db 1 ATCCGCAAGAGGATCGAGGC 20

RESULT 194  
US-10-189-267-234  
; Sequence 234, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 234  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-234

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1321 AGAGGATCGAGGCCATCCGC 1340  
|||||  
Db 1 AGAGGATCGAGGCCATCCGC 20

RESULT 195  
US-10-189-267-235  
; Sequence 235, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 235  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-235

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1335 ATCCGGCGGCAGATCCTGAG 1354  
|||||  
Db 1 ATCCGGCGGCAGATCCTGAG 20

RESULT 196  
US-10-189-267-236  
; Sequence 236, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 236  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-236

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1376 CCCGGAAGACTATCCGAGC 1395  
|||||  
Db 1 CCCGGAAGACTATCCGAGC 20

RESULT 197  
US-10-189-267-237  
; Sequence 237, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284

; SEQ ID NO 237  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-237

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CCGGAGGTGATTCATCT 1428  
Db 1 CCGGAGGTGATTCATCT 20  
|||||

## RESULT 198

US-10-189-267-238  
; Sequence 238, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 238  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-238

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTCATCTACAC 1433  
Db 1 AGGTGATTCATCTACAC 20  
|||||

## RESULT 199

US-10-189-267-239  
; Sequence 239, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 239  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-239

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1422 TCATCTACACAGTACCAG 1441  
Db 1 TCATCTACACAGTACCAG 20  
|||||

## RESULT 200

US-10-189-267-240  
; Sequence 240, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 240  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-240

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1463 AAGCCGAGGCGCGCCT 1482  
Db 1 AAGCCGAGGCGCGCCT 20  
|||||

## RESULT 201

US-10-189-267-241  
; Sequence 241, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 241  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-241

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTAGCCAGGAGGTT 1526  
Db 1 AGTACTAGCCAGGAGGTT 20  
|||||

## RESULT 202

US-10-189-267-242  
; Sequence 242, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION



;  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 242  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-242

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1515 GCCAAGGAGGTTTATAAAAT 1534  
DB 1 GCCAAGGAGGTTTATAAAAT 20

## RESULT 203

US-10-189-267-243  
; Sequence 243, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION

; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 243  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-243

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 TTTATAAAATCGACATGCCG 1544  
DB 1 TTTATAAAATCGACATGCCG 20

## RESULT 204

US-10-189-267-244  
; Sequence 244, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION

; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 244  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-244

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CCTCCGAAAAATCCCATCCCG 1574  
DB 1 CCTCCGAAAAATCCCATCCCG 20

## RESULT 205

US-10-189-267-245  
; Sequence 245, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION

; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 245  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-245

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 CCACCTTTCTACAGACCCCTAC 1595  
DB 1 CCACCTTTCTACAGACCCCTAC 20

## RESULT 206

US-10-189-267-246  
; Sequence 246, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION

; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 246  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-246

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 TTTCTACAGACCCCTACTTCA 1599  
DB 1 TTTCTACAGACCCCTACTTCA 20

## RESULT 207

US-10-189-267-247  
; Sequence 247, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION

; FILE REFERENCE: PTS-0038

; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 247

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-247

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1584 TACAGACCTACTTCAGAAAT 1603  
DB 1 TACAGACCTACTTCAGAAAT 20

## RESULT 208

US-10-189-267-248  
; Sequence 248, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobbie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 248

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-248

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 TACTTCAGAAATCGTCGCTT 1612  
DB 1 TACTTCAGAAATCGTCGCTT 20

## RESULT 209

US-10-189-267-249  
; Sequence 249, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobbie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 249

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-249

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1854 CACAAAGACAGGAACCTGGG 1873

DB 1 CACAAAGACAGGAACCTGGG 20

## RESULT 210

US-10-189-267-250  
; Sequence 250, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobbie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 250

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-250

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1877 TAAATAAGTTTACACTGCC 1896  
DB 1 TAAATAAGTTTACACTGCC 20

## RESULT 211

US-10-189-267-251  
; Sequence 251, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobbie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 251

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-251

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1967 TGCAGGTATTGATGGCACCT 1986  
DB 1 TGCAGGTATTGATGGCACCT 20

## RESULT 212

US-10-189-267-252  
; Sequence 252, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobbie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267

```
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 252
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-252

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1996 CCAGTGGTGATCAGAAAAC 2015
Db 1 CCAGTGGTGATCAGAAAAC 20

RESULT 213
US-10-189-267-253
; Sequence 253, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 253
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-253

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2000 TGCTGATCAGAAAACATATA 2019
Db 1 TGCTGATCAGAAAACATATA 20

RESULT 214
US-10-189-267-254
; Sequence 254, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 254
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-254

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2060 CCTGCTAATGTTGTCCT 2079
Db 1 CCTGCTAATGTTGTCCT 2079

RESULT 215
US-10-189-267-255
; Sequence 255, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 255
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-255

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2075 GCCCTCCTACAGACTGGAGT 2094
Db 1 GCCCTCCTACAGACTGGAGT 20

RESULT 216
US-10-189-267-256
; Sequence 256, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 256
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-256

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2142 TGCCTTAGAAATGTCAGGA 2161
Db 1 TGCCTTAGAAATGTCAGGA 20

RESULT 217
US-10-189-267-257
; Sequence 257, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
```

```
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 257
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-257

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TGCCTTCGCCCTCTTACAT 2188
Db 1 TGCCTTCGCCCTCTTACAT 20

RESULT 218
US-10-189-267-258
; Sequence 258, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 258
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-258

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 GATTTTAAGAGGATCTTGG 2209
Db 1 GATTTTAAGAGGATCTTGG 20

RESULT 219
US-10-189-267-259
; Sequence 259, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 259
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-259

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TGGATCCATGAACCCCAAGG 2236
Db 1 TGGATCCATGAACCCCAAGG 20
```

```
RESULT 220
US-10-189-267-260
; Sequence 260, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 260
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-260

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2226 GAACCCAAAGGTACAATGC 2245
Db 1 GAACCCAAAGGTACAATGC 20

RESULT 221
US-10-189-267-261
; Sequence 261, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 261
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-261

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2238 TACAATGCTAACTTCTGTGC 2257
Db 1 TACAATGCTAACTTCTGTGC 20

RESULT 222
US-10-189-267-262
; Sequence 262, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
```

```
; SEQ ID NO 262
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-262

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2349 CCTTGCTGTGTGCCAGGA 2368
      |||||
Db 1 CCTTGCTGTGTGCCAGGA 20

RESULT 223
US-10-189-267-263
; Sequence 263, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 263
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-263

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2444 GTCCTGTAATGCAGCTAAA 2463
      |||||
Db 1 GTCCTGTAATGCAGCTAAA 20

RESULT 224
US-10-189-267-264
; Sequence 264, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 264
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-264

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2451 AAATGACGCTAAAGTCCTTG 2470
      |||||
Db 1 AAATGACGCTAAAGTCCTTG 20
```

```
RESULT 225
US-10-189-267-265
; Sequence 265, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 265
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-265

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2487 AAAATCACGGTGACAATGAC 2506
      |||||
Db 1 AAAATCACGGTGACAATGAC 20

RESULT 226
US-10-189-267-266
; Sequence 266, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 266
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-266

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2635 GTTCTGTTTGTAAAACTGG 2654
      |||||
Db 1 GTTCTGTTTGTAAAACTGG 20

RESULT 227
US-10-189-267-267
; Sequence 267, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 267
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-267
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2640 GTTGTAAACTGGCATCT 2659
      |||||||
Db 1 GTTGTAAACTGGCATCT 20

RESULT 228
US-10-189-267-268
; Sequence 268, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 268
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-268
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2970 TGTGTACTATATAATGAAC 2989
      |||||||
Db 1 TGTGTACTATATAATGAAC 20

RESULT 229
US-10-189-267-269
; Sequence 269, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 269
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-269
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2988 ACCTTTCATTACCTTGGAA 3007
      |||||||
Db 1 ACCTTTCATTACCTTGGAA 20
```

```
RESULT 230
US-10-189-267-270
; Sequence 270, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 270
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-270
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3049 AAATCATGATGGCTTAAG 3068
      |||||||
Db 1 AAATCATGATGGCTTAAG 20

RESULT 231
US-10-189-267-271
; Sequence 271, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 271
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-271
Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3279 AATTGTAATGTTCTTTGC 3298
      |||||||
Db 1 AATTGTAATGTTCTTTGC 20

RESULT 232
US-10-189-267-272
; Sequence 272, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 272
; LENGTH: 20
```

```
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-272

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3292 TCCTTGCCAGTTTAAGCAAG 3311
      |||||
Db 1 TCCTTGCCAGTTTAAGCAAG 20

RESULT 233
US-10-189-267-273
; Sequence 273, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 273
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-273

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3520 CATGTAATGTGTAGATCTTA 3539
      |||||
Db 1 CATGTAATGTGTAGATCTTA 20

RESULT 236
US-10-189-267-276
; Sequence 276, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 276
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-276

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3505 ACAGTAACACTTTTACATGT 3524
      |||||
Db 1 ACAGTAACACTTTTACATGT 20

RESULT 234
US-10-189-267-274
; Sequence 274, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 274
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-274

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3512 CTACTTTACATGTAATGTGT 3531
      |||||
Db 1 CTACTTTACATGTAATGTGT 20

RESULT 235
US-10-189-267-275
; Sequence 275, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 275
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-275

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3642 GCTGGCCAGTACCTTTGAAT 3661
      |||||
Db 1 GCTGGCCAGTACCTTTGAAT 20

RESULT 237
US-10-189-267-277
; Sequence 277, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 277
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: M. musculus
; FEATURE:
US-10-189-267-277

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4245 CTTTCAGGCTGATTAAAAA 4264
Db      1 CTTTCAGGCTGATTAAAAA 20

RESULT 238
US-10-633-163-48/c
; Sequence 48, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-48

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAAACTGCCGC 53
Db      20 GAGCTGCTGAAACTGCCGC 1

RESULT 239
US-10-633-163-49/c
; Sequence 49, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-49

; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-49

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 AAGCTAGGGAAGGTCGCGAG 278
Db      20 AAGCTAGGGAAGGTCGCGAG 1

RESULT 240
US-10-633-163-50/c
; Sequence 50, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-50

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 TGGCCGCTCGAGCAAGAAA 381
Db      20 TGGCCGCTCGAGCAAGAAA 1

RESULT 241
US-10-633-163-51/c
; Sequence 51, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-51
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US-10-633-163-51

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GGGATCCTCGCGCCTGCTC 512  
|||||  
DB 20 GGGATCCTCGCGCCTGCTC 1

RESULT 242

US-10-633-163-52/c  
; Sequence 52, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 52  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-52

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 ACACGTGTGGAAGGCAGGCG 690  
|||||  
DB 20 ACACGTGTGGAAGGCAGGCG 1

RESULT 243

US-10-633-163-53/c  
; Sequence 53, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 53  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-53

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 830 TCAGATCAGCCACTCGGCAC 849  
|||||  
DB 20 TCAGATCAGCCACTCGGCAC 1

RESULT 244

US-10-633-163-54/c  
; Sequence 54, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 54  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-54

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1016 TTGGGAACGCGTTGCATTTT 1035  
|||||  
DB 20 TTGGGAACGCGTTGCATTTT 1

RESULT 245

US-10-633-163-55/c  
; Sequence 55, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 55  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-55

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 GCTCTGCAATCGTCCCGG 1266  
| | | | | | | | | | | | | | | | | | | | | |  
DB 20 GCTCTGCAATCGTCCCGG 1

RESULT 246  
US-10-633-163-56/c  
; Sequence 56, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 56  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-56

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 GCAGGAGGAGGCAAGCCGA 1470  
| | | | | | | | | | | | | | | | | | | | | |  
DB 20 GCAGGAGGAGGCAAGCCGA 1

RESULT 247  
US-10-633-163-57/c  
; Sequence 57, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 57  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-57

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 GTCTTCGCTTGCAAAACCC 1687  
| | | | | | | | | | | | | | | | | | | | | |  
DB 20 GTCTTCGCTTGCAAAACCC 1

RESULT 248  
US-10-633-163-58/c  
; Sequence 58, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 58  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-58

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1754 TCCACCCAGCGCTACATCG 1773  
| | | | | | | | | | | | | | | | | | | | | |  
DB 20 TCCACCCAGCGCTACATCG 1

RESULT 249  
US-10-633-163-59/c  
; Sequence 59, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 59  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-59

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2032 AAAAAACCAAGTGGGAAGACC 2051  
|||||  
Db 20 AAAAAACCAAGTGGGAAGACC 1

RESULT 250  
US-10-633-163-60/c  
; Sequence 60, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 60  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-60

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2321 CACCATAAATCCGAAGCTT 2340  
|||||  
Db 20 CACCATAAATCCGAAGCTT 1

RESULT 251  
US-10-633-163-61/c  
; Sequence 61, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 61  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-61

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2478 CAGGACACGAAATCACGGT 2497  
|||||  
Db 20 CAGGACACGAAATCACGGT 1

RESULT 252  
US-10-633-163-62/c  
; Sequence 62, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 62  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-62

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2854 ACGTATTGTTCCAGCCGCG 2873  
|||||  
Db 20 ACGTATTGTTCCAGCCGCG 1

RESULT 253  
US-10-633-163-63/c  
; Sequence 63, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; TITLE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 63  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-63

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3075 GAACTCAATAAGCCAGGG 3094  
|||||  
Db 20 GAACTCAATAAGCCAGGG 1

RESULT 254  
US-10-633-163-64/c  
; Sequence 64, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; FILE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-64

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3297 GCAGTTTAAGCAAGCCGGT 3316  
|||||  
Db 20 GCAGTTTAAGCAAGCCGGT 1

RESULT 255  
US-10-633-163-65/c  
; Sequence 65, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; FILE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-65

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3352 TTTGACCGTGAAGTGGCTG 3371

Db 20 TTTGACCGTGAAGTGGCTG 1  
|||||

RESULT 256  
US-10-633-163-66/c  
; Sequence 66, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; FILE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 66  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-66

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3753 CATGAGCTACCTGGGTCCAT 3772  
|||||  
Db 20 CATGAGCTACCTGGGTCCAT 1

RESULT 257  
US-10-633-163-67/c  
; Sequence 67, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; FILE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 67  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-67

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3874 TGTGATCATGTGGCGGTG 3893  
|||||

Db 20 TGTGACTCATGTGGCGGTG 1

RESULT 258

US-10-633-163-68/c  
; Sequence 68, Application US/10633163  
; Publication No. US20040063655A1  
; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean  
; APPLICANT: Susan F. Murray  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH  
; FILE OF INVENTION: FACTOR BETA EXPRESSION  
; FILE REFERENCE: ISPH-0607  
; CURRENT APPLICATION NUMBER: US/10/633,163  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US/09/948,002  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 09/661,753  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/154,546  
; PRIOR FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 71  
; SEQ ID NO 68  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-633-163-68

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4097 TTTGGTGTCTCATGGGTGTA 4116

Db 20 TTTGGTGTCTCATGGGTGTA 1

RESULT 259

US-09-894-799-22  
; Sequence 22, Application US/09894799  
; Publication No. US20030009784A1  
; GENERAL INFORMATION:

; APPLICANT: No. US20030009784A1artis  
; TITLE OF INVENTION: Expression of trehalose biosynthetic genes in plants  
; FILE REFERENCE: trehalose  
; CURRENT APPLICATION NUMBER: US/09/894,799  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 09/262,615  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: CGC1990/PROV  
; PRIOR FILING DATE: 1998-03-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide  
US-09-894-799-22

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.9e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 AGATTCCTCCCTCCCTCCCAAGCT 991

Db 1 AGCTTCCCTCCCTCCCTCCCAAGCT 24

RESULT 260

US-09-954-556-13  
; Sequence 13, Application US/09954556  
; Publication No. US20030078219A1  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Scott Cooper  
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 EXPRES  
; FILE REFERENCE: RTS-0250  
; CURRENT APPLICATION NUMBER: US/09/954,556  
; CURRENT FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 108  
; SEQ ID NO 13  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Probe  
US-09-954-556-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.9e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2927 CCTCCCTCCCTCCCTCCCAAGCT 2950

Db 1 CCACACCGTCCATCTCCCAAGCT 24

RESULT 261

US-10-648-984-22  
; Sequence 22, Application US/10648984  
; Publication No. US20040078848A1  
; GENERAL INFORMATION:

; APPLICANT: Novartis  
; TITLE OF INVENTION: Expression of trehalose biosynthetic genes in plants  
; FILE REFERENCE: trehalose  
; CURRENT APPLICATION NUMBER: US/10/648,984  
; CURRENT FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: US/09/894,799  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 09/262,615  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: CGC1990/PROV  
; PRIOR FILING DATE: 1998-03-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide  
US-10-648-984-22

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.9e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 AGATTCCTCCCTCCCTCCCAAGCT 991

Db 1 AGCTTCCCTCCCTCCCTCCCAAGCT 24

RESULT 262

US-10-189-267-13/c  
; Sequence 13, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier

; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 13  
 ; LENGTH: 19  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: PCR Primer  
 US-10-189-267-13

Query Match 0.4%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 CCTTCGACGTGACAGACGC 1834  
 Db 19 CCTTCGACGTGACAGACGC 1

RESULT 263  
 US-10-189-267-74/c  
 ; Sequence 74, Application US/10189267  
 ; Publication No. US20040006030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 74  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-10-189-267-74

Query Match 0.4%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 GCAAGCTGAAGCTCACCAG 1372  
 Db 20 GCAAGCTGAAGCTCACCAG 2

RESULT 264  
 US-10-189-267-214  
 ; Sequence 214, Application US/10189267  
 ; Publication No. US20040006030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Susan M. Freier  
 ; APPLICANT: Kenneth W. Dobie  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
 ; FILE REFERENCE: PTS-0038  
 ; CURRENT APPLICATION NUMBER: US/10/189,267  
 ; CURRENT FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 284  
 ; SEQ ID NO 214  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: H. sapiens  
 ; FEATURE:  
 US-10-189-267-214

Query Match 0.4%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 GCAAGCTGAAGCTCACCAG 1372  
 Db 1 GCAAGCTGAAGCTCACCAG 19

RESULT 265  
 US-10-155-407A-18  
 ; Sequence 18, Application US/10155407A  
 ; Publication No. US20030077267A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frenz, John  
 ; APPLICANT: Shire, Steven J.  
 ; APPLICANT: Silkowski, Mary B.  
 ; TITLE OF INVENTION: PURIFIED FORMS OF DNase  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/155,407A  
 ; FILING DATE: 22-May-2002  
 ; CLASSIFICATION: <unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/638112  
 ; FILING DATE: 11-Aug-2000  
 ; APPLICATION NUMBER: 08/942561  
 ; FILING DATE: 01-OCT-1997  
 ; APPLICATION NUMBER: 08/634125  
 ; FILING DATE: 19-Apr-1996  
 ; APPLICATION NUMBER: 08/409631  
 ; FILING DATE: 22-Mar-1995  
 ; APPLICATION NUMBER: 08/348284  
 ; FILING DATE: 30-No. US20030077267A1-1994  
 ; APPLICATION NUMBER: 08/116186  
 ; FILING DATE: 02-Sep-1993  
 ; APPLICATION NUMBER: 07/895300  
 ; FILING DATE: 08-Jun-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Evans, David W.  
 ; REGISTRATION NUMBER: NONE  
 ; REFERENCE/DOCKET NUMBER: P0747C9  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-1739  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 22 base pairs  
 ; TYPE: Nucleic Acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-155-407A-18

Query Match 0.4%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCAGCGCGCGC 636  
 Db 1 GCGCGCGCGCAGCGCGCGC 22

```
RESULT 266
US-10-155-407A-18/C
; Sequence 18, Application US/10155407A
; Publication No. US2003007267A1
; GENERAL INFORMATION:
; APPLICANT: Frenz, John
; Shire, Steven J.
; Sliwowski, Mary B.
; TITLE OF INVENTION: PURIFIED FORMS OF DNase
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,407A
; FILING DATE: 22-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/638112
; FILING DATE: 11-Aug-2000
; APPLICATION NUMBER: 08/942561
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: 08/634125
; FILING DATE: 19-Apr-1996
; APPLICATION NUMBER: 08/409631
; FILING DATE: 22-Mar-1995
; APPLICATION NUMBER: 08/348284
; FILING DATE: 30-No. US20030077267A1-1994
; APPLICATION NUMBER: 08/116186
; FILING DATE: 02-Sep-1993
; APPLICATION NUMBER: 07/895300
; FILING DATE: 08-Jun-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P0747C8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-155-407A-18
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCAGCAGCGCGC 636
DB 22 GCGCGCGCGCGCGCGCGC 1

RESULT 267
US-09-823-634A-15
; Sequence 15, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-634A-15
Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
DB 1 AAAAAAAAAATTGGAGAAAAA 20

RESULT 268
US-09-823-647B-15
; Sequence 15, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-647B-15
Query Match 0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
DB 1 AAAAAAAAAATTGGAGAAAAA 20

RESULT 269
US-10-367-470-15
; Sequence 15, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
```

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; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-10-367-470-15

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAATTGGAGAAAA 2599
Db 1 AAAAAAATTGGAGAAAAA 20

RESULT 270
US-10-189-267-31/c
; Sequence 31, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-31

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACCTGCAGCACCTCGA 1300
Db 20 TCTACCTGCAGCACACTCGA 1

RESULT 271
US-10-189-267-39/c
; Sequence 39, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-39

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACCTGCAGCACCTCGA 1300
Db 20 TCTACCTGCAGCACACTCGA 1

RESULT 272
US-10-189-267-42/c
; Sequence 42, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-42

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2442 AGTCTTGTAAATGCAGCTA 2461
Db 20 AGTCTTGTAAATGCAGCTA 1

RESULT 273
US-10-189-267-49/c
; Sequence 49, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-49

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2224 ATGAACCCCAAGGGTACAAT 2243
Db 20 ACGAACCCCAAGGGTACAAT 1

RESULT 274
US-10-189-267-50/c
; Sequence 50, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:

```



```
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-50

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTGATTTTAAGAGGGATCT 2206
      ||||| ||||| ||||| |||||
Db 20 ATTGATTTCAAGAGGGATCT 1

RESULT 275
US-10-189-267-57/c
; Sequence 57, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-57

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1310 GTTATGCGCAAGAGGATCG 1329
      ||| ||||| ||||| |||||
Db 20 GTTATGCGCAAGAGGATCG 1

RESULT 276
US-10-189-267-76/c
; Sequence 76, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-76

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACTGCGCAGCACCCTCGA 1300
      ||||| ||||| ||||| |||||
Db 1 TCTACTGCGCAGCACCCTCGA 20

RESULT 277
US-10-189-267-78/c
; Sequence 78, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-78

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2240 CAATGCTAACTTCTGTGCTG 2259
      ||||| ||||| ||||| |||||
Db 20 CAATGCTAACTTCTGTGCTG 1

RESULT 278
US-10-189-267-180
; Sequence 180, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 180
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-180

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TCTACTGCGCAGCACCCTCGA 1300
      ||||| ||||| ||||| |||||
Db 1 TCTACTGCGCAGCACCCTCGA 20

RESULT 279
US-10-189-267-192
```



Db 2 GUGGCAACUGGAAGAUUUU 21

## RESULT 284

US-10-028-158-9/c  
; Sequence 9, Application US/10028158  
; Publication No. US20020110833A1  
; GENERAL INFORMATION:  
; APPLICANT: Caniggia, Isabella  
; APPLICANT: Post, Martin  
; APPLICANT: Lye, Stephen  
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF  
; TITLE OF INVENTION: TROPHOBLAST  
; FILE REFERENCE: 11757.38USWO  
; CURRENT APPLICATION NUMBER: US/10/028,158  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US/09/380,662  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: PCT/CA98/00180  
; PRIOR FILING DATE: 1998-03-05  
; PRIOR APPLICATION NUMBER: US 60/039,919  
; PRIOR FILING DATE: 1997-03-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-028-158-9

Query Match 0.4%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 CCCTACTTCAGATCGTC 1607

Db 18 CCCTACTTCAGATCGTC 1

## RESULT 285

US-10-146-058-67/c  
; Sequence 67, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-10-146-058-67

Query Match 0.4%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCATCTACA 1431

Db 18 AGGTGATTTCCATCTACA 1

## RESULT 286

US-10-146-058-104/c  
; Sequence 104, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666

```
; TELEPAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-104

Query Match
Best Local Similarity 0.4%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1

RESULT 287
US-10-789-119-2
; Sequence 2, Application US/10789119
; Publication No. US20040170157A1
; GENERAL INFORMATION:
; APPLICANT: Chung, Yih-Lin
; TITLE OF INVENTION: METHOD FOR INCREASING THERAPEUTIC GAIN
; FILE REFERENCE: 13206-004002
; CURRENT APPLICATION NUMBER: US/10/789,119
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US 10/205,738
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-789-119-2

Query Match
Best Local Similarity 0.4%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACACTACTGTGTGCT 1234
Db 1 CATGCACACTACTGTGTGCT 18

RESULT 288
US-10-189-267-33/c
; Sequence 33, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-33
```

```
Query Match
Best Local Similarity 0.4%; Score 17.4; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1746 TTAACATCTCCACCACG 1764
Db 19 TTAACATCTCCACCACG 1

RESULT 289
US-10-189-267-43/c
; Sequence 43, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-43

Query Match
Best Local Similarity 0.4%; Score 17.4; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2084 CAGACTGCAGTCACACAG 2102
Db 20 CAGACTGCAGTCACACAG 2

RESULT 290
US-10-189-267-58/c
; Sequence 58, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-58

Query Match
Best Local Similarity 0.4%; Score 17.4; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 800 TCTCGTCCCTTTTGGCCG 818
Db 19 TCTCTCCCTTTTGGCCG 1

RESULT 291
US-10-189-267-70/c
; Sequence 70, Application US/10189267
```

```
; FEATURE:  
US-10-189-267-201  
  
Query Match          0.4%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 2.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0;  
  
QY      800 TCTCGTCCCTTTGGCCGG 818  
         ||||| |||||||  
DB       2 TCTCTTCCTTTTGGCCGG 20  
         ||||| |||||||  
  
RESULT 294  
US-10-189-267-211  
; Sequence 211, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 211  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-189-267-211  
  
Query Match          0.4%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 2.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0;  
  
QY      3027 TCGAGACCAAAATACTTTGC 3045  
         ||||| |||||||  
DB       2 TCGAGACCAAAATACTTTGC 20  
         ||||| |||||||  
  
RESULT 295  
US-10-786-720-12633  
; Sequence 12633, Application US/10786720  
; Publication No. US20040191818A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: O'Toole, Margot  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING DISEASES  
; FILE REFERENCE: 031896-023000 (AM101331L)  
; CURRENT APPLICATION NUMBER: US/10/786,720  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 21135  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12633  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNAI-antisense strand  
US-10-786-720-12633  
  
Query Match          0.4%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 63.2%; Pred. No. 2.4e+02;  
Matches 12; Conservative 6; Mismatches 1; Indels 0;  
  
QY      4 TATCTGCTGGCAGCAGGT 22  
         :||:|||  
DB       3 UAUUCUGCGCACACAGGU 21  
         :||:|||  
  
RESULT 296  
US-10-792-280-85
```

; Sequence 85, Application US/10792280  
; Publication No. US20040234517A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Bowman, Michael  
; APPLICANT: Follettie, Maximilian  
; APPLICANT: Chen, Heng  
; APPLICANT: Williams, Cara  
; APPLICANT: Ellis, Debra  
; APPLICANT: Winkler, Aaron  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING ASTHMA OR  
; FILE OF INVENTION: OTHER ALLERGIC OR INFLAMMATORY DISEASES  
; FILE REFERENCE: AM101023-2  
; CURRENT APPLICATION NUMBER: US/10/792,280  
; CURRENT FILING DATE: 2004-03-04  
; NUMBER OF SEQ ID NOS: 1535  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 85  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNAi-sense strand  
US-10-792-280-85

Query Match 0.4%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 68.4%; Pred. No. 2.4e+02;  
Matches 13; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3248 GTGGCAATCTGGAAGATT 3266  
|:||||| |:|||||:::  
Db 3 GUGGCAACUGGAAGAUU 21

RESULT 297  
US-09-953-047-49/c  
; Sequence 49, Application US/09953047  
; Publication No. US20030087854A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE  
; FILE REFERENCE: RTS-0157  
; CURRENT APPLICATION NUMBER: US/09/953,047  
; CURRENT FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 95  
; SEQ ID NO 49  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-953-047-49

Query Match 0.4%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 TTGCTGTGTGCCCAGG 2367  
|:||||| |:|||||:::  
Db 17 TTGCTGTGTGCCCAGG 1

RESULT 298  
US-10-630-401-49/c  
; Sequence 49, Application US/10630401  
; Publication No. US20040048824A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE  
; FILE REFERENCE: RTS-0157  
; CURRENT APPLICATION NUMBER: US/10/630,401  
; CURRENT FILING DATE: 2003-07-30

; PRIOR APPLICATION NUMBER: US/09/953,047  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 95  
; SEQ ID NO 49  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-630-401-49

Query Match 0.4%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 TTGCTGTGTGCCCAGG 2367  
|:||||| |:|||||:::  
Db 17 TTGCTGTGTGCCCAGG 1

RESULT 299  
US-10-663-189-7/c  
; Sequence 7, Application US/10663189  
; Publication No. US20050026158A1  
; GENERAL INFORMATION:  
; APPLICANT: The Johns Hopkins School of Medicine  
; APPLICANT: Nelson, William  
; APPLICANT: Tchou, Julia  
; APPLICANT: Bakker, Jilla  
; APPLICANT: Lin, Xiaohui  
; TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DIS  
; FILE REFERENCE: JHU1660-1  
; CURRENT APPLICATION NUMBER: US/10/663,189  
; CURRENT FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US/09/687,246B  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/159,168  
; PRIOR FILING DATE: 1999-10-13  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: primer N-F1  
US-10-663-189-7

Query Match 0.4%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAATT 2590  
|:||||| |:|||||:::  
Db 19 TTAAAAAATAAAATT 3

RESULT 300  
US-09-725-265-42/c  
; Sequence 42, Application US/09725265  
; Publication No. US20010000175A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KANAGAWA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLI  
; FILE REFERENCE: THE METHOD  
; FILE REFERENCE: 199953US0XDIV

```
/ CURRENT APPLICATION NUMBER: US/09/725,265
/ CURRENT FILING DATE: 2000-11-29
/ PRIOR APPLICATION NUMBER: US 09/556,127
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: JP 1999-111601
/ PRIOR FILING DATE: 1999-04-20
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 42
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: ARTIFICIAL SEQUENCE
/ FEATURE:
/ OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-42

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATATATTT 1171
Db 20 TTTTATATATATATAT 1

RESULT 301
US-09-823-634A-13
/ Sequence 13, Application US/09823634A
/ Patent No. US20020142308A1
/ GENERAL INFORMATION:
/ APPLICANT: Applied Gene Technologies, Inc.
/ APPLICANT: Dattagupta, Nanibhushan
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
/ TITLE OF INVENTION: METHODS USING RNASE H
/ FILE REFERENCE: 47541-20006.00
/ CURRENT APPLICATION NUMBER: US/09/823,634A
/ CURRENT FILING DATE: 2002-02-28
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGAGAAAAA 2599
Db 1 AAAAAAAATTGAAAAAAA 20

RESULT 302
US-09-823-634A-14
/ Sequence 14, Application US/09823634A
/ Patent No. US20020142308A1
/ GENERAL INFORMATION:
/ APPLICANT: Applied Gene Technologies, Inc.
/ APPLICANT: Dattagupta, Nanibhushan
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
/ TITLE OF INVENTION: METHODS USING RNASE H
/ FILE REFERENCE: 47541-20006.00
/ CURRENT APPLICATION NUMBER: US/09/823,634A
/ CURRENT FILING DATE: 2002-02-28
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14
/ LENGTH: 20
/ TYPE: DNA
```

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligo AGT02021
US-09-823-634A-14

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGAGAAAAA 2599
Db 1 AAAAAAAATTGAAAAAAA 20

RESULT 303
US-09-823-647B-13
/ Sequence 13, Application US/09823647B
/ Patent No. US20020142309A1
/ GENERAL INFORMATION:
/ APPLICANT: Applied Gene Technologies, Inc.
/ APPLICANT: Dattagupta, Nanibhushan
/ TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 47541-20004.20
/ CURRENT APPLICATION NUMBER: US/09/823,647B
/ CURRENT FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: US 09/616,761
/ PRIOR FILING DATE: 2000-07-14
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGAGAAAAA 2599
Db 1 AAAAAAAATTGAAAAAAA 20

RESULT 304
US-09-823-647B-14
/ Sequence 14, Application US/09823647B
/ Patent No. US20020142309A1
/ GENERAL INFORMATION:
/ APPLICANT: Applied Gene Technologies, Inc.
/ APPLICANT: Dattagupta, Nanibhushan
/ TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 47541-20004.20
/ CURRENT APPLICATION NUMBER: US/09/823,647B
/ CURRENT FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: US 09/616,761
/ PRIOR FILING DATE: 2000-07-14
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
```

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTCGAGAAAA 2599  
 |||||  
 Db 1 AAAAAAAAAATTGAAAAAA 20

RESULT 305  
 US-09-888-326-192  
 ; Sequence 192, Application US/09888326  
 ; Publication No. US20030026801A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weiner, George  
 ; APPLICANT: Hartmann, Gunther  
 ; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
 ; FILE REFERENCE: C1039/7052 (AWS)  
 ; CURRENT APPLICATION NUMBER: US/09/888,326  
 ; CURRENT FILING DATE: 2001-06-22  
 ; PRIOR APPLICATION NUMBER: US 60/213,346  
 ; PRIOR FILING DATE: 2000-06-22  
 ; NUMBER OF SEQ ID NOS: 848  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 192  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic oligonucleotide  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (0)...(0)  
 ; OTHER INFORMATION: phosphorothioate backbone  
 US-09-888-326-192

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635  
 |||||  
 Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 306  
 US-09-888-326-192/c  
 ; Sequence 192, Application US/09888326  
 ; Publication No. US20030026801A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weiner, George  
 ; APPLICANT: Hartmann, Gunther  
 ; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
 ; FILE REFERENCE: C1039/7052 (AWS)  
 ; CURRENT APPLICATION NUMBER: US/09/888,326  
 ; CURRENT FILING DATE: 2001-06-22  
 ; PRIOR APPLICATION NUMBER: US 60/213,346  
 ; PRIOR FILING DATE: 2000-06-22  
 ; NUMBER OF SEQ ID NOS: 848  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 192  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic oligonucleotide  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (0)...(0)  
 ; OTHER INFORMATION: phosphorothioate backbone  
 US-09-888-326-192

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635  
 |||||  
 Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 307  
 US-09-888-326-193  
 ; Sequence 193, Application US/09888326  
 ; Publication No. US20030026801A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weiner, George  
 ; APPLICANT: Hartmann, Gunther  
 ; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
 ; FILE REFERENCE: C1039/7052 (AWS)  
 ; CURRENT APPLICATION NUMBER: US/09/888,326  
 ; CURRENT FILING DATE: 2001-06-22  
 ; PRIOR APPLICATION NUMBER: US 60/213,346  
 ; PRIOR FILING DATE: 2000-06-22  
 ; NUMBER OF SEQ ID NOS: 848  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 193  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic oligonucleotide  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (0)...(0)  
 ; OTHER INFORMATION: phosphodiester backbone  
 US-09-888-326-193

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635  
 |||||  
 Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 308  
 US-09-888-326-193/c  
 ; Sequence 193, Application US/09888326  
 ; Publication No. US20030026801A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weiner, George  
 ; APPLICANT: Hartmann, Gunther  
 ; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
 ; FILE REFERENCE: C1039/7052 (AWS)  
 ; CURRENT APPLICATION NUMBER: US/09/888,326  
 ; CURRENT FILING DATE: 2001-06-22  
 ; PRIOR APPLICATION NUMBER: US 60/213,346  
 ; PRIOR FILING DATE: 2000-06-22  
 ; NUMBER OF SEQ ID NOS: 848  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 193  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic oligonucleotide  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (0)...(0)  
 ; OTHER INFORMATION: phosphodiester backbone  
 US-09-888-326-193

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



Qy 616 CGCGCGCACGACGCGCG 635  
|||  
pb 20 CGCGCGCGCGCGCGCG 1

```

RESULT 309
US-09-948-002-69/c
; Sequence 69, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-69

```

|                          |       |                    |        |            |
|--------------------------|-------|--------------------|--------|------------|
| Query Match              | 0.4%  | Score 16.8;        | DB 1;  | Length 20; |
| Best Local Similarity    | 90.0% | Pred. No. 2.5e+02; |        |            |
| Matches 18: Conservative | 0;    | Mismatches 2;      | Indels |            |

Qy 1247 GCTCCTGCATCTGGTCCCG 1266  
| | | | | | | | | | | | | | | | | |  
Db 20 GATCCTGCATCTGGTACGG 1

```

RESULT 310
US-09-776-479-520
; Sequence 520, Application US/09776479
; Publication No. US2003008748A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulator
; TITLE OF INVENTION: Treatment of As
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/77
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: Fast-SEQ for Windows Versio
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequen
US-09-776-479-520

```

|                          |       |                   |        |           |
|--------------------------|-------|-------------------|--------|-----------|
| Query Match              | 0.4%  | Score 16.8        | DB 1   | Length 20 |
| Best Local Similarity    | 90.0% | Pred. No. 2.5e+02 |        |           |
| Matches 18: Conservative | 0     | Mismatches 2      | Indels |           |

Qy 616 CGCGCGGCACGCACGCGCG 635  
|||  
pb 1 CGCGCGCGCGCGCGCGCGCG 20

```

RESULT 311
US-09-776-479-520/c
; Sequence 520, Application US/09776479
; Publication No. US2003008748A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TREATMENT OF: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-520

```

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18: Conservative 0; Mismatches 2; Indels

QY 616 CGCGGCGCACGCGCGCG 635  
Db 20 CGCGGCGCGCGCGCGCGCG 1

```

RESULT 312
US-09-776-479-520
; Sequence 520, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TREATMENT OF: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-520

```

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18: Conservative 0; Mismatches 2; Indels

Qy 616 CGCGGCGCACGACGCGCG 635  
pB 1 CGCGGCGCGCGCGCGCGCG 20

RESULT 313  
US-09-776-479-520/c  
; Sequence 520, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:

; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 520  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
DB 20 CGCGCGCGCGCGCGCGCG 1  
|||||

## RESULT 314

US-09-776-479-769  
; Sequence 769, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 769  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
DB 1 CGCGCGCGCGCGCGCGCG 20  
|||||

## RESULT 315

US-09-776-479-769/c  
; Sequence 769, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE OF INVENTION: Treatment of Asthma and Allergy

; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 769  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
DB 20 CGCGCGCGCGCGCGCGCG 1  
|||||

## RESULT 316

US-09-776-479-769  
; Sequence 769, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 769  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
DB 1 CGCGCGCGCGCGCGCGCG 20  
|||||

## RESULT 317

US-09-776-479-769/c  
; Sequence 769, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03

; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 769  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
|||||  
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 318  
US-09-965-101-22  
; Sequence 22, Application US/09965101  
; Publication No. US20040186067A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; FILE REFERENCE: C1039/7057 (HCL/NAT)  
; CURRENT APPLICATION NUMBER: US/09/965,101  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233  
; PRIOR FILING DATE: 1997-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,209  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-09-965-101-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
|||||  
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 319  
US-09-965-101-22/c  
; Sequence 22, Application US/09965101  
; Publication No. US20040186067A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; FILE REFERENCE: C1039/7057 (HCL/NAT)  
; CURRENT APPLICATION NUMBER: US/09/965,101  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649

; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233  
; PRIOR FILING DATE: 1997-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,209  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-09-965-101-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
|||||  
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 320  
US-09-965-101-76  
; Sequence 76, Application US/09965101  
; Publication No. US20040186067A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; FILE REFERENCE: C1039/7057 (HCL/NAT)  
; CURRENT APPLICATION NUMBER: US/09/965,101  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233  
; PRIOR FILING DATE: 1997-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,209  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 76  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-09-965-101-76

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGCG 634  
|||||  
DB 1 GCGCGCGCGCGCGCGCGCG 20

RESULT 321  
US-09-965-101-76/c  
; Sequence 76, Application US/09965101  
; Publication No. US20040186067A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or

```

; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/WAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-76

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCGCGCGCGCG 634
Db 20 GCGCGCGCGCGCGCGCGCG 1

RESULT 322
US-10-146-058-99/c
; Sequence 99, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF INVENTIONS: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350

```

```

; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-99

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAACGG 1947
Db 20 CATCATCCCGAATAAAAGTG 1

RESULT 323
US-10-112-653-497
; Sequence 497, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Daniel J.
; APPLICANT: Berg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 497
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-497

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGCGCGCGCGCG 635
Db 1 GCGCGCGCGCGCGCGCGCG 20

RESULT 324
US-10-112-653-497/c
; Sequence 497, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Daniel J.
; APPLICANT: Berg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 497
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```
;
; FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-497

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 325
US-10-112-653-742
; Sequence 742, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 742
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-742

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 326
US-10-112-653-742/c
; Sequence 742, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 742
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-742

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 327
US-10-017-995-520
; Sequence 520, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-520

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 328
US-10-017-995-520/c
; Sequence 520, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-520

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 329
US-10-017-995-769
; Sequence 769, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
```

; APPLICANT: Bratzler, Robert L.  
 ; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
 ; FILE REFERENCE: C1037/7025 (HCL/WAT)  
 ; CURRENT APPLICATION NUMBER: US/10/017,995  
 ; PRIOR FILING DATE: 2001-12-18  
 ; PRIOR APPLICATION NUMBER: US 60/255,534  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 1093  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 769  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Sequence  
 US-10-017-995-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635  
 Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 330  
 US-10-017-995-769/c  
 ; Sequence 769, Application US/10017995  
 ; Publication No. US20030055014A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bratzler, Robert L.  
 ; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
 ; FILE REFERENCE: C1037/7025 (HCL/WAT)  
 ; CURRENT APPLICATION NUMBER: US/10/017,995  
 ; PRIOR FILING DATE: 2001-12-18  
 ; PRIOR APPLICATION NUMBER: US 60/255,534  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 1093  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 769  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Sequence  
 US-10-017-995-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635  
 Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 331  
 US-10-209-608-42/c  
 ; Sequence 42, Application US/10209608  
 ; Publication No. US20030082592A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KURANE, RYUICHIRO  
 ; APPLICANT: KANAGAWA, TAKAHIRO  
 ; APPLICANT: KAMAGATA, YOICHI  
 ; APPLICANT: YAMADA, KAZUTAKA  
 ; APPLICANT: YOKOMAKU, TOYOKAZU  
 ; APPLICANT: KOYAMA, OSAMU  
 ; APPLICANT: FURUSHO, KENTA  
 ; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI  
 ; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
 ; TITLE OF INVENTION: THE METHOD  
 ; FILE REFERENCE: 199953US0XDIV

; CURRENT APPLICATION NUMBER: US/10/209,608  
 ; CURRENT FILING DATE: 2002-08-01  
 ; PRIOR APPLICATION NUMBER: US/09/725,265  
 ; PRIOR FILING DATE: 2000-11-29  
 ; PRIOR APPLICATION NUMBER: US 09/556,127  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: JP 1999-111601  
 ; PRIOR FILING DATE: 1999-04-20  
 ; NUMBER OF SEQ ID NOS: 70  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 42  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: ARTIFICIAL SEQUENCE  
 ; FEATURE:  
 ; OTHER INFORMATION: SYNTHETIC DNA  
 US-10-209-608-42

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTCTTTTTTATATATTT 1171  
 Db 20 TTTTATATATATATATAT 1

RESULT 332  
 US-10-367-470-13  
 ; Sequence 13, Application US/10367470  
 ; Publication No. US20030165963A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Applied Gene Technologies, Inc.  
 ; APPLICANT: Dattagupta, Nanibhushan  
 ; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: 47541-20004.20  
 ; CURRENT APPLICATION NUMBER: US/10/367,470  
 ; CURRENT FILING DATE: 2003-02-13  
 ; PRIOR APPLICATION NUMBER: US/09/823,647B  
 ; PRIOR FILING DATE: 2002-05-07  
 ; PRIOR APPLICATION NUMBER: US 09/616,761  
 ; PRIOR FILING DATE: 2000-07-14  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligo AGT02020  
 US-10-367-470-13

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGAGAAAAA 2599  
 Db 1 AAAAAAAAAATTGAAAAAAA 20

RESULT 333  
 US-10-367-470-14  
 ; Sequence 14, Application US/10367470  
 ; Publication No. US20030165963A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Applied Gene Technologies, Inc.  
 ; APPLICANT: Dattagupta, Nanibhushan  
 ; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: 47541-20004.20  
 ; CURRENT APPLICATION NUMBER: US/10/367,470

; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/823,647B  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US/09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligo AGT02021  
US-10-367-470-14

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGGAGAAAAA 2599  
||||||| - |||||  
Db 1 AAAAAAAATTGTAATAAAA 20

## RESULT 334

US-10-314-578-520  
; Sequence 520, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; PRIOR FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 520  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
||||||| - |||||  
Db 1 CGCGCGCGCGCGCGCGCG 20

## RESULT 335

US-10-314-578-520/c  
; Sequence 520, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; CURRENT FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 520  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
||||||| - |||||  
Db 20 CGCGCGCGCGCGCGCGCG 1

## RESULT 336

US-10-314-578-769  
; Sequence 769, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; PRIOR FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 769  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
||||||| - |||||  
Db 1 CGCGCGCGCGCGCGCGCG 20

## RESULT 337

US-10-314-578-769/c  
; Sequence 769, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schetter, Christian  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578

| Query Match | Best Local Similarity | Score | DB 1 | Length | DB 2 | Length | DB 3 | Length | DB 4 | Length | DB 5 | Length | DB 6 | Length | DB 7 | Length | DB 8 | Length | DB 9 | Length | DB 10 | Length | DB 11 | Length | DB 12 | Length | DB 13 | Length | DB 14 | Length | DB 15 | Length | DB 16 | Length | DB 17 | Length | DB 18 | Length | DB 19 | Length | DB 20 | Length | DB 21 | Length | DB 22 | Length | DB 23 | Length | DB 24 | Length | DB 25 | Length | DB 26 | Length | DB 27 | Length | DB 28 | Length | DB 29 | Length | DB 30 | Length | DB 31 | Length | DB 32 | Length | DB 33 | Length | DB 34 | Length | DB 35 | Length | DB 36 | Length | DB 37 | Length | DB 38 | Length | DB 39 | Length | DB 40 | Length | DB 41 | Length | DB 42 | Length | DB 43 | Length | DB 44 | Length | DB 45 | Length | DB 46 | Length | DB 47 | Length | DB 48 | Length | DB 49 | Length | DB 50 | Length | DB 51 | Length | DB 52 | Length | DB 53 | Length | DB 54 | Length | DB 55 | Length | DB 56 | Length | DB 57 | Length | DB 58 | Length | DB 59 | Length | DB 60 | Length | DB 61 | Length | DB 62 | Length | DB 63 | Length | DB 64 | Length | DB 65 | Length | DB 66 | Length | DB 67 | Length | DB 68 | Length | DB 69 | Length | DB 70 | Length | DB 71 | Length | DB 72 | Length | DB 73 | Length | DB 74 | Length | DB 75 | Length | DB 76 | Length | DB 77 | Length | DB 78 | Length | DB 79 | Length | DB 80 | Length | DB 81 | Length | DB 82 | Length | DB 83 | Length | DB 84 | Length | DB 85 | Length | DB 86 | Length | DB 87 | Length | DB 88 | Length | DB 89 | Length | DB 90 | Length | DB 91 | Length | DB 92 | Length | DB 93 | Length | DB 94 | Length | DB 95 | Length | DB 96 | Length | DB 97 | Length | DB 98 | Length | DB 99 | Length | DB 100 | Length | DB 101 | Length | DB 102 | Length | DB 103 | Length | DB 104 | Length | DB 105 | Length | DB 106 | Length | DB 107 | Length | DB 108 | Length | DB 109 | Length | DB 110 | Length | DB 111 | Length | DB 112 | Length | DB 113 | Length | DB 114 | Length | DB 115 | Length | DB 116 | Length | DB 117 | Length | DB 118 | Length | DB 119 | Length | DB 120 | Length | DB 121 | Length | DB 122 | Length | DB 123 | Length | DB 124 | Length | DB 125 | Length | DB 126 | Length | DB 127 | Length | DB 128 | Length | DB 129 | Length | DB 130 | Length | DB 131 | Length | DB 132 | Length | DB 133 | Length | DB 134 | Length | DB 135 | Length | DB 136 | Length | DB 137 | Length | DB 138 | Length | DB 139 | Length | DB 140 | Length | DB 141 | Length | DB 142 | Length | DB 143 | Length | DB 144 | Length | DB 145 | Length | DB 146 | Length | DB 147 | Length | DB 148 | Length | DB 149 | Length | DB 150 | Length | DB 151 | Length | DB 152 | Length | DB 153 | Length | DB 154 | Length | DB 155 | Length | DB 156 | Length | DB 157 | Length | DB 158 | Length | DB 159 | Length | DB 160 | Length | DB 161 | Length | DB 162 | Length | DB 163 | Length | DB 164 | Length | DB 165 | Length | DB 166 | Length | DB 167 | Length | DB 168 | Length | DB 169 | Length | DB 170 | Length | DB 171 | Length | DB 172 | Length | DB 173 | Length | DB 174 | Length | DB 175 | Length | DB 176 | Length | DB 177 | Length | DB 178 | Length | DB 179 | Length | DB 180 | Length | DB 181 | Length | DB 182 | Length | DB 183 | Length | DB 184 | Length | DB 185 | Length | DB 186 | Length | DB 187 | Length | DB 188 | Length | DB 189 | Length | DB 190 | Length | DB 191 | Length | DB 192 | Length | DB 193 | Length | DB 194 | Length | DB 195 | Length | DB 196 | Length | DB 197 | Length | DB 198 | Length | DB 199 | Length | DB 200 | Length | DB 201 | Length | DB 202 | Length | DB 203 | Length | DB 204 | Length | DB 205 | Length | DB 206 | Length | DB 207 | Length | DB 208 | Length | DB 209 | Length | DB 210 | Length | DB 211 | Length | DB 212 | Length | DB 213 | Length | DB 214 | Length | DB 215 | Length | DB 216 | Length | DB 217 | Length | DB 218 | Length | DB 219 | Length | DB 220 | Length | DB 221 | Length | DB 222 | Length | DB 223 | Length | DB 224 | Length | DB 225 | Length | DB 226 | Length | DB 227 | Length | DB 228 | Length | DB 229 | Length | DB 230 | Length | DB 231 | Length | DB 232 |
|-------------|-----------------------|-------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
|-------------|-----------------------|-------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|



```
RESULT 342
US-10-189-267-44/c
; Sequence 44, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-44
Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2127 TTGGATGCTGCCTACTGCTT 2146
      ||||| ||||| ||||| |||||
Db 20 TTGGATGGCGCCTATTGCTT 1

RESULT 343
US-10-189-267-46/c
; Sequence 46, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-46
Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAAGT 2465
      ||||| ||||| ||||| |||||
Db 20 CTTGCAATGCAGCTAAAT 1

RESULT 344
US-10-189-267-71/c
; Sequence 71, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
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; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-71
Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3056 TCGATGGCTTAAGGAGTTTG 3075
      ||||| ||||| ||||| |||||
Db 20 TGGATGGCTTAAGGAACTTG 1

RESULT 345
US-10-189-267-174
; Sequence 174, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 174
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-174
Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2349 CCTTGCTGTGTCTCCAGGA 2368
      ||||| ||||| ||||| |||||
Db 1 CCTTGCTGTGTCTCCAGA 20

RESULT 346
US-10-189-267-181
; Sequence 181, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 181
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-181
Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2094 TCACAACAGTCACGCCGGCG 2113
      ||||| ||||| ||||| |||||
Db 1 TCACAACAGCACCAACCGCG 20
```

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; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-42

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATATATTT 1171
DB 20 TTTTATATATATATATAT 1

RESULT 350
US-10-633-163-69/c
; Sequence 69, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-69

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1247 GCTCTGCATCTGTCCTGG 1266
DB 20 GATCTGCATCTGTCACGG 1

RESULT 351
US-10-831-778-520
; Sequence 520, Application US/10831778
; Publication No. US2004023574A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the

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; TITLE OF INVENTION: A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-42

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1870 TGGGGTTTAAATAAGTTTA 1889
DB 1 TGGGATTTAAATAAGCTTA 20

RESULT 348
US-10-189-267-188
; Sequence 188, Application US/10189267
; Publication No. US2004006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 188
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-189-267-188

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2127 TTGGATGCTGCCTACTGCTT 2146
DB 1 TTGGATGCGCGCTATTGCTT 20

RESULT 349
US-10-683-386-42/c
; Sequence 42, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI

```

; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/831,778  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 520  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 352  
US-10-831-778-520/c  
; Sequence 520, Application US/10831778  
; Publication No. US20040235774A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/831,778  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 520  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-520

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 353  
US-10-831-778-769  
; Sequence 769, Application US/10831778  
; Publication No. US20040235774A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/831,778  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/179,991

; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 769  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 354  
US-10-831-778-769/c  
; Sequence 769, Application US/10831778  
; Publication No. US20040235774A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/831,778  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 769  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-769

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 355  
US-10-838-659-22  
; Sequence 22, Application US/10838659  
; Publication No. US20050032734A1  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; TITLE OF INVENTION: Therapeutic Protocols  
; FILE REFERENCE: C1039.70057US01  
; CURRENT APPLICATION NUMBER: US/10/838,659  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: US 09/965,101  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233

```

; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-22

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 356
US-10-838-659-22/c
; Sequence 22, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-22

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 357
US-10-838-659-76
; Sequence 76, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or

```

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; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-76

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634
Db 1 GCGCGCGCGCGCGCGCGC 20

RESULT 358
US-10-838-659-76/c
; Sequence 76, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-76

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634
Db 20 GCGCGCGCGCGCGCGCGC 1

RESULT 359

```

US-10-146-058-76/c  
; Sequence 76, Application US/10146058

; Publication No. US20030040499A1

; GENERAL INFORMATION:

; APPLICANT: Schlingsiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingsiepen, Karl-Hermann

; APPLICANT: Schlingsiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; immunosuppressive effect of transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/146,058

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/535,249

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666

; TELEFAX: (202) 393-5350

; TELE: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 76:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-10-146-058-76

Query Match 0.4%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 2.3e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGAAATCGT 1606

DB 18 ACCCTACTTCAGAAATGT 1

RESULT 360

US-10-146-058-133/c

; Sequence 133, Application US/10146058

; Publication No. US20030040499A1

; GENERAL INFORMATION:

; APPLICANT: Schlingsiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlingsiepen, Karl-Hermann

; APPLICANT: Schlingsiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; immunosuppressive effect of transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/146,058

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/535,249

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666

; TELEFAX: (202) 393-5350

; TELE: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 133:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-10-146-058-133

Query Match

Best Local Similarity 0.4%; Score 16.4; DB 1; Length 18;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463

DB 18 CTTGTAATGCAGCTAAA 1

RESULT 361

US-10-789-119-4/c

; Sequence 4, Application US/10789119

; Publication No. US20040170157A1

; GENERAL INFORMATION:

; APPLICANT: Chung, Yih-Lin

; TITLE OF INVENTION: METHOD FOR INCREASING THERAPEUTIC GAIN

; FILE REFERENCE: 13206-004002

; CURRENT APPLICATION NUMBER: US/10/789,119

; CURRENT FILING DATE: 2004-03-11

; PRIOR APPLICATION NUMBER: US 10/205,738

; PRIOR FILING DATE: 2002-07-25

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

FEATURE:  
US-10-789-119-4  
Query Match 0.4%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2454 TGCAGCTAAAGTCCTGG 2471  
|||||  
Db 18 TGCAGCTAAAGTCCTCGG 1  
RESULT 362  
US-09-766-450-48  
; Sequence 48, Application US/09766450  
; Publication No. US20030022166A1  
; GENERAL INFORMATION:  
; APPLICANT: Collins, Colin  
; APPLICANT: Volik, Stanislav  
; APPLICANT: Gray, Joe W.  
; APPLICANT: Albertson, Donna G.  
; APPLICANT: Pinkel, Daniel  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Repeat-Free Probes for Molecular  
; FILE REFERENCE: 023071-111800US  
; CURRENT APPLICATION NUMBER: US/09/766,450  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 48  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer 768.348.r1  
US-09-766-450-48  
Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 645 ACACATCCACGCCACAC 662  
|||||  
Db 2 ACACATGCCACGCCACAC 19  
RESULT 363  
US-10-683-990-59  
; Sequence 59, Application US/10683990  
; Publication No. US20040198682A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics  
; APPLICANT: McSwiggen, James  
; APPLICANT: Usman, Nassim  
; APPLICANT: Pavco, Pamela  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor  
; FILE REFERENCE: 400/134 (02-742-H)  
; CURRENT APPLICATION NUMBER: US/10/683,990  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: PCT/US03/05022  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/393,796  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/399,348  
; PRIOR FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 256  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 156  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-683-990-156

PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 256  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 59  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r  
US-10-683-990-59  
Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 66 GGGAGAGAAAGAGAGAGAG 83  
|||||  
Db 2 GUGAGAGAAAGAGAGAGAG 19  
RESULT 364  
US-10-683-990-156/c  
; Sequence 156, Application US/10683990  
; Publication No. US20040198682A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics  
; APPLICANT: McSwiggen, James  
; APPLICANT: Usman, Nassim  
; APPLICANT: Pavco, Pamela  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor  
; FILE REFERENCE: 400/134 (02-742-H)  
; CURRENT APPLICATION NUMBER: US/10/683,990  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: PCT/US03/05022  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/393,796  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/399,348  
; PRIOR FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: US 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US 60/440,129  
; PRIOR FILING DATE: 2003-01-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 256  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 156  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-683-990-156

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; Query Match          0.4%; Score 16.4; DB 1; Length 19;
; Best Local Similarity 94.4%; Pred. No. 2.5e+02;
; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 GCGAGAGAAAGAGAGAGAG 83
DB 18 GTGAGAGAAAGAGAGAGAG 1

RESULT 365
US-09-791-942-10
; Sequence 10, Application US/09791942
; Patent No. US20020147166A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Robert Rothlein
; APPLICANT: Takashi Kei Kishimoto
; APPLICANT: Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0099
; CURRENT APPLICATION NUMBER: US/09/791,942
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-791-942-10

Query Match          0.4%; Score 16.4; DB 1; Length 20;
; Best Local Similarity 94.4%; Pred. No. 2.8e+02;
; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3393 TCCTTTGCTTGGTATAT 3410
DB 2 TCCTTGCTTGGTATAT 19

RESULT 366
US-10-189-267-27/c
; Sequence 27, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-27

Query Match          0.4%; Score 16.4; DB 1; Length 20;
; Best Local Similarity 94.4%; Pred. No. 2.8e+02;
; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1693 AACCCCAAGCCAGAGTG 1700
DB 19 AACCCCAAGCCAGAGTG 2

RESULT 367
US-10-189-267-177
```

```
; Sequence 177, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 177
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-267-177

Query Match          0.4%; Score 16.4; DB 1; Length 20;
; Best Local Similarity 94.4%; Pred. No. 2.8e+02;
; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1683 AACCCCAAGCCAGAGTG 1700
DB 2 AACCCCAAGCCAGAGTG 19

RESULT 368
US-10-289-762-2628
; Sequence 2628, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2628
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2628

Query Match          0.4%; Score 16.4; DB 1; Length 20;
; Best Local Similarity 94.4%; Pred. No. 2.8e+02;
; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1055 GCCAGGACGTTTCTA 1072
DB 2 GCCAGGACGTTTCTA 19

RESULT 369
US-10-415-463-10
; Sequence 10, Application US/10415463
; Publication No. US20040110705A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0198
; CURRENT APPLICATION NUMBER: US/10/415,463
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 09/702,251
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-415-463-10

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3393 TCCTTTGCTCTGGTATAT 3410
Db 2 TCCCTCGCTCTGGTATAT 19

RESULT 370
US-10-728-399-292/c
; Sequence 292, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455.1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-292

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588
Db 20 TGTTTAAACAAAAA 3

RESULT 371
US-10-728-399-369/c
; Sequence 369, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455.1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 369
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-369

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588
Db 19 TGTTTAAACAAAAA 2

RESULT 372
US-10-728-399-475/c
; Sequence 475, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MITONEET EXPRESSION
; FILE REFERENCE: 01455.1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 475
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoneet antisense
US-10-728-399-475

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2588
Db 18 TGTTTAAACAAAAA 1

RESULT 373
US-10-028-158-16/c
; Sequence 16, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/10/028,158
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-028-158-16

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACACTACTGTGTG 1232
Db 16 CATGCACACTACTGTGTG 1

RESULT 374
US-10-028-158-17
; Sequence 17, Application US/10028158
; Publication No. US20020110833A1
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
```



APPLICANT: Post, Martin  
APPLICANT: Lye, Stephen  
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF  
TROPICBLAST  
FILE REFERENCE: 11757 38USWO  
CURRENT APPLICATION NUMBER: US/10/028,158  
CURRENT FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: US/09/380,662  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: PCT/CA98/00180  
PRIOR FILING DATE: 1998-03-05  
PRIOR APPLICATION NUMBER: US 60/039,919  
PRIOR FILING DATE: 1997-03-07  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 17  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-028-158-17

Query Match 0.4%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2e+02; 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACCTACTGTGTG 1232  
Db 1 CATGCACCTACTGTGTG 16

RESULT 375  
US-10-146-058-105/c  
Sequence 105, Application US/10146058  
Publication No. US20030040499A1  
GENERAL INFORMATION:  
APPLICANT: Schlingensiepen, Georg-Ferdinand  
APPLICANT: Brysch, Wolfgang  
APPLICANT: Schlingensiepen, Karl-Hermann  
APPLICANT: Schlingensiepen, Reimar  
APPLICANT: Bogdahn, Ulrich  
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1  
NUMBER OF SEQUENCES: 137  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/146,058  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/535,249  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 089.0  
FILING DATE: 30-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 849.7  
FILING DATE: 13-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELEPHONE: (202)638-6666

TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-10-146-058-105

Query Match 0.4%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2e+02; 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAAA 2035  
Db 16 AGTCCACTAGGAAAAA 1

RESULT 376  
US-10-146-058-113/c  
Sequence 113, Application US/10146058  
Publication No. US20030040499A1  
GENERAL INFORMATION:  
APPLICANT: Schlingensiepen, Georg-Ferdinand  
APPLICANT: Brysch, Wolfgang  
APPLICANT: Schlingensiepen, Karl-Hermann  
APPLICANT: Schlingensiepen, Reimar  
APPLICANT: Bogdahn, Ulrich  
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1  
NUMBER OF SEQUENCES: 137  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/146,058  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/535,249  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 089.0  
FILING DATE: 30-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 849.7  
FILING DATE: 13-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELEPHONE: (202)638-6666  
TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)

```
; ANTI-SENSE: YES
US-10-146-058-113

Query Match          0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATTCG 2168
DB 16 TGTGCAGGATAATTCG 1

RESULT 377
US-10-156-306-524/c
; Sequence 524, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 524
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-524

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2588
DB 17 TTTAAAAA 2

RESULT 378
US-10-156-306-525/c
; Sequence 525, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-525

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2588
DB 16 TTTAAAAA 1

RESULT 379
US-10-238-700-8
; Sequence 8, Application US/10238700
```

```
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels
; FILE REFERENCE: 400/057 (MBH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-8

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 AGGCAGCAGCGCGGC 439
DB 1 AGGCAGCAGCGCGGC 16

RESULT 380
US-09-775-479-3/c
; Sequence 9, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: LECIERC, Guy
; APPLICANT: MARTEL, R.mi
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
; FILE REFERENCE: 12168-1US-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-9

Query Match          0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2588
DB 18 TTTAAAAA 3

RESULT 381
US-10-713-900-164292/c
; Sequence 164292, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 164292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-164292
```

```
Query Match          0.4%; Score 16; DB 1; Length 25;
Best Local Similarity 79.2%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3165 AAGCCCGACGACGCTGCTGC 3188
      ||||| ||||| ||||| ||||| |||||
Db 25 AAGCTTCGACGACGCTGTTGC 2
```

```
RESULT 382
US-09-888-326-342
; Sequence 342, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-342
```

```
Query Match          0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 633
      ||||| ||||| ||||| |||||
Db 1 GCGCGCGCGCGCGCGCG 19
```

```
RESULT 383
US-09-888-326-342/c
; Sequence 342, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 342
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-342
```

```
Query Match          0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGCACGCGCG 634
      ||||| ||||| ||||| |||||
Db 19 GCGCGCGCGCGCGCGCG 1
```

```
RESULT 384
US-09-776-479-138
; Sequence 138, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-138
```

```
Query Match          0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 633
      ||||| ||||| ||||| |||||
Db 1 GCGCGCGCGCGCGCGCG 19
```

```
RESULT 385
US-09-776-479-138/c
; Sequence 138, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGCACGCGCGC 634
Db 19 CGCGCGCGCGCGCGCGC 1

RESULT 386
US-09-776-479-138
; Sequence 138, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 387
US-09-776-479-138/c
; Sequence 138, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-138

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 388
US-10-112-653-131
; Sequence 131, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-131

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 633
Db 1 GCGCGCGCGCGCGCGCGC 19

RESULT 389
US-10-112-653-131/c
; Sequence 131, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-131

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGCACGCGCGC 634

```

```
Db      19  CGCGCGCGCGCGCGCGC 1
RESULT 390
US-10-017-995-138
; Sequence 138, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-138
Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      615  GCGCGCGCGCACGCGCGC 633
Db      19  CGCGCGCGCGCGCGCGC 1

RESULT 391
US-10-017-995-138/c
; Sequence 138, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-138
Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616  CGCGCGCGCGCACGCGCGC 634
Db      19  CGCGCGCGCGCGCGCGC 1

RESULT 392
US-10-314-578-138
; Sequence 138, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-138
Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616  CGCGCGCGCGCACGCGCGC 634
Db      19  CGCGCGCGCGCGCGCGC 1

RESULT 394
US-10-683-990-97
; Sequence 97, Application US/10683990
; Publication No. US20040198682A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; APPLICANT: McSwiggen, James
```

APPLICANT: Usman, Nassim  
APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor  
FILE REFERENCE: 400/134 (02-742-H)  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 256  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 97  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense  
US-10-683-990-97  
Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 2.9e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2570 GTGTTTAAAAA 2588  
Db 1 GUGUGGAAAAA 19  
RESULT 395  
US-10-683-990-194/c  
Sequence 194, Application US/10683990  
Publication No. US2004019862A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Usman, Nassim  
APPLICANT: Pavco, Pamela  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Placental Growth Factor  
FILE REFERENCE: 400/134 (02-742-H)  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: US/10/683,990  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: PCT/US03/05022  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/393,796  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 60/399,348  
PRIOR FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 256  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 194  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-683-990-194  
Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2570 GTGTTTAAAAA 2588  
Db 19 GTGTGMAAAAAA 1  
RESULT 396  
US-10-831-778-138  
Sequence 138, Application US/10831778  
Publication No. US20040235774A1  
GENERAL INFORMATION:  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Petersen, Deanna M.  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
FILE REFERENCE: C1037/7013 (HCL/MAT)  
CURRENT FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US/10/831,778  
PRIOR FILING DATE: 2000-02-03  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 138  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-138  
Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 615 GCGCGCGCGCGCGCGCG 633  
Db 1 GCGCGCGCGCGCGCGCG 19  
RESULT 397  
US-10-831-778-138/c  
Sequence 138, Application US/10831778  
Publication No. US20040235774A1  
GENERAL INFORMATION:  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Petersen, Deanna M.  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
FILE REFERENCE: C1037/7013 (HCL/MAT)

; CURRENT APPLICATION NUMBER: US/10/831,778  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 138  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-138

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 GCGCGCGCGACGCGCGC 634  
|||||  
DB 19 GCGCGCGCGCGCGCGC 1

RESULT 398  
US-09-750-401-32/c  
; Sequence 32, Application US/09750401  
; Publication No. US20020004211A1  
; GENERAL INFORMATION:  
; APPLICANT: Keene, Jack D.  
; APPLICANT: Carson, Craig C.  
; APPLICANT: Tenenbaum, Scott A.  
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
; FILE REFERENCE: RBN-001  
; CURRENT APPLICATION NUMBER: US/09/750,401  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,338  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2  
US-09-750-401-32

Query Match 0.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAGAAAA 2599  
|||||  
DB 22 AAAAAAACCAATTAAGAAAA 1

RESULT 399  
US-10-309-788-32/c  
; Sequence 32, Application US/10309788  
; Publication No. US20030211466A1  
; GENERAL INFORMATION:  
; APPLICANT: Keene, Jack D.  
; APPLICANT: Tenenbaum, Scott A.  
; APPLICANT: Carson, Craig C.  
; APPLICANT: Phelps, William C.  
; TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Target  
; FILE REFERENCE: RBN-001CP  
; CURRENT APPLICATION NUMBER: US/10/309,788  
; CURRENT FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: US 60/173,338  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 09/750,401

; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 3'-UTR consensus sequence of TGF beta 2  
US-10-309-788-32

Query Match 0.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAGAAAA 2599  
|||||  
DB 22 AAAAAAACCAATTAAGAAAA 1

RESULT 400  
US-10-238-306B-32/c  
; Sequence 32, Application US/10238306B  
; Publication No. US20030235830A1  
; GENERAL INFORMATION:  
; APPLICANT: Keene, Jack D.  
; APPLICANT: Tenenbaum, Scott A.  
; APPLICANT: Carson, Craig C.  
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
; FILE REFERENCE: RBN-001CN  
; CURRENT APPLICATION NUMBER: US/10/238,306B  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: US 09/750,401  
; PRIOR FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,338  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2  
US-10-238-306B-32

Query Match 0.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAATTGGAGAAAA 2599  
|||||  
DB 22 AAAAAAACCAATTAAGAAAA 1

RESULT 401  
US-10-629-453-32/c  
; Sequence 32, Application US/10629453  
; Publication No. US20040096878A1  
; GENERAL INFORMATION:  
; APPLICANT: Keene, Jack D.  
; APPLICANT: Carson, Craig C.  
; APPLICANT: Tenenbaum, Scott A.  
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
; FILE REFERENCE: RBN-001DV  
; CURRENT APPLICATION NUMBER: US/10/629,453  
; CURRENT FILING DATE: 2003-07-29  
; PRIOR APPLICATION NUMBER: US 09/750,401  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,338  
; PRIOR FILING DATE: 1999-12-28

[illegible]



```

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-112

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2136 GCCTACTGCTTTAGAAA 2152
Db 17 GCCTATTGCTTTAGAAA 1

RESULT 408
US-10-209-608-18/c
; Sequence 18, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOKAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/10/209,608
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-18

Query Match 0.4%; Score 15.4; DB 1; Length 18;

```

Best Local Similarity 94.1%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177  
Db 17 TATATATTTTCTT 1

## RESULT 409

US-10-232-881-3/c  
; Sequence 3, Application US/10232881  
; Publication No. US2003008088A1  
; GENERAL INFORMATION:  
; APPLICANT: Ravikumar, Vasulinga  
; APPLICANT: Manoharan, Muthiah  
; APPLICANT: Capaldi, Daniel  
; APPLICANT: Krotz, Achim  
; APPLICANT: Cole, Douglas  
; APPLICANT: Guzaev, Andrei  
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric  
; FILE REFERENCE: ISIS3380  
; CURRENT APPLICATION NUMBER: US/10/232,881  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US/09/288,679  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/118,564  
; PRIOR FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Phosphorothioate backbone  
US-10-232-881-3

Query Match 0.4%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATGGAG 2594  
Db 18 AAAAAAAAAAATGGG 2

## RESULT 410

US-10-232-881-5/c  
; Sequence 5, Application US/10232881  
; Publication No. US2003008088A1  
; GENERAL INFORMATION:  
; APPLICANT: Ravikumar, Vasulinga  
; APPLICANT: Manoharan, Muthiah  
; APPLICANT: Capaldi, Daniel  
; APPLICANT: Krotz, Achim  
; APPLICANT: Cole, Douglas  
; APPLICANT: Guzaev, Andrei  
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric  
; FILE REFERENCE: ISIS3380  
; CURRENT APPLICATION NUMBER: US/10/232,881  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US/09/288,679  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 60/118,564  
; PRIOR FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial

FEATURE:  
; OTHER INFORMATION: No. US2003008088A1el Sequence  
US-10-232-881-5

Query Match 0.4%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATGGAG 2594  
Db 18 AAAAAAAAAAATGGG 2

## RESULT 411

US-10-683-386-18/c  
; Sequence 18, Application US/10683386  
; Publication No. US20040063137A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KAWAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/10/683,386  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US/09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-10-683-386-18

Query Match 0.4%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177  
Db 17 TATATATTTTCTT 1

## RESULT 412

US-10-760-940-3/c  
; Sequence 3, Application US/10760940  
; Publication No. US20040219577A1  
; GENERAL INFORMATION:  
; APPLICANT: Ravikumar, Vasulinga  
; APPLICANT: Manoharan, Muthiah  
; APPLICANT: Capaldi, Daniel C.  
; APPLICANT: Krotz, Achim  
; APPLICANT: Cole, Douglas L.  
; APPLICANT: Guzaev, Andrei  
; TITLE OF INVENTION: IMPROVED PROCESS FOR THE SYNTHESIS OF OLIGOMERIC COMPOUNDS  
; FILE REFERENCE: ISIS-5422  
; CURRENT APPLICATION NUMBER: US/10/760,940  
; CURRENT FILING DATE: 2004-01-20  
; PRIOR APPLICATION NUMBER: US 10/232,881  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: US 09/288,679  
; PRIOR FILING DATE: 1999-04-09

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; PRIOR APPLICATION NUMBER: US 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phosphorothioate backbone
US-10-760-940-3

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2

RESULT 413
US-10-473-126-1002/c
; Sequence 1002, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 1002
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for N-MYC
US-10-473-126-1002

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2807 AAAAAAAAAACATCAAAAC 2823
Db 18 AAAAAAAAAACCAAAAC 2

RESULT 414
US-09-569-193A-3
; Sequence 3, Application US/09569193A
; Patent No. US20020076697A1
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Kinase Assays Using Polyclonals
; FILE REFERENCE: 100/07930
; CURRENT APPLICATION NUMBER: US/09/569,193A
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 09/316,447
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/156,366
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/139,562
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-473-126-1002
```

```
; OTHER INFORMATION: PNA probe
US-09-569-193A-3

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCT 2139
Db 1 CGCTGTGGATGCTGCT 17

RESULT 415
US-09-865-044-3
; Sequence 3, Application US/09865044
; Patent No. US20020146703A1
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Assay Methods and Systems
; FILE REFERENCE: 09316447
; CURRENT APPLICATION NUMBER: US/09/865,044
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/316,447
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-865-044-3

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCT 2139
Db 1 CGCTGTGGATGCTGCT 17

RESULT 416
US-10-057-812-3
; Sequence 3, Application US/10057812
; Publication No. US20020197619A1
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Kinase Assays Using Polyclonals
; FILE REFERENCE: 100/07930
; CURRENT APPLICATION NUMBER: US/10/057,812
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US/09/569,193A
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/156,366
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/139,562
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-057-812-3

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2123 CGCTTTGGATGCTGCCT 2139  
|||||  
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 417  
US-10-397-887-3  
; Sequence 3, Application US/10397887  
; Publication No. US20030175815A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikiforov, Theo T.  
; TITLE OF INVENTION: Assay Methods and Systems  
; FILE REFERENCE: 09316447  
; CURRENT APPLICATION NUMBER: US/10/397,887  
; CURRENT FILING DATE: 2003-03-26  
; PRIOR APPLICATION NUMBER: US/09/316,447A  
; PRIOR FILING DATE: 1999-02-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Nucleic Acid  
US-10-397-887-3

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 3.2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139  
|||||  
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 418  
US-10-349-143-4619  
; Sequence 4619, Application US/10349143  
; Publication No. US20040005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilva  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.0200CF1  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 4619  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..19  
; OTHER INFORMATION: upstream amplification primer 99-16399 for SEQ 685,  
US-10-349-143-4619

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 3.2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3126 GTTGTATAGGACTAAG 3142  
|||||  
Db 2 GTTGTATAGGACTAAG 18

RESULT 419  
US-10-701-550-3  
; Sequence 3, Application US/10701550  
; Publication No. US20040058406A1  
; GENERAL INFORMATION:  
; APPLICANT: Nikiforov, Theo T.  
; TITLE OF INVENTION: Kinase Assays Using Polycations  
; FILE REFERENCE: 100/07930  
; CURRENT APPLICATION NUMBER: US/10/701,550  
; CURRENT FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: US 09/569,193  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 09/316,447  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: US 60/156,366  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/139,562  
; PRIOR FILING DATE: 1999-06-16  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PNA probe  
US-10-701-550-3

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 3.2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139  
|||||  
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 420  
US-10-670-011-33/c  
; Sequence 33, Application US/10670011  
; Publication No. US20040209832A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Pavco, Pamela  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial  
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor  
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/132 (MBHB02-742-G)  
; CURRENT APPLICATION NUMBER: US/10/670,011  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US03/05022  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US60/393,796  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US60/399,348  
; PRIOR FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: US60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US60/408,378  
; PRIOR FILING DATE: 2002-09-05

```
/ PRIOR APPLICATION NUMBER: US60/409,293
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: US60/440,129
/ PRIOR FILING DATE: 2003-01-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 427
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 33
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region
US-10-670-011-33

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 CCTCCCCGGGCTCGCC 601
Db 17 CCTGCCGGGCTCGCC 1

RESULT 421
US-10-670-011-129
/ Sequence 129, Application US/10670011
/ Publication No. US20040209832A1
/ GENERAL INFORMATION:
/ APPLICANT: Sina Therapeutics, Inc.
/ APPLICANT: McSwiggen, James
/ APPLICANT: Beigelman, Leonid
/ APPLICANT: Pavco, Pamela
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
/ TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
/ TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
/ FILE REFERENCE: 400/132 (MBH02-742-G)
/ CURRENT FILING DATE: 2003-09-23
/ PRIOR APPLICATION NUMBER: PCT/US03/05022
/ PRIOR FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: US60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US60/386,782
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: US60/393,796
/ PRIOR FILING DATE: 2002-07-03
/ PRIOR APPLICATION NUMBER: US60/399,348
/ PRIOR FILING DATE: 2002-07-29
/ PRIOR APPLICATION NUMBER: US60/406,784
/ PRIOR FILING DATE: 2002-08-29
/ PRIOR APPLICATION NUMBER: US60/408,378
/ PRIOR FILING DATE: 2002-09-05
/ PRIOR APPLICATION NUMBER: US60/409,293
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: US60/440,129
/ PRIOR FILING DATE: 2003-01-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 427
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 129
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-670-011-129

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 3.2e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 585 CCTCCCCGGGCTCGCC 601
Db 3 CCUGCCCGCGGCUCCGCC 19

RESULT 422
US-10-663-189-7
/ Sequence 7, Application US/10663189
/ Publication No. US20050026158A1
/ GENERAL INFORMATION:
/ APPLICANT: The Johns Hopkins School of Medicine
/ APPLICANT: Nelson, William
/ APPLICANT: Tchou, Julia
/ APPLICANT: Bakker, Jila
/ APPLICANT: Lin, Xiaohui
/ TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DIS
/ FILE REFERENCE: JHU1660-1
/ CURRENT APPLICATION NUMBER: US/10/663,189
/ CURRENT FILING DATE: 2003-09-15
/ PRIOR APPLICATION NUMBER: US/09/687,246B
/ PRIOR FILING DATE: 2000-10-12
/ PRIOR APPLICATION NUMBER: 60/159,168
/ PRIOR FILING DATE: 1999-10-13
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 7
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: primer N-F1
US-10-663-189-7

Query Match          0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTTTTTTAAAG 2758
Db 4 ATTTTTTTTTTTTAAAG 20

RESULT 423
US-10-156-306-523/c
/ Sequence 523, Application US/10156306
/ Publication No. US20030119017A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: McSwiggen, James
/ TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
/ TITLE OF INVENTION: Levels of IKK-Gamma and PKR
/ FILE REFERENCE: MBH01-664-A (400/050)
/ CURRENT APPLICATION NUMBER: US/10/156,306
/ CURRENT FILING DATE: 2002-05-28
/ NUMBER OF SEQ ID NOS: 8013
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 523
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-10-156-306-523

Query Match          0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAATAAAAAA 2588
Db 17 TTAAAAAATAAAAAA 3

RESULT 424
```

```
US-10-735-592-47
; Sequence 47, Application US/10735592
; Publication No. US2004017157A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70039US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; NUMBER OF SEQ ID NOS: 11
; PRIOR FILING DATE: 2003-12-11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-47

Query Match          0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2572 GTTTAAAAA 2586
Db 3 GTTTAAAAA 17

RESULT 425
US-09-775-479-8
; Sequence 8, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: MARTEL, Guy
; APPLICANT: LECLERC, Guy
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF PREPARATION AND
; FILE REFERENCE: 12168-IUS-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-8

Query Match          0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAA 2590
Db 3 AAAAAA 17

RESULT 426
US-09-725-265-20/c
; Sequence 20, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: YOICHI
```

```
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-20

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179
Db 18 ATATATATTTTCTTTC 1

RESULT 427
US-09-891-517-20/c
; Sequence 20, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS C
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA C
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-20

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179
Db 18 ATATATATTTTCTTTC 1
```

Db 18 ATATATATTTTTTTTTTC 1

## RESULT 428

US-09-969-373-2296

; Sequence 2296, Application US/09969373

; Patent No. US20020133852A1

; GENERAL INFORMATION:

; APPLICANT: Effertz, Roger J.

; APPLICANT: Haug, Brian M.

; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

; FILE REFERENCE: 38-10(52679)A

; CURRENT APPLICATION NUMBER: US/09/969,373

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 09/754,853

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US 09/760,427

; PRIOR FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US 09/855,768

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 2296

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Glycine max

US-09-969-373-2296

Query Match

Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2053 CACATCTCTGCTAATGT 2070

Db 1 CCCATCTCTGCTAGGT 18

## RESULT 429

US-09-904-744-3/c

; Sequence 3, Application US/09904744

; Patent No. US20020150905A1

; GENERAL INFORMATION:

; APPLICANT: Barbera-Guillem, Emilio

; APPLICANT: Nelson, M. Bud

; APPLICANT: Castro, Stephanie

; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form

; FILE REFERENCE: B-73

; CURRENT APPLICATION NUMBER: US/09/904,744

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: 09/437076

; PRIOR FILING DATE: 1999-11-09

; PRIOR APPLICATION NUMBER: 60/107828

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthesized

US-09-904-744-3

Query Match

Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCCCC 990

Db 18 CCCCCCCCCCCCCCCCC 1

## RESULT 430

US-09-949-305B-2

; Sequence 2, Application US/09949305B

; Publication No. US20030022318A1

; GENERAL INFORMATION:

; APPLICANT: Lin, Shi-Lung

; APPLICANT: Ying, Shao-yao

; TITLE OF INVENTION: Method for Thermocycling Amplification of Nucleic Acid Sequences

; FILE REFERENCE: 266/014

; CURRENT APPLICATION NUMBER: US/09/949,305B

; CURRENT FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: 09/494,212

; PRIOR FILING DATE: 2000-01-25

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 18

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: poly(C) primer

US-09-949-305B-2

Query Match

Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCCCC 990

Db 1 CCCCCCCCCCCCCCCCC 18

## RESULT 431

US-10-146-058-72/c

; Sequence 72, Application US/10146058

; Publication No. US20030040499A1

; GENERAL INFORMATION:

; APPLICANT: Schlengersiepen, Georg-Ferdinand

; APPLICANT: Brysach, Wolfgang

; APPLICANT: Schlengersiepen, Karl-Hermann

; APPLICANT: Schlengersiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS: 137

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/146,058

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/535,249

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)638-6666  
 TELEFAX: (202) 393-5350  
 TELEX: RCA 248593 IDEA UR  
 INFORMATION FOR SEQ ID NO: 72:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 ANTI-SENSE: YES  
 US-10-146-058-72

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1527 TATTAATCGATCGCG 1544  
 |||||  
 Db 18 TACAAATAGATCGCG 1

RESULT 432

US-10-146-058-79/c  
 Sequence 79, Application US/10146058  
 Publication No. US2003004099A1  
 GENERAL INFORMATION:  
 APPLICANT: Schlingensiepen, Georg-Ferdinand  
 APPLICANT: Brysch, Wolfgang  
 APPLICANT: Schlingensiepen, Karl-Hermann  
 APPLICANT: Schlingensiepen, Reimar  
 APPLICANT: Bogdahn, Ulrich  
 TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
 TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
 NUMBER OF SEQUENCES: 137  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Jacobson, Price, Holman & Stern  
 STREET: 400 Seventh St. N.W.  
 CITY: Washington D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/146,058  
 FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/535,249  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 93 107 089.0  
 FILING DATE: 30-APR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 93 107 849.7  
 FILING DATE: 13-MAY-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Player, William E.  
 REGISTRATION NUMBER: 31,409  
 REFERENCE/DOCKET NUMBER: 10577/P58418  
 TELEPHONE: (202)638-6666  
 TELEFAX: (202) 393-5350  
 TELEX: RCA 248593 IDEA UR  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown

TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 ANTI-SENSE: YES  
 US-10-146-058-79

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1636 ATGCTTCCAATCTGCTGA 1653  
 |||||  
 Db 18 ATGCTTCCAATTTGCTGA 1

RESULT 433

US-10-146-058-85/c  
 Sequence 85, Application US/10146058  
 Publication No. US20030040499A1  
 GENERAL INFORMATION:  
 APPLICANT: Schlingensiepen, Georg-Ferdinand  
 APPLICANT: Brysch, Wolfgang  
 APPLICANT: Schlingensiepen, Karl-Hermann  
 APPLICANT: Schlingensiepen, Reimar  
 APPLICANT: Bogdahn, Ulrich  
 TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
 TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
 NUMBER OF SEQUENCES: 137  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Jacobson, Price, Holman & Stern  
 STREET: 400 Seventh St. N.W.  
 CITY: Washington D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/146,058  
 FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/535,249  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 93 107 089.0  
 FILING DATE: 30-APR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 93 107 849.7  
 FILING DATE: 13-MAY-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Player, William E.  
 REGISTRATION NUMBER: 31,409  
 REFERENCE/DOCKET NUMBER: 10577/P58418  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)638-6666  
 TELEFAX: (202) 393-5350  
 TELEX: RCA 248593 IDEA UR  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 ANTI-SENSE: YES  
 US-10-146-058-85

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



QY 1711 GGATTGAACGTATCAGA 1728  
|||||  
Db 18 GGATTGAGCTATATCAGA 1

RESULT 434

US-10-146-058-96/c  
; Sequence 96, Application US/10146058  
; Publication No. US20030040499A1

GENERAL INFORMATION:

APPLICANT: Schlengersiepen, Georg-Ferdinand  
APPLICANT: Brysch, Wolfgang  
APPLICANT: Schlengersiepen, Karl-Hermann  
APPLICANT: Schlengersiepen, Reimar  
APPLICANT: Bogdahn, Ulrich

TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
NUMBER OF SEQUENCES: 137

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C.  
COUNTRY: U.S.A.  
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/146,058

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/535,249

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93 107 089.0

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93 107 849.7

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.

REGISTRATION NUMBER: 31,409

REFERENCE/DOCKET NUMBER: 10577/P58418

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)638-6666

TELEFAX: (202) 393-5350

TELEX: RCA 248593 IDEA UR

INFORMATION FOR SEQ ID NO: 96:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: YES

US-10-146-058-96

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1880 AATAAGTTTACACTGCC 1897

Db 18 AATAAGCTTACACTGCC 1

RESULT 435

US-10-146-058-115/c  
; Sequence 115, Application US/10146058  
; Publication No. US20030040499A1

GENERAL INFORMATION:  
APPLICANT: Schlengersiepen, Georg-Ferdinand  
APPLICANT: Brysch, Wolfgang  
APPLICANT: Schlengersiepen, Karl-Hermann  
APPLICANT: Schlengersiepen, Reimar  
APPLICANT: Bogdahn, Ulrich

TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
NUMBER OF SEQUENCES: 137

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C.  
COUNTRY: U.S.A.  
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/146,058

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/535,249

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93 107 089.0

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93 107 849.7

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Player, William E.

REGISTRATION NUMBER: 31,409

REFERENCE/DOCKET NUMBER: 10577/P58418

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)638-6666

TELEFAX: (202) 393-5350

TELEX: RCA 248593 IDEA UR

INFORMATION FOR SEQ ID NO: 115:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: YES

US-10-146-058-115

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2175 CGCCCTCTTTACATTGAT 2192

Db 18 CGTCCACTTACATTGAT 1

RESULT 436

US-10-146-058-128/c

; Sequence 128, Application US/10146058

; Publication No. US20030040499A1

GENERAL INFORMATION:

APPLICANT: Schlengersiepen, Georg-Ferdinand

APPLICANT: Brysch, Wolfgang

APPLICANT: Schlengersiepen, Karl-Hermann

APPLICANT: Schlengersiepen, Reimar

APPLICANT: Bogdahn, Ulrich

TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1

NUMBER OF SEQUENCES: 137

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jacobson, Price, Holman & Stern  
;; STREET: 400 Seventh St. N.W.  
;; CITY: Washington D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/146,058  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/535,249  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 089.0  
;; FILING DATE: 30-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/146,058  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/535,249  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 089.0  
;; FILING DATE: 30-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 849.7  
;; FILING DATE: 13-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Player, William E.  
;; REGISTRATION NUMBER: 31,409  
;; REFERENCE/DOCKET NUMBER: 10577/P58418  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 638-6666  
;; TELEFAX: (202) 393-5350  
;; TELEX: RCA 248593 IDEA UR  
;; INFORMATION FOR SEQ ID NO: 128:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: DNA (genomic)  
;; ANTI-SENSE: YES  
US-10-146-058-128

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2375 ACCACTGACCAATCTCTA 2392  
DB 18 ACCTCTAACCATTCTCTA 1

RESULT 437  
US-10-146-058-132/c  
; Sequence 132, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingsiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingsiepen, Karl-Hermann  
; APPLICANT: Schlingsiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/146,058  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/535,249  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 089.0  
;; FILING DATE: 30-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 849.7  
;; FILING DATE: 13-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Player, William E.  
;; REGISTRATION NUMBER: 31,409  
;; REFERENCE/DOCKET NUMBER: 10577/P58418  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 638-6666  
;; TELEFAX: (202) 393-5350  
;; TELEX: RCA 248593 IDEA UR  
;; INFORMATION FOR SEQ ID NO: 132:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: DNA (genomic)  
;; ANTI-SENSE: YES  
US-10-146-058-132

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2439 GTCAAGTCTTTGAAATGC 2456  
DB 18 GTAAAGTCTTGCAATGC 1

RESULT 438  
US-10-085-906-135/c  
; Sequence 135, Application US/10085906  
; Publication No. US20030054371A1  
; GENERAL INFORMATION:  
; APPLICANT: Ying, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
; FILE REFERENCE: GNM-5343CP2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/126,215  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 09/534,061  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PCT/US00/07938  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 135  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-906-135

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

; FILING DATE: 28-Jan-2003
; CLASSIFICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELETYPE: RCA 248593 IDEA UR
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: 1..18
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
;
US-10-352-704-24
;
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCACCCGCCGCC 990
Db 1 CCCCCCCCACCCGCCGCC 18

RESULT 441
US-10-220-033-4/c
; Sequence 4, Application US/10220033
; Publication No. US20030186906A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
; TITLE OF INVENTION: and a molecule binding to an expression product of that
; TITLE OF INVENTION: gene
; FILE REFERENCE: P68119US0
; CURRENT APPLICATION NUMBER: US/10/220,033
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: PCT/EP01/02694
; PRIOR FILING DATE: 2001-03-10
; PRIOR APPLICATION NUMBER: EP00105190.3
; PRIOR FILING DATE: 2000-03-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: oligonucleotide
US-10-220-033-4
;
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATGCCG 1544

```

```

Db      18 TACAAATAGACATGCG 1
      || ||||| ||||| |||||
RESULT 442
US-10-328-578-142/c
; Sequence 142, Application US/10328578
; Publication No. US20030225016A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE OF INVENTION: METHODS OF USING THE SAME-III
; FILE REFERENCE: 377882002020
; CURRENT FILING DATE: 2003-05-16
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2002-04-23
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-328-578-142

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      931 AAAAAAAAAACCACTT 948
      ||||| ||||| |||||
Db      18 AAAAAAAAAAAAAACCT 1

RESULT 443
US-10-297-068-282/c
; Sequence 282, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 282
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-282

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1162 ATATATATTTTCTTAC 1179
      ||||| ||||| |||||
Db      18 ATATATATTTTCTTTC 1

RESULT 445
US-10-623-371-142/c
; Sequence 142, Application US/10623371
; Publication No. US20040132677A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; APPLICANT: TUCK, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE OF INVENTION: METHODS OF USING THE SAME-IV
; FILE REFERENCE: 377882002021
; CURRENT FILING DATE: 2003-07-18
; PRIOR FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2914 CTGCAGTGGTGCCCTCC 2931
      ||||| ||||| ||||| ||
Db      18 CTGCAGTAGTGCCACC 1

RESULT 444
US-10-683-386-20/c
; Sequence 20, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; FILE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 0163-0758-0X
; CURRENT FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 1999-04-20
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-20

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1162 ATATATATTTTCTTAC 1179
      ||||| ||||| |||||
Db      18 ATATATATTTTCTTTC 1

RESULT 445
US-10-623-371-142/c
; Sequence 142, Application US/10623371
; Publication No. US20040132677A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; APPLICANT: TUCK, Stephen F.
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE OF INVENTION: METHODS OF USING THE SAME-IV
; FILE REFERENCE: 377882002021
; CURRENT FILING DATE: 2003-07-18
; PRIOR FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2002-06-21
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 142
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic construct
US-10-623-371-142

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACAACCTT 948
Db 18 AAAAAAAAAAAAAACCT 1

RESULT 446
US-10-849-072-22
; Sequence 22, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: High density labeling of DNA with modified or
; FILE OF INVENTION: "chromophore" carrying nucleotides and DNA polymerases
; FILE REFERENCE: 4780/00/WO
; CURRENT APPLICATION NUMBER: US/10/849,072
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: second
; OTHER INFORMATION: fragment of SEQ ID NO: 6
US-10-849-072-22

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCCGCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 447
US-10-849-072-24/c
; Sequence 24, Application US/10849072
; Publication No. US20040214221A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: High density labeling of DNA with modified or
; FILE OF INVENTION: "chromophore" carrying nucleotides and DNA polymerases
; FILE REFERENCE: 4780/00/WO
; CURRENT APPLICATION NUMBER: US/10/849,072
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: second
; OTHER INFORMATION: fragment of SEQ ID NO: 6
US-10-849-072-24

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCCGCCCC 990
Db 18 CCCCCCCCCCCCCCCCCC 1

Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCCGCCCC 990
Db 18 CCCCCCCCCCCCCCCCCC 1

RESULT 448
US-10-701-347-6
; Sequence 6, Application US/10701347
; Publication No. US20050026161A1
; GENERAL INFORMATION:
; APPLICANT: LEUCADIA TECHNOLOGIES, INC.
; TITLE OF INVENTION: DISPLACEMENT SANDWICH IMMUNO-PCR
; FILE REFERENCE: 45283.0002.UTL
; CURRENT APPLICATION NUMBER: US/10/701,347
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: 60/423,173
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-701-347-6

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2344 CTTCCCTTCTGTGTGT 2361
Db 1 CTTCCCTTCTGTGTGT 18

RESULT 449
US-10-701-347-11
; Sequence 11, Application US/10701347
; Publication No. US20050026161A1
; GENERAL INFORMATION:
; APPLICANT: LEUCADIA TECHNOLOGIES, INC.
; TITLE OF INVENTION: DISPLACEMENT SANDWICH IMMUNO-PCR
; FILE REFERENCE: 45283.0002.UTL
; CURRENT APPLICATION NUMBER: US/10/701,347
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: 60/423,173
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: PNA backbone
US-10-701-347-11

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2344 CTTCCCTTCTGTGTGT 2361
Db 1 CTTCCCTTCTGTGTGT 18
```

RESULT 450  
US-09-882-945A-280/c  
; Sequence 280, Application US/09882945A  
; Publication No. US2003014353A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 280  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-882-945A-280

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 TGGGAGAGAAAGAGAG 80  
Db 16 TGGGAGAGAAACAGAG 1  
|||||

RESULT 451  
US-10-146-058-94/c  
; Sequence 94, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.

REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-6666  
TELEFAX: (202)393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-10-146-058-94

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1851 CACCACAAAGACAGGA 1866  
Db 16 CACCATTAAGACAGGA 1  
|||||

RESULT 452  
US-10-146-058-107/c  
; Sequence 107, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202)393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-10-146-058-107

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2060 CCTGCTAATGTTGTTG 2075  
Db 16 CCTGCTAATGTTATTG 1

## RESULT 453

US-10-807-114-280/c  
; Sequence 280, Application US/10807114  
; Publication No. US20040235024A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/10/807,114  
; CURRENT FILING DATE: 2004-03-23  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 280  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-807-114-280

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 TGGGAGAGAAAGACAG 80  
Db 16 TGGGAGAGAAACACAG 1

## RESULT 454

US-10-156-306-526  
; Sequence 526, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; FILE REFERENCE: Levels of IKK-Gamma and PKR  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 526  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-526

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 25.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;  
QY 2745 TTTTNTTTTAAAGGA 2760  
Db 2 UUUUUUUUUUAAAGA 17

## RESULT 455

US-10-156-306-527  
; Sequence 527, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; FILE REFERENCE: Levels of IKK-Gamma and PKR  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 527  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-527

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 25.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAAAGGA 2760  
Db 1 UUUUUUUUUUAAAGA 16

## RESULT 456

US-09-780-533A-233  
; Sequence 233, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MHB00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 233  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-233

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 3.4e+02;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1587 AGACCTTACTTCAGAA 1602  
Db 2 AGAUCUACUUCAGAA 17

## RESULT 457

US-09-776-474-942  
; Sequence 942, Application US/09776474  
; Publication No. US20030087847A1

```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaev, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 942
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; US-09-776-474-942

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 932 AAAAAAAAAACAACCT 947
Db 1 AAAAAAAAAACAUAACU 16

RESULT 458
US-09-930-423-998
; Sequence 998, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 998
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
; US-09-930-423-998

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GGGCAGCGCTCAGGA 119
Db 1 GGGCAGCGCCAGGGA 16

RESULT 459
US-09-930-423-1179
; Sequence 1179, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 942
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
; US-09-930-423-1179

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GGGCAGCGCTCAGGA 119
Db 1 GGGCAGCGCCAGGGA 16

RESULT 460
US-09-745-237A-998
; Sequence 998, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 998
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-745-237A-998

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GGGCAGCGCTCAGGGA 119
Db 1 GGGCAGCGCCAGGGA 16

RESULT 461
US-09-745-237A-1179
; Sequence 1179, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-745-237A-1179

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 103 GGGCAGCGCTCAGGG 118
Db 2 GGGCAGCGCCAGGG 17

RESULT 462
US-09-745-237A-1179
; Sequence 1179, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-745-237A-1179

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 103 GGGCAGCGCTCAGGG 118
Db 2 GGGCAGCGCCAGGG 17
```



Db 2 GGGGAGGCCGCCAGG 17

## RESULT 462

US-10-041-856-35  
; Sequence 35, Application US/10041856  
; Publication No. US2002016929A1  
; GENERAL INFORMATION:  
; APPLICANT: SLAUGENHAUPT, SUSAN  
; APPLICANT: GUSELLA, JAMES F.  
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL  
; TITLE OF INVENTION: DYSAUTONOMIA  
; FILE REFERENCE: 1829-4004US1  
; CURRENT APPLICATION NUMBER: US/10/041,856  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: 60/260,080  
; PRIOR FILING DATE: 2001-01-06  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Mus sp.  
US-10-041-856-35

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2745 TTTTTCATTTTAAAGGA 2760  
|||||  
Db 2 TTTTTCATTTTTCAGGA 17

## RESULT 463

US-10-156-306-528/c  
; Sequence 528, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 528  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-528

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2570 GTCTTTAAAAA 2585  
|||  
Db 16 GTCTTTAAAAA 1

## RESULT 464

US-10-238-700-7  
; Sequence 7, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/057 (MBH01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700

; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-7

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 422 GCAGGCAGCAGCGCG 437  
|||  
Db 2 GGAGGCAGCAGCGCG 17

## RESULT 465

US-10-339-793-439/c  
; Sequence 439, Application US/10339793  
; Publication No. US20030180764A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Shang, Jin  
; APPLICANT: Bowen, Benjamin  
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS  
; FILE REFERENCE: 37-000310US  
; CURRENT APPLICATION NUMBER: US/10/339,793  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 443  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 439  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-339-793-439

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2138 CTACTGCTTTAGAAAT 2153  
|||||  
Db 17 CTACTGCTTTAGAGAT 2

## RESULT 466

US-10-138-674-1773  
; Sequence 1773, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1773  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-1773



```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1773
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1773

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1813 TCTCTTCGACGTGAC 1828
      :|::|::|::|::|::|
Db 2 UCUCUCCACGUGAC 17

RESULT 472
US-10-287-949A-3612/c
; Sequence 3612, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3612
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3612

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2666 ACAGCAACAACAACA 2681
      |||||
Db 17 ACAGCAACAACAACA 2

RESULT 473
US-10-287-949A-6425
; Sequence 6425, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 6425
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6425

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1813 TCTCTTCGACGTGAC 1828
      :|::|::|::|::|::|
Db 1 UCUCUCCACGUGAC 16

RESULT 474
US-10-287-949A-7146
; Sequence 7146, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7146
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7146

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 425 GGCAGCAGCGCGGCT 440
      |||||
Db 2 GGCAGCAGCGCGGCGCU 17

RESULT 475
US-10-287-949A-7538
; Sequence 7538, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7538
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7538

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 2671 AACAAACACCAAAA 2686  
Db 2 AAAAACACCAAAA 17

## RESULT 476

```

US-10-712-672-716/c
; Sequence 716, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 716
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-716

```

|                          |       |                    |        |            |
|--------------------------|-------|--------------------|--------|------------|
| Query Match              | 0.3%  | Score 14.4;        | DB 1;  | Length 17; |
| Best Local Similarity    | 93.8% | Pred. No. 3.4e+02; |        |            |
| Matches 15: Conservative | 0;    | Mismatches 1;      | Indels |            |

Qy 97 AGCTCTGGGCGCAGGCG 112  
Db 17 AGCGCTGGGCGCAGGCG 2

RESULT, T 477

```

US-10-712-672-717/c
; Sequence 717, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowirra, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 717
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-717

```

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 1. Indels

Qy 97 AGCTCTGGGCGAGGCG 112  
Db 16 AGCGTGGGCGAGGCG 1

RESULT 478

```

US-10-712-633-4
; Sequence 4, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEOTIC ACID BASED FOR THE TREATMENT OF HIV
; FILE REFERENCE: MEH02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US 10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-4

```

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.4e+02;  
Matches 14: Conservative 1; Mismatches 1; Indels

Qy 425 GGCAGCAGCGCGGCT 440  
 |||||  
 db 2 GGCAGCGCGCGGCU 17

## RESIN.T 479

```

US00-712-633-551
; Sequence 551, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MOLECULES
; TITLE OF INVENTION: RECEPTOR FOR THE PRESENTATION OF A LIGAND
; FILE REFERENCE: MHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772

```

```
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 551
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-551

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2671 AACACCAACCCACAAA 2686
Db 2 AAAAAACACCCACAAA 17

RESULT 480
US-10-498-462-47
; Sequence 47, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 47
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-47

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 616 CGCGCGGCACGCACG 631
Db 2 CGCGCGCACACGCACG 17

RESULT 481
US-10-498-462-48
; Sequence 48, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aeomica Sequence Listing Engine
```

```
; SEQ ID NO 48
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-48

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 616 CGCGCGGCACGCACG 631
Db 1 CGCGCGCACACGCACG 16

RESULT 482
US-09-725-265-15/c
; Sequence 15, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-15

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTCCT 1177
Db 18 ATATATATTTTTCCT 3

RESULT 483
US-09-725-265-16/c
; Sequence 16, Application US/09725265
; Publication No. US20010000175A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
```

; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-725-265-16

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
|||||  
Db 18 ATATATATTTT 3

RESULT 484  
US-09-725-265-17/c  
; Sequence 17, Application US/09725265  
; Publication No. US20010000175A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KANAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 199953USOXDIV  
; CURRENT APPLICATION NUMBER: US/09/725,265  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-725-265-17

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
|||||  
Db 18 ATATATATTTT 3

RESULT 485  
US-09-725-265-19/c  
; Sequence 19, Application US/09725265  
; Publication No. US20010000175A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KANAGATA, YOICHI

; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 199953USOXDIV  
; CURRENT APPLICATION NUMBER: US/09/725,265  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-725-265-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
|||||  
Db 18 ATATATATTTT 3

RESULT 486  
US-09-891-517-15/c  
; Sequence 15, Application US/09891517  
; Patent No. US20020106653A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KANAGATA, YOICHI  
; APPLICANT: TORIMURA, MASAKI  
; APPLICANT: KURATA, SHINYA  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS (C  
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA (C  
; TITLE OF INVENTION: METHOD  
; FILE REFERENCE: 210352US-1994-163-0-X  
; CURRENT APPLICATION NUMBER: US/09/891,517  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: JP2000-193133  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: JP2000-236115  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP2000-292483  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-09-891-517-15

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
|||||

Db 18 ATATATATTTTTTTT 3

RESULT 487

US-09-891-517-16/c

; Sequence 16, Application US/09891517

; Patent No. US20020106653A1

; GENERAL INFORMATION:

; APPLICANT: KURANE, RYUICHIRO

; APPLICANT: KANAGAWA, TAKAHIRO

; APPLICANT: KAWAGATA, YOICHI

; APPLICANT: TORIMURA, MASAKI

; APPLICANT: KURATA, SHINYA

; APPLICANT: YAMADA, KAZUTAKA

; APPLICANT: YOKOMAKU, TOYOKAZU

; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS

; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA

; TITLE OF INVENTION: METHOD

; FILE REFERENCE: 210352US-1994-163-0-X

; CURRENT APPLICATION NUMBER: US/09/891,517

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: JP2000-193133

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: JP2000-236115

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP2000-292483

; PRIOR FILING DATE: 2000-09-26

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic DNA

US-09-891-517-16

Query Match 0.3%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177

Db 18 ATATATATTTTTTTT 3

RESULT 488

US-09-891-517-17/c

; Sequence 17, Application US/09891517

; Patent No. US20020106653A1

; GENERAL INFORMATION:

; APPLICANT: KURANE, RYUICHIRO

; APPLICANT: KANAGAWA, TAKAHIRO

; APPLICANT: KAWAGATA, YOICHI

; APPLICANT: TORIMURA, MASAKI

; APPLICANT: KURATA, SHINYA

; APPLICANT: YAMADA, KAZUTAKA

; APPLICANT: YOKOMAKU, TOYOKAZU

; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS

; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA

; TITLE OF INVENTION: METHOD

; FILE REFERENCE: 210352US-1994-163-0-X

; CURRENT APPLICATION NUMBER: US/09/891,517

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: JP2000-193133

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: JP2000-236115

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP2000-292483

; PRIOR FILING DATE: 2000-09-26

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic DNA

US-09-891-517-17

Query Match 0.3%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177

Db 18 ATATATATTTTTTTT 3

RESULT 489

US-09-891-517-19/c

; Sequence 19, Application US/09891517

; Patent No. US20020106653A1

; GENERAL INFORMATION:

; APPLICANT: KURANE, RYUICHIRO

; APPLICANT: KANAGAWA, TAKAHIRO

; APPLICANT: KAWAGATA, YOICHI

; APPLICANT: TORIMURA, MASAKI

; APPLICANT: KURATA, SHINYA

; APPLICANT: YAMADA, KAZUTAKA

; APPLICANT: YOKOMAKU, TOYOKAZU

; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS

; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA

; TITLE OF INVENTION: METHOD

; FILE REFERENCE: 210352US-1994-163-0-X

; CURRENT APPLICATION NUMBER: US/09/891,517

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: JP2000-193133

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: JP2000-236115

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP2000-292483

; PRIOR FILING DATE: 2000-09-26

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic DNA

US-09-891-517-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177

Db 18 ATATATATTTTTTTT 3

RESULT 490

US-09-904-744-2/c

; Sequence 2, Application US/09904744

; Patent No. US20020150905A1

; GENERAL INFORMATION:

; APPLICANT: Barbera-Guillem, Emilio

; APPLICANT: Nelson, M. Bud

; APPLICANT: Castro, Stephanie

; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form

; TITLE OF INVENTION: dendrimers in a signal amplification system

; FILE REFERENCE: B-73

; CURRENT APPLICATION NUMBER: US/09/904,744

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: 09/437076

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic DNA

US-09-891-517-17

Query Match 0.3%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177

Db 18 ATATATATTTTTTTT 3

RESULT 489

US-09-891-517-19/c

; Sequence 19, Application US/09891517

; Patent No. US20020106653A1

; GENERAL INFORMATION:

; APPLICANT: KURANE, RYUICHIRO

; APPLICANT: KANAGAWA, TAKAHIRO

; APPLICANT: KAWAGATA, YOICHI

; APPLICANT: TORIMURA, MASAKI

; APPLICANT: KURATA, SHINYA

; APPLICANT: YAMADA, KAZUTAKA

; APPLICANT: YOKOMAKU, TOYOKAZU

; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS

; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA

; TITLE OF INVENTION: METHOD

; FILE REFERENCE: 210352US-1994-163-0-X

; CURRENT APPLICATION NUMBER: US/09/891,517

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: JP2000-193133

; PRIOR FILING DATE: 2000-06-27

; PRIOR APPLICATION NUMBER: JP2000-236115

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP2000-292483

; PRIOR FILING DATE: 2000-09-26

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic DNA

US-09-891-517-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177

Db 18 ATATATATTTTTTTT 3

RESULT 490

US-09-904-744-2/c

; Sequence 2, Application US/09904744

; Patent No. US20020150905A1

; GENERAL INFORMATION:

; APPLICANT: Barbera-Guillem, Emilio

; APPLICANT: Nelson, M. Bud

; APPLICANT: Castro, Stephanie

; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form

; TITLE OF INVENTION: dendrimers in a signal amplification system

; FILE REFERENCE: B-73

; CURRENT APPLICATION NUMBER: US/09/904,744

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: 09/437076

; PRIOR FILING DATE: 1999-11-09  
 ; PRIOR APPLICATION NUMBER: 60/107828  
 ; PRIOR FILING DATE: 1998-11-10  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthesized  
 US-09-904-744-2

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 931 AAAAAAAAAAAACC 946  
 Db 17 AAAAAAAAAAAACC 2

RESULT 491

US-09-961-077-1157  
 ; Sequence 1157, Application US/09961077  
 ; Publication No. US20030014775A1

; GENERAL INFORMATION:  
 ; APPLICANT: Zwick, Michael G.  
 ; Edington, Brent B.  
 ; McSwiggen, James A.  
 ; Merlo, Patricia Ann Owens  
 ; Guo, Lining  
 ; Skokut, Thomas A.  
 ; Young, Scott A.  
 ; Folkerts, Otto  
 ; Merlo, Donald J.  
 ; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
 ; MODULATION OF GENE EXPRESSION  
 ; IN PLANTS

; NUMBER OF SEQUENCES: 1263  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/961,077  
 ; FILING DATE: 21-Sep-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/679,645  
 ; FILING DATE: July 12, 1996  
 ; APPLICATION NUMBER: 60/001,135  
 ; FILING DATE: July 13, 1995  
 ; APPLICATION NUMBER: 08/300,726  
 ; FILING DATE: September 2, 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 219/247  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1157:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1157:  
 US-09-961-077-1157

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 81.2%; Pred. No. 3.8e+02;  
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 586 CTCCTCCGGCTCGCC 601  
 Db 2 CUCCCCGCCGCGCC 17

RESULT 492

US-09-994-311-7/c  
 ; Sequence 7, Application US/09994311  
 ; Publication No. US20030082556A1

; GENERAL INFORMATION:  
 ; APPLICANT: Kaufman, Joseph C.  
 ; APPLICANT: Roth, Matthew E.  
 ; APPLICANT: Lizardi, Paul M.  
 ; APPLICANT: Feng, Li  
 ; APPLICANT: Latimer, Darin R.  
 ; TITLE OF INVENTION: Binary Encoded Sequence Tags  
 ; FILE REFERENCE: AGL 100  
 ; CURRENT APPLICATION NUMBER: US/09/994,311  
 ; CURRENT FILING DATE: 2001-11-26  
 ; PRIOR APPLICATION NUMBER: US/09/637,751  
 ; PRIOR FILING DATE: 2000-08-11  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 7  
 ; LENGTH: 18  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-994-311-7  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACA 2816  
 Db 18 TGAATAAAAAAAAAACA 3

RESULT 493

US-10-077-383-27  
 ; Sequence 27, Application US/10077383  
 ; Publication No. US2003005044A1

; GENERAL INFORMATION:  
 ; APPLICANT: Haydock, Paul V.  
 ; APPLICANT: U'Ren, Jack  
 ; APPLICANT: Saigene Corporation  
 ; TITLE OF INVENTION: Nucleic Acid Amplification Using an RNA Polymerase and  
 ; DNA/RNA Mixed Polymer Intermediate Products  
 ; FILE REFERENCE: 018048-001710US  
 ; CURRENT APPLICATION NUMBER: US/10/077,383  
 ; CURRENT FILING DATE: 2002-02-15  
 ; PRIOR APPLICATION NUMBER: US 60/296,812  
 ; PRIOR FILING DATE: 2001-06-07  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 27  
 ; LENGTH: 18  
 ; TYPE: DNA



```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: spacer sequence
US-10-077-383-27
Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 GGGAGAGAGAGAGAGA 81
Db 1 GGGAGAGAGAGAGAGA 16

RESULT 494
US-10-209-608-15/c
; Sequence 15, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-15

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 495
US-10-209-608-16/c
; Sequence 16, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-15

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 496
US-10-209-608-17/c
; Sequence 17, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-17

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 497
US-10-209-608-19/c
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; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-16

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 496
US-10-209-608-17/c
; Sequence 17, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-17

Query Match          0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 497
US-10-209-608-19/c
```

; Sequence 19, Application US/10209608  
; Publication No. US20030082592A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KAMAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 199953U50XDIV  
; CURRENT APPLICATION NUMBER: US/10/209,608  
; CURRENT FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US/09/725,265  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-10-209-608-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
|||||  
18 ATATATATTTTCTT 3

Db 18 ATATATATTTTCTT 3

RESULT 498  
US-10-145-857-19  
; Sequence 19, Application US/10145857  
; Publication No. US20030092654A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-ALPHA EXPRESSION  
; FILE REFERENCE: RTSP-0117  
; CURRENT APPLICATION NUMBER: US/10/145,857  
; CURRENT FILING DATE: 2002-05-13  
; PRIOR APPLICATION NUMBER: US/09/856,074  
; PRIOR FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: US/09/197,360  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: US/09/856,074  
; PRIOR FILING DATE: 2001-05-17  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 19  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-145-857-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3727 TATTTATGTTGTC 3742  
|||||

Db 1 TATTTTATGTTATTC 16

RESULT 499  
US-10-683-386-15/c  
; Sequence 15, Application US/10683386  
; Publication No. US20040063137A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KAMAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/10/683,386  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US/09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-10-683-386-15

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
|||||  
18 ATATATATTTTCTT 3

Db 18 ATATATATTTTCTT 3

RESULT 500  
US-10-683-386-16/c  
; Sequence 16, Application US/10683386  
; Publication No. US20040063137A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KAMAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/10/683,386  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US/09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:

; OTHER INFORMATION: SYNTHETIC DNA  
US-10-683-386-16

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177  
| | | | | | | | | | | | | | | | | |  
Db 18 ATATATATTTTCTT 3

## RESULT 501

US-10-683-386-17/c  
; Sequence 17, Application US/10683386  
; Publication No. US20040063137A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KANAGAWA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/10/683,386  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US/09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-10-683-386-17

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177  
| | | | | | | | | | | | | | | | | |  
Db 18 ATATATATTTTCTT 3

## RESULT 502

US-10-683-386-19/c  
; Sequence 19, Application US/10683386  
; Publication No. US20040063137A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KANAGAWA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/10/683,386  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US/09/556,127  
; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-10-683-386-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177  
| | | | | | | | | | | | | | | | | |  
Db 18 ATATATATTTTCTT 3

## RESULT 503

US-10-473-126-652/c  
; Sequence 652, Application US/10473126  
; Publication No. US20040234973A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell  
; TITLE OF INVENTION: proliferative disorders  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/473,126  
; CURRENT FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 1258  
; SEQ ID NO 652  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Detection oligonucleotide for ELK1  
US-10-473-126-652

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 935 AAAAACAACCTTTC 950  
| | | | | | | | | | | | | | | | | |  
Db 16 AAAAACAACCTTTC 1

## RESULT 504

US-10-473-126-1066/c  
; Sequence 1066, Application US/10473126  
; Publication No. US20040234973A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell  
; TITLE OF INVENTION: proliferative disorders  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/473,126  
; CURRENT FILING DATE: 2003-09-26  
; NUMBER OF SEQ ID NOS: 1258  
; SEQ ID NO 1066  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Detection oligonucleotide for ELK1  
US-10-473-126-1066

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950  
Db 16 AAAAAACAACCTTC 1

RESULT 505  
US-10-872-984-7/c  
; Sequence 7, Application US/10872984  
; Publication No. US2004026588A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaufman, Joseph C.  
; APPLICANT: Roth, Matthew E.  
; APPLICANT: Lizardi, Paul M.  
; APPLICANT: Feng, Li  
; APPLICANT: Latimer, Darin R.  
; TITLE OF INVENTION: Binary Encoded Sequence Tags  
; FILE REFERENCE: AGL 100  
; CURRENT APPLICATION NUMBER: US/10/872,984  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: US/09/994,311  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-872-984-7

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAAGAAAAAACA 2816  
Db 18 TGAAGAAAAAACA 3

RESULT 506  
US-10-845-667-682  
; Sequence 682, Application US/10845667  
; Publication No. US20050026183A1  
; GENERAL INFORMATION:  
; APPLICANT: Fan, Jian-Bing  
; APPLICANT: Bibikova, Marina  
; TITLE OF INVENTION: Methods and Compositions For Diagnosing  
; FILE REFERENCE: 67234-091  
; CURRENT APPLICATION NUMBER: US/10/845,667  
; CURRENT FILING DATE: 2004-05-14  
; PRIOR FILING DATE: 2003-05-15  
; NUMBER OF SEQ ID NOS: 1506  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 682  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-845-667-682

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3772 TTCTCTCCCAACCCC 3787  
Db 1 TTCTCTCTCCCAACCCC 16

RESULT 507  
US-10-845-667-1432  
; Sequence 1432, Application US/10845667  
; Publication No. US20050026183A1  
; GENERAL INFORMATION:  
; APPLICANT: Fan, Jian-Bing  
; APPLICANT: Bibikova, Marina  
; TITLE OF INVENTION: Methods and Compositions For Diagnosing  
; FILE REFERENCE: 67234-091  
; CURRENT APPLICATION NUMBER: US/10/845,667  
; CURRENT FILING DATE: 2004-05-14  
; PRIOR FILING DATE: 2003-05-15  
; NUMBER OF SEQ ID NOS: 1506  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1432  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-845-667-1432

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.8e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3772 TTCTCTCCCAACCCC 3787  
Db 1 TTCTCTCTCCCAACCCC 16

RESULT 508  
US-10-719-900-164291/c  
; Sequence 164291, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 164291  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-164291

Query Match 0.3%; Score 14.4; DB 1; Length 25;  
Best Local Similarity 75.0%; Pred. No. 5.7e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3165 AAGCCCCAGCAACACGTGTCTGC 3188  
Db 25 AAGCTTCGCGAGTCACGTGTTCG 2

RESULT 509  
US-09-263-959-816/c  
; Sequence 816, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,959  
FILING DATE: 05-MAR-1999  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McWaters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 320010.426C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 816:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-263-959-816

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 GAGAGAAAGAGAGA 81  
Db 14 GAGAGAAAGAGAGA 1

RESULT 510  
US-10-146-058-57/c  
Sequence 57, Application US/10146058  
Publication No. US20030040499A1  
GENERAL INFORMATION:  
APPLICANT: Schlingensiepen, Georg-Ferdinand  
APPLICANT: Brysch, Wolfgang  
APPLICANT: Schlingensiepen, Karl-Hermann  
APPLICANT: Schlingensiepen, Reimar  
APPLICANT: Bogdahn, Ulrich  
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
NUMBER OF SEQUENCES: 137  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/146,058  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/535,249  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 089.0  
FILING DATE: 30-APR-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 393-5350  
TELEFAX: (202) 393-5350

APPLICATION NUMBER: EP 93 107 849.7  
FILING DATE: 13-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: DNA (genomic)  
MOLECULE TYPE: YES  
ANTI-SENSE: YES  
US-10-146-058-57

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1219 TGCACACTGTGTG 1232  
Db 14 TGCACACTGTGTG 1

RESULT 511  
US-10-146-058-63/c  
Sequence 63, Application US/10146058  
Publication No. US20030040499A1  
GENERAL INFORMATION:  
APPLICANT: Schlingensiepen, Georg-Ferdinand  
APPLICANT: Brysch, Wolfgang  
APPLICANT: Schlingensiepen, Karl-Hermann  
APPLICANT: Schlingensiepen, Reimar  
APPLICANT: Bogdahn, Ulrich  
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
NUMBER OF SEQUENCES: 137  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/146,058  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/535,249  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 089.0  
FILING DATE: 30-APR-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 393-5350  
TELEFAX: (202) 393-5350

Qy 1561 AAAATGCCATCCCG 1574  
pb 14 AAAATGCCATCCCG 1

RESULT 514  
 US-10-146-058-75/c  
 ; Sequence 75, Application US/10146058  
 ; Publication No. US20030040499A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlingsiepen, Georg-Ferdinand  
 ; APPLICANT: Brysch, Wolfgang  
 ; APPLICANT: Schlingsiepen, Karl-Hermann  
 ; APPLICANT: Schlingsiepen, Reimar  
 ; APPLICANT: Bogdahn, Ulrich  
 ; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
 ; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
 ; NUMBER OF SEQUENCES: 137  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Jacobson, Price, Holman & Stern  
 ; STREET: 400 Seventh St. N.W.  
 ; CITY: Washington D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/146,058  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/535,249  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 93 107 089.0  
 ; FILING DATE: 30-APR-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 93 107 849.7  
 ; FILING DATE: 13-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Player, William E.  
 ; REGISTRATION NUMBER: 31,409  
 ; REFERENCE/DOCKET NUMBER: 10577/P58418  
 ; TELEPHONE: (202) 638-6666  
 ; TELEFAX: (202) 393-5350  
 ; TELEX: RCA 248593 IDEA UR  
 ; INFORMATION FOR SEQ ID NO: 75:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: DNA (genomic)  
 ; MOLECULE TYPE: YES  
 ; ANTI-SENSE: YES  
 ; US-10-146-058-75

Query Match 0.3%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1575 CCCACTTTCTACAG 1588  
 Db 14 CCCACTTTCTACAG 1

RESULT 515  
 US-10-146-058-91/c  
 ; Sequence 91, Application US/10146058  
 ; Publication No. US20030040499A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlingsiepen, Georg-Ferdinand  
 ; APPLICANT: Brysch, Wolfgang  
 ; APPLICANT: Schlingsiepen, Karl-Hermann  
 ; APPLICANT: Schlingsiepen, Reimar  
 ; APPLICANT: Bogdahn, Ulrich  
 ; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
 ; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
 ; NUMBER OF SEQUENCES: 137  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Jacobson, Price, Holman & Stern  
 ; STREET: 400 Seventh St. N.W.

; APPLICANT: Schlingsiepen, Karl-Hermann  
 ; APPLICANT: Schlingsiepen, Reimar  
 ; APPLICANT: Bogdahn, Ulrich  
 ; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
 ; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
 ; NUMBER OF SEQUENCES: 137  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Jacobson, Price, Holman & Stern  
 ; STREET: 400 Seventh St. N.W.  
 ; CITY: Washington D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/146,058  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/535,249  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 93 107 089.0  
 ; FILING DATE: 30-APR-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 93 107 849.7  
 ; FILING DATE: 13-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Player, William E.  
 ; REGISTRATION NUMBER: 31,409  
 ; REFERENCE/DOCKET NUMBER: 10577/P58418  
 ; TELEPHONE: (202) 638-6666  
 ; TELEFAX: (202) 393-5350  
 ; TELEX: RCA 248593 IDEA UR  
 ; INFORMATION FOR SEQ ID NO: 91:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: DNA (genomic)  
 ; ANTI-SENSE: YES  
 ; US-10-146-058-91

Query Match 0.3%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1807 AATGGCTCTCCTTC 1820  
 Db 14 AATGGCTCTCCTTC 1

RESULT 516  
 US-10-146-058-101/c  
 ; Sequence 101, Application US/10146058  
 ; Publication No. US20030040499A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlingsiepen, Georg-Ferdinand  
 ; APPLICANT: Brysch, Wolfgang  
 ; APPLICANT: Schlingsiepen, Karl-Hermann  
 ; APPLICANT: Schlingsiepen, Reimar  
 ; APPLICANT: Bogdahn, Ulrich  
 ; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
 ; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
 ; NUMBER OF SEQUENCES: 137  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Jacobson, Price, Holman & Stern  
 ; STREET: 400 Seventh St. N.W.

;; CITY: Washington D.C  
;; COUNTRY: U.S.A.  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/146,058  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/535,249  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 089.0  
;; FILING DATE: 30-APR-1993  
;; NAME: Player, William E.  
;; REGISTRATION NUMBER: 31,409  
;; REFERENCE/DOCKET NUMBER: 10577/P58418  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)638-6666  
;; TELEX: RCA 248593 IDEA UR  
;; INFORMATION FOR SEQ ID NO: 101:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: DNA (genomic)  
;; ANTI-SENSE: YES  
US-10-146-058-101

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTTATTGGTGCAC 1984  
DB 14 GGTTATTGGTGCAC 1

RESULT 517  
US-10-146-058-103/c  
; Sequence 103, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/146,058  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/535,249  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 93 107 089.0  
;; FILING DATE: 30-APR-1993  
;; NAME: Player, William E.  
;; REGISTRATION NUMBER: 31,409  
;; REFERENCE/DOCKET NUMBER: 10577/P58418  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)638-6666  
;; TELEX: RCA 248593 IDEA UR  
;; INFORMATION FOR SEQ ID NO: 103:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: DNA (genomic)  
;; ANTI-SENSE: YES  
US-10-146-058-103

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 CAGTGGTGATCAGA 2010  
DB 14 CAGTGGTGATCAGA 1

RESULT 518  
US-10-146-058-106/c  
; Sequence 106, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993



;/ PRIOR APPLICATION DATA: EP 93 107 849.7  
;/ APPLICATION NUMBER: EP 93 107 849.7  
;/ FILING DATE: 13-MAY-1993  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Player, William E.  
;/ REGISTRATION NUMBER: 31,409  
;/ REFERENCE/DOCKET NUMBER: 10577/P58418  
;/ TELEPHONE: (202)638-6666  
;/ TELEFAX: (202) 393-5350  
;/ TELEX: RCA 248593 IDEA UR  
;/ INFORMATION FOR SEQ ID NO: 106:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 14 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: unknown  
;/ TOPOLOGY: unknown  
;/ MOLECULE TYPE: DNA (genomic)  
;/ ANTI-SENSE: YES  
US-10-146-058-106

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AAGACCCCATCT 2059  
Db 14 AAGACCCCATCT 1

RESULT 519  
US-10-146-058-122/c  
; Sequence 122, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666

;/ TELEFAX: (202) 393-5350  
;/ TELEX: RCA 248593 IDEA UR  
;/ INFORMATION FOR SEQ ID NO: 122:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 14 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: unknown  
;/ TOPOLOGY: unknown  
;/ MOLECULE TYPE: DNA (genomic)  
;/ ANTI-SENSE: YES  
US-10-146-058-122

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACACT 2291  
Db 14 GGAGTTCAGACACT 1

RESULT 520  
US-10-146-058-136/c  
; Sequence 136, Application US/10146058  
; Publication No. US20030040499A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/146,058  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/535,249  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
;/ INFORMATION FOR SEQ ID NO: 136:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 14 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: unknown  
;/ TOPOLOGY: unknown  
;/ MOLECULE TYPE: DNA (genomic)



TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic DNA  
US-10-468-753-48  
Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2575 TAAAAAAAAAAAAA 2588  
Db 14 TAAAAAAAAAAAAA 1

RESULT 525  
US-10-855-595-17/c  
Sequence 17, Application US/108555595  
Publication No. US20040235057A1  
GENERAL INFORMATION:  
APPLICANT: Petkovich, P. Martin, White, Jay A.,  
Beckett, Barbara R., Jones, Glenville  
TITLE OF INVENTION: Retinoid Metabolizing Protein  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5L 1A9  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/855,595  
FILING DATE: 28-May-2004  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/668,482  
FILING DATE: 25-Sep-2000  
APPLICATION NUMBER: 08/882,164  
FILING DATE: June 25, 1997  
APPLICATION NUMBER: 08/667,546  
FILING DATE: June 21, 1996  
APPLICATION NUMBER: 08/724,466  
FILING DATE: October 1, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 50767/00010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 17  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 17  
US-10-855-595-17  
Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2574 TAAAAAAAAAAAAA 2587  
Db 14 TAAAAAAAAAAAAA 1

6,306,624  
RESULT 526  
US-10-855-595-21/c  
Sequence 21, Application US/108555595  
Publication No. US20040235057A1  
GENERAL INFORMATION:  
APPLICANT: Petkovich, P. Martin, White, Jay A.,  
Beckett, Barbara R., Jones, Glenville  
TITLE OF INVENTION: Retinoid Metabolizing Protein  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5L 1A9  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/855,595  
FILING DATE: 28-May-2004  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/668,482  
FILING DATE: 25-Sep-2000  
APPLICATION NUMBER: 08/882,164  
FILING DATE: June 25, 1997  
APPLICATION NUMBER: 08/667,546  
FILING DATE: June 21, 1996  
APPLICATION NUMBER: 08/724,466  
FILING DATE: October 1, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 50767/00010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 21  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 21  
US-10-855-595-21  
Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2801 TGAIAAAAAAAAAA 2814  
Db 14 TGAIAAAAAAAAAA 1  
RESULT 527  
US-10-855-532-17/c  
Sequence 17, Application US/10855532  
Publication No. US20040259074A1  
GENERAL INFORMATION:  
APPLICANT: Petkovich, P. Martin, White, Jay A.,  
Beckett, Barbara R., Jones, Glenville  
TITLE OF INVENTION: Retinoid Metabolizing Protein  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada

ZIP: MSL 1A9  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA: US/10/855,532  
FILING DATE: 28-May-2004  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/668,482  
FILING DATE: 25-Sep-2000  
APPLICATION NUMBER: 08/882,164  
FILING DATE: June 25, 1997  
APPLICATION NUMBER: 08/667,546  
FILING DATE: June 21, 1996  
APPLICATION NUMBER: 08/724,466  
FILING DATE: October 1, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 50767/00010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 17  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 17  
US-10-855-532-17  
Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2574 TTAATAAAAAAAAAA 2587  
DB 14 TTAATAAAAAAAAAA 1  
RESULT 528  
US-10-855-532-21/c  
Sequence 21, Application US/10855532  
Publication No. US20040259074A1  
GENERAL INFORMATION:  
APPLICANT: Pekovich, P. Martin, White, Jay A.,  
Beckett, Barbara R., Jones, Glenville  
TITLE OF INVENTION: Retinoid Metabolizing Protein  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: MSL 1A9  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/855,532  
FILING DATE: 28-May-2004  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/668,482  
FILING DATE: 25-Sep-2000  
APPLICATION NUMBER: 08/882,164  
FILING DATE: June 25, 1997  
APPLICATION NUMBER: 08/667,546

FILING DATE: June 21, 1996  
APPLICATION NUMBER: 08/724,466  
FILING DATE: October 1, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 50767/00010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 21  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 21  
US-10-855-532-21  
Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2801 TGAATAAAAAAAAA 2814  
DB 14 TGAATAAAAAAAAA 1  
RESULT 529  
US-09-504-231A-321/c  
Sequence 321, Application US/09504231A  
Patent No. US20020013458A1  
GENERAL INFORMATION:  
APPLICANT: Blatt, Lawrence  
APPLICANT: McSwiggen, James  
APPLICANT: Roberts, Beth  
APPLICANT: Pavco, Pamela  
APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI  
FILE REFERENCE: rpi 247/282  
CURRENT APPLICATION NUMBER: US/09/504,231A  
CURRENT FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: 09/274,553  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3242  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 321  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-321  
Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3210 TGCCCAAGAGGCCT 3223  
DB 15 TGCCCAAGAGGCCT 2  
RESULT 530  
US-09-504-231A-322/c  
Sequence 322, Application US/09504231A

Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 322  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-322  
  
Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3210 TGCCCAAGGCCT 3223  
Db 14 TGCCCAAGGCCT 1  
  
RESULT 531  
US-09-274-553D-321/c  
; Sequence 321, Application US/09274553D  
; Patent No. US2002008225A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/274,553D  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3148  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 321  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553D-321

QY 3210 TGCCCAAGGCCT 3223  
Db 15 TGCCCAAGGCCT 2  
  
RESULT 532  
US-09-274-553D-322/c  
; Sequence 322, Application US/09274553D  
; Patent No. US2002008225A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; FILE REFERENCE: fpi 247/282  
; CURRENT APPLICATION NUMBER: US/09/274,553D  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3148  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 322  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553D-322  
  
Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3210 TGCCCAAGGCCT 3223  
Db 14 TGCCCAAGGCCT 1  
  
RESULT 533  
US-10-027-632-52311  
; Sequence 52311, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 52311
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52311

Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 ATTTCTTCTCTTA 885
   |||||
Db 1 ATTTCTTCTCTTA 14

RESULT 534
US-10-027-632-52311
; Sequence 52311, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52311
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52311

Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 872 ATTTCTTCTCTTA 885
   |||||
Db 1 ATTTCTTCTCTTA 14

RESULT 535
US-10-230-007B-17
; Sequence 17, Application US/10230007B
; Publication No. US20030170667A1
; GENERAL INFORMATION:
; APPLICANT: Kaytes, Paul
; APPLICANT: Teng, Chi-Hse
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Diagnostic for Schizophrenia
; FILE REFERENCE: 00458.PRO1
; CURRENT APPLICATION NUMBER: US/10/230,007B
; CURRENT FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA

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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-230-007B-17

Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3718 CCTGCGCTGTATTT 3731
   |||||
Db 1 CCTGCGCTGTATTT 14

RESULT 536
US-10-647-982A-17
; Sequence 17, Application US/10647982A
; Publication No. US20040115699A1
; GENERAL INFORMATION:
; APPLICANT: Kaytes, Paul
; APPLICANT: Teng, Chi-Hse
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Diagnostic for Schizophrenia
; FILE REFERENCE: 01313.PRO1
; CURRENT APPLICATION NUMBER: US/10/647,982A
; CURRENT FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-647-982A-17

Query Match      0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3718 CCTGCGCTGTATTT 3731
   |||||
Db 1 CCTGCGCTGTATTT 14

RESULT 537
US-10-041-856-35/c
; Sequence 35, Application US/10041856
; Publication No. US20020169299A1
; GENERAL INFORMATION:
; APPLICANT: SLAUGENHAUPT, SUSAN
; APPLICANT: GUSELLA, JAMES F.
; TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL
; TITLE OF INVENTION: DYSAUTONOMIA
; FILE REFERENCE: 1829-4004US1
; CURRENT APPLICATION NUMBER: US/10/041,856
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/260,080
; PRIOR FILING DATE: 2001-01-06
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Mus sp.
US-10-041-856-35

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814
   |||||
Db 14 TGAATAAAAAAAAAA 1

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RESULT 538  
US-09-090-672B-105/c  
; Sequence 105, Application US/09090672B  
; Patent No. US20020068707A1  
; GENERAL INFORMATION:  
; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,  
; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tateunari; Kuga, Tetsuro; Sawada,  
; APPLICANT: Shigenaga; Takei, Masami  
; TITLE OF INVENTION: Iga Nephropathy-Related Genes  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; ZIP: 10112-3801  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: Compaq PC  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect 8.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/090,672B  
; FILING DATE: 04-JUNE-1998  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP97/04468  
; FILING DATE: 03-DEC-1997  
; APPLICATION NUMBER: JP-8-325763  
; FILING DATE: 05-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perry, Lawrence S.  
; REGISTRATION NUMBER: 31865  
; REFERENCE/DOCKET NUMBER: 766.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 218-2100  
; TELEFAX: (212) 218-2200  
; INFORMATION FOR SEQ ID NO: 105:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid, synthetic DNA  
US-09-090-672B-105  
Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2575 TAAAAA-857/c  
Db 17 TAAAAA-857/c  
RESULT 539  
US-09-780-533A-857/c  
; Sequence 857, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MEH800,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2400  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-2400

6,828,428  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 857  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-857  
Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 565 GCGCTCCGGGCG 578  
Db 17 GCGCTCCGGGCG 4  
RESULT 540  
US-09-780-533A-2399/c  
; Sequence 2399, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MEH800,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2399  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-2399  
Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 565 GCGCTCCGGGCG 578  
Db 16 GCGCTCCGGGCG 3  
RESULT 541  
US-09-780-533A-2400/c  
; Sequence 2400, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MEH800,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2400  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-2400

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCGGCTCCGGGGCG 578  
DB 15 GCGGCTCCGGGGCG 2

RESULT 542  
US-09-730-559B-107/c  
; Sequence 107, Application US/09730559B  
; Publication No. US20030207828A1  
; GENERAL INFORMATION:  
; APPLICANT: ISHIWATA, TETSUYOSHI  
; APPLICANT: SAKURADA, MIKIRO  
; APPLICANT: KAWABATA, AYAKO  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: NISHI, TATSUNARI  
; APPLICANT: KUGA, TETSURO  
; APPLICANT: SAWADA, SHIGEMASA  
; APPLICANT: TAKEI, MASAMI  
; APPLICANT: SHIBATA, KENJI  
; APPLICANT: FURUYA, AKIKO  
; TITLE OF INVENTION: IGA NEPHROPATHY-ASSOCIATED GENE  
; FILE REFERENCE: 766.21 CIP  
; CURRENT APPLICATION NUMBER: US/09/730,559B  
; CURRENT FILING DATE: 2000-12-07  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
US-09-730-559B-107

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAATGA 2588  
DB 17 TAAAAAATAATGA 4

RESULT 543  
US-10-163-552-948/c  
; Sequence 948, Application US/10163552  
; Publication No. US20030105051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level  
; TITLE OF INVENTION: HER2  
; FILE REFERENCE: MBH01-1653-A (400/014)  
; CURRENT APPLICATION NUMBER: US/10/163,552  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 1997  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 948  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-163-552-948

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2362 CCCAGGATCTGGAA 2375

DB 16 CCCAGGATCTGGAA 3

RESULT 544  
US-10-156-306-522/c  
; Sequence 522, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 522  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-522

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAATGA 2588  
DB 17 TAAAAAATAATGA 4

RESULT 545  
US-10-156-306-631/c  
; Sequence 631, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBH01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 631  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-631

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3599 TTTTITTTTAAATGA 3612  
DB 17 TTTTITTTTAAATGA 4

RESULT 546  
US-10-061-201-2011/c  
; Sequence 2011, Application US/10061201  
; Publication No. US20030166229A1  
; GENERAL INFORMATION:  
; APPLICANT: Shanon, Mark  
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1  
; FILE REFERENCE: PB0178  
; CURRENT APPLICATION NUMBER: US/10/061,201  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666



```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2011
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-2011

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCCCTGCTG 1903
DB 17 CACTGCCCCCTGCTG 4

RESULT 547
US-10-061-201-2012/c
; Sequence 2012, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2012
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-2012
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Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCCCTGCTG 1903
DB 16 CACTGCCCCCTGCTG 3

RESULT 548
US-10-061-201-2013/c
; Sequence 2013, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2013
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-2013

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCCCTGCTG 1903
DB 15 CACTGCCCCCTGCTG 2

RESULT 549
US-10-061-201-2014/c
; Sequence 2014, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/328,205  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 4162  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 2014  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-061-201-2014

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCTGCTG 1903  
Db 14 CACTGCCCTGCTG 1

## RESULT 550

US-10-309-152A-3/c  
; Sequence 3, Application US/10309152A  
; Publication No. US20030175759A1  
; GENERAL INFORMATION:  
; APPLICANT: Hitachi Ltd.  
; TITLE OF INVENTION: A method for prediction of genes and a method for providing a list  
; FILE REFERENCE: H02001031A  
; CURRENT APPLICATION NUMBER: US/10/309,152A  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: JP 2002-047297  
; PRIOR FILING DATE: 2002-02-25  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Oligo-d(T) primer by Nippon Flour Mills  
US-10-309-152A-3

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588  
Db 17 TAAAAA 4

## RESULT 551

US-10-220-373-7/c  
; Sequence 7, Application US/10220373  
; Publication No. US20030180743A1  
; GENERAL INFORMATION:  
; APPLICANT: NAGASU, Takeshi  
; APPLICANT: OSHIDA, Tadashi  
; APPLICANT: OBAYASHI, Izumi  
; APPLICANT: MATSUI, Keiko  
; APPLICANT: SAITO, Hirohisa  
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASE  
; FILE REFERENCE: SH2-010US

; CURRENT APPLICATION NUMBER: US/10/220,373  
; CURRENT FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: JP 2000-61832  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Artificially  
; OTHER INFORMATION: Synthesized Primer Sequence  
US-10-220-373-7

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588  
Db 17 TAAAAA 4

## RESULT 552

US-10-291-808-63/c  
; Sequence 63, Application US/10291808  
; Publication No. US20030224382A1  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John  
; APPLICANT: Trenkle, Thomas  
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
; TITLE OF INVENTION: Using Same  
; FILE REFERENCE: P-PH 3457  
; CURRENT APPLICATION NUMBER: US/10/291,808  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US/09/300,958  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,331  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/098,070  
; PRIOR FILING DATE: 1998-08-27  
; PRIOR APPLICATION NUMBER: 60/118,624  
; PRIOR FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-291-808-63

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588  
Db 17 TAAAAA 4

## RESULT 553

US-10-380-255-6/c  
; Sequence 6, Application US/10380255  
; Publication No. US20040023263A1  
; GENERAL INFORMATION:  
; APPLICANT: Sugita et al.  
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES  
; FILE REFERENCE: 6235-64935  
; CURRENT APPLICATION NUMBER: US/10/380,255

; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: PCT/JP01/08247  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: JP 2000-293021  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:an artificially  
; OTHER INFORMATION: synthesized primer sequence  
US-10-380-255-6

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA-2588  
Db 17 TAAAAA-4

RESULT 554  
US-10-380-254-3/c  
; Sequence 3, Application US/10380254  
; Publication No. US2004003825A1  
; GENERAL INFORMATION:  
; APPLICANT: Sugita et al.  
; TITLE OF INVENTION: METHOD OF TESTING FOR ALLERGIC DISEASES  
; FILE REFERENCE: 6235-64773  
; CURRENT APPLICATION NUMBER: US/10/380,254  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: PCT/JP01/08246  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: JP 2000-291318  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:an artificially  
; OTHER INFORMATION: synthesized primer sequence  
US-10-380-254-3

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA-2588  
Db 17 TAAAAA-4

RESULT 555  
US-10-398-885A-2/c  
; Sequence 2, Application US/10398885A  
; Publication No. US20040053282A1  
; GENERAL INFORMATION:  
; APPLICANT: Sugita, Yuji  
; APPLICANT: Hashida, Ryoichi  
; APPLICANT: Ogawa, Kaoru  
; APPLICANT: Nagasu, Takeshi  
; APPLICANT: Obayashi, Masaya  
; APPLICANT: Saito, Hirohisa  
; APPLICANT: Takahashi, Eiki  
; TITLE OF INVENTION: Method of Testing For Allergic Diseases  
; FILE REFERENCE: SHIMIZU-07907

; CURRENT APPLICATION NUMBER: US/10/398,885A  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: PCT/JP01/08937  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: JP 2000-314093  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-398-885A-2

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA-2588  
Db 17 TAAAAA-4

RESULT 556  
US-10-398-877-18/c  
; Sequence 18, Application US/10398877  
; Publication No. US20040058351A1  
; GENERAL INFORMATION:  
; APPLICANT: Sugita, Yuji  
; APPLICANT: Hashida, Ryoichi  
; APPLICANT: Ogawa, Kaoru  
; APPLICANT: Nagasu, Takeshi  
; APPLICANT: Obayashi, Masaya  
; APPLICANT: Saito, Hirohisa  
; TITLE OF INVENTION: Method of Testing for Allergic Diseases  
; FILE REFERENCE: SHIMIZU-07906  
; CURRENT APPLICATION NUMBER: US/10/398,877  
; CURRENT FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP01/08574  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: JP 2000-314093  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-398-877-18

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA-2588  
Db 17 TAAAAA-4

RESULT 557  
US-10-239-734-3/c  
; Sequence 3, Application US/10239734  
; Publication No. US20040161746A1  
; GENERAL INFORMATION:  
; APPLICANT: GENOX RESEARCH, INC.  
; APPLICANT: JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF AGENCY OF NATIONAL CENTER FOR  
; APPLICANT: CHILD HEALTH AND DEVELOPMENT  
; APPLICANT: Matsumoto, Yoshiko  
; APPLICANT: Tsujimoto, Gozoh

```

; APPLICANT: Nagasu, Takeshi
; APPLICANT: Sugita, Yuji
; APPLICANT: Oshida, Tadahi
; APPLICANT: Imai, Yukiko
; TITLE OF INVENTION: Method of Testing For Allergic Disease
; FILE REFERENCE: SHIMIZU-07379
; CURRENT APPLICATION NUMBER: US/10/239,734
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/JP01/11286
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 2000-389476 JP
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: "Grt15A", an artificially synthesized primer sequence
US-10-239-734-3
```

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAAA 2588  
|||||

Db 17 TAAAAAATAAAAAA 4

RESULT 558

```

US-10-735-592-17/c
; Sequence 17, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-17
```

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2803 AAAAAAATAACA 2816  
|||||

Db 15 AAAAAAATAACA 2

RESULT 559

```

US-10-735-592-46
; Sequence 46, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
```

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-46
```

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAAA 2588  
|||||

Db 4 TAAAAAATAAAAAA 17

RESULT 560

```

US-10-735-592-56/c
; Sequence 56, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/735,592
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-592-56
```

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2803 AAAAAAATAACA 2816  
|||||

Db 15 AAAAAAATAACA 2

RESULT 561

```

US-10-608-863-3/c
; Sequence 3, Application US/10608863
; Publication No. US20040214192A1
; GENERAL INFORMATION:
; APPLICANT: Hashida, Ryoichi
; APPLICANT: Kagaya, Shinji
; APPLICANT: Yanoi, Yoshihiro
; APPLICANT: Sugita, Yuji
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: METHODS FOR EXAMINATION FOR ALLERGIC DISEASES, AND DRUGS FOR TREATING ALLERGIC DISEASES
; FILE REFERENCE: 3462.1003-000
; CURRENT APPLICATION NUMBER: US/10/608,863
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: JP 2002-188490
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially
```

OTHER INFORMATION: Synthesized Primer Sequence  
US-10-608-863-3

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAA 2588  
| | | | | | | | | | | | | | | | | | | | | |  
DB 17 TAAAAAATAAAAA 4

RESULT 562  
US-10-156-306-525  
; Sequence 525, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 525  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-525

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 17.6%; Pred. No. 4e+02;  
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 2743 TCTTTTCTTTTAAAGG 2759  
:  
DB 1 UUUUUUUUUUUUAAAG 17

RESULT 563  
US-10-156-306-523  
; Sequence 523, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 523  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-523

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 17.6%; Pred. No. 4e+02;  
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 2743 TCTTTTCTTTTAAAGG 2759  
:  
DB 1 UUUUUUUUUUUUAAAG 17

RESULT 562  
US-10-156-306-525  
; Sequence 525, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 525  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-525

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 17.6%; Pred. No. 4e+02;  
Matches 3; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 2741 CATCTTTTCTTTTAA 2757  
| :  
DB 1 CUUUUUUUUUUUUAA 17

RESULT 564  
US-10-735-592-47/c  
; Sequence 47, Application US/10735592

Publication No. US20040171571A1  
; GENERAL INFORMATION:  
; APPLICANT: Art, Krieg  
; APPLICANT: Joerg, Vollmer  
; TITLE OF INVENTION: 5' CPG Nucleic Acids and Methods of Use  
; FILE REFERENCE: C1037.70038US01  
; CURRENT APPLICATION NUMBER: US/10/735,592  
; CURRENT FILING DATE: 2003-12-11  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-735-592-47

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1032 TTTTCTTTTAAAGGA 1048  
| | | | | | | | | | | | | | | | | | | | | |  
DB 17 TTTTCTTTTAAAGGA 1

RESULT 565  
US-10-156-306-528  
; Sequence 528, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 528  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-528

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 29.4%; Pred. No. 4e+02;  
Matches 5; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTCTTTTAAAGGAA 2762  
:  
DB 1 UUUUUUUUUUUUAAAGCA 17

RESULT 566  
US-10-291-808-63  
; Sequence 63, Application US/10291808  
; Publication No. US20030224382A1  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John  
; APPLICANT: Trenkle, Thomas  
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
; TITLE OF INVENTION: Using Same  
; FILE REFERENCE: P-PH 3457  
; CURRENT APPLICATION NUMBER: US/10/291,808  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US/09/300,958  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,331  
; PRIOR FILING DATE: 1998-04-27

```
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-63
```

```
Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred.No.4e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3263 ATTTTTCCTTTTAA 3279
Db 1 ATTTTTCCTTTTAA 17
```

```
RESULT 567
US-09-775-479-9
; Sequence 9, Application US/09775479
; Publication No. US20040067197A1
; GENERAL INFORMATION:
; APPLICANT: LECLERC, Guy
; APPLICANT: MARTEL, R.m1
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 12168-IUS-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-9
```

```
Query Match      0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred.No.4.3e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTAA 3280
Db 1 TTTTTCCTTTTAA 17
```

Search completed: February 25, 2005, 09:49:58  
Job time : 28 secs

| Result No. | Score | Query |        | DB | ID               | Description          |
|------------|-------|-------|--------|----|------------------|----------------------|
|            |       | Match | Length |    |                  |                      |
| C          | 1     | 35.8  | 0.8    | 39 | 1                | US-08-486-057B-6     |
|            | 2     | 35.8  | 0.8    | 39 | 1                | US-08-789-588-6      |
|            | 3     | 34.2  | 0.8    | 39 | 1                | US-08-486-057B-7     |
|            | 4     | 34.2  | 0.8    | 39 | 1                | US-08-789-588-7      |
|            | 5     | 33    | 0.8    | 33 | 1                | US-09-750-401-29     |
| C          | 6     | 25    | 0.6    | 25 | 1                | US-09-750-401-31     |
|            | 7     | 25    | 0.6    | 25 | 1                | US-09-396-196G-60887 |
|            | 8     | 25    | 0.6    | 25 | 1                | US-09-396-196G-60888 |
|            | 9     | 25    | 0.6    | 25 | 1                | US-09-396-196G-60889 |
|            | 10    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60890 |
|            | 11    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60891 |
|            | 12    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60892 |
|            | 13    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60893 |
|            | 14    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60894 |
|            | 15    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60895 |
|            | 16    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60896 |
|            | 17    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60897 |
|            | 18    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60898 |
|            | 19    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60899 |
|            | 20    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60900 |
|            | 21    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60901 |
|            | 22    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60902 |
|            | 23    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60903 |
|            | 24    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60904 |
|            | 25    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60905 |
|            | 26    | 25    | 0.6    | 25 | 1                | US-09-396-196G-60906 |
|            | 27    | 22    | 0.5    | 22 | 1                | US-09-750-401-32     |
|            | 28    | 20    | 0.5    | 20 | 1                | US-09-380-662-8      |
|            | 29    | 20    | 0.5    | 20 | 1                | US-09-661-753-48     |
|            | 30    | 20    | 0.5    | 20 | 1                | US-09-661-753-49     |
|            | 31    | 20    | 0.5    | 20 | 1                | US-09-661-753-50     |
|            | 32    | 20    | 0.5    | 20 | 1                | US-09-661-753-51     |
| 33         | 20    | 0.5   | 20     | 1  | US-09-661-753-52 |                      |

|       |      |     |    |   |                     |                    |       |      |     |    |   |                     |                    |
|-------|------|-----|----|---|---------------------|--------------------|-------|------|-----|----|---|---------------------|--------------------|
| 107   | 16   | 0.4 | 16 | 1 | US-09-380-662-17    | Sequence 17, Appl  | C 180 | 14.8 | 0.3 | 18 | 1 | US-08-535-249-96    | Sequence 96, Appl  |
| C 108 | 16   | 0.4 | 16 | 1 | US-08-535-249-105   | Sequence 105, App  | C 181 | 14.8 | 0.3 | 18 | 1 | US-08-535-249-115   | Sequence 115, App  |
| C 109 | 16   | 0.4 | 16 | 1 | US-08-535-249-113   | Sequence 113, App  | C 182 | 14.8 | 0.3 | 18 | 1 | US-08-535-249-128   | Sequence 128, App  |
| C 110 | 16   | 0.4 | 17 | 1 | US-09-601-144-2     | Sequence 2, Appl   | C 183 | 14.8 | 0.3 | 18 | 1 | US-08-535-249-132   | Sequence 132, App  |
| C 111 | 16   | 0.4 | 18 | 1 | US-08-330-000-1     | Sequence 1, Appl   | C 184 | 14.8 | 0.3 | 18 | 1 | US-09-725-265-20    | Sequence 20, Appl  |
| C 112 | 16   | 0.4 | 18 | 1 | US-08-365-908-1     | Sequence 1, Appl   | C 185 | 14.8 | 0.3 | 18 | 1 | US-09-704-640-122   | Sequence 122, App  |
| C 113 | 16   | 0.4 | 19 | 1 | US-09-026-601-25    | Sequence 25, Appl  | C 186 | 14.8 | 0.3 | 18 | 1 | US-09-556-127-20    | Sequence 20, Appl  |
| C 114 | 16   | 0.4 | 20 | 1 | US-08-842-079-4     | Sequence 4, Appl   | C 187 | 14.8 | 0.3 | 18 | 1 | US-10-352-704-24    | Sequence 24, Appl  |
| C 115 | 16   | 0.4 | 20 | 1 | US-09-638-857-4     | Sequence 4, Appl   | C 188 | 14.8 | 0.3 | 18 | 1 | US-09-904-744-3     | Sequence 3, Appl   |
| C 116 | 16   | 0.4 | 24 | 1 | US-08-478-470-13    | Sequence 13, Appl  | C 189 | 14.8 | 0.3 | 18 | 1 | US-09-904-744-3     | Sequence 3, Appl   |
| C 117 | 16   | 0.4 | 24 | 1 | US-08-214-599-13    | Sequence 13, Appl  | C 190 | 14.8 | 0.3 | 18 | 1 | US-09-904-744-3     | Sequence 3, Appl   |
| C 118 | 16   | 0.4 | 24 | 1 | US-08-473-015-13    | Sequence 13, Appl  | C 191 | 14.8 | 0.3 | 18 | 1 | US-09-904-744-3     | Sequence 3, Appl   |
| C 119 | 16   | 0.4 | 24 | 1 | US-08-465-368-13    | Sequence 13, Appl  | C 192 | 14.4 | 0.3 | 16 | 1 | US-08-535-249-94    | Sequence 94, Appl  |
| C 120 | 16   | 0.4 | 24 | 1 | US-08-477-306-13    | Sequence 13, Appl  | C 193 | 14.4 | 0.3 | 16 | 1 | US-08-535-249-107   | Sequence 107, Appl |
| C 121 | 16   | 0.4 | 24 | 1 | US-08-700-448-13    | Sequence 13, Appl  | C 194 | 14.4 | 0.3 | 17 | 1 | US-08-050-073-155   | Sequence 155, App  |
| C 122 | 16   | 0.4 | 24 | 1 | US-08-923-386A-13   | Sequence 13, Appl  | C 195 | 14.4 | 0.3 | 17 | 1 | US-08-390-850-578   | Sequence 578, App  |
| C 123 | 15.8 | 0.4 | 19 | 1 | US-08-899-029-1     | Sequence 1, Appl   | C 196 | 14.4 | 0.3 | 17 | 1 | US-08-390-850-581   | Sequence 581, App  |
| C 124 | 15.8 | 0.4 | 19 | 1 | US-09-696-791-4067  | Sequence 4067, App | C 197 | 14.4 | 0.3 | 17 | 1 | US-08-373-124A-2153 | Sequence 2153, App |
| C 125 | 15.6 | 0.4 | 22 | 1 | US-09-750-401-32    | Sequence 32, Appl  | C 198 | 14.4 | 0.3 | 17 | 1 | US-08-373-124A-2159 | Sequence 2159, App |
| C 126 | 15.4 | 0.4 | 17 | 1 | US-08-390-850-579   | Sequence 579, App  | C 199 | 14.4 | 0.3 | 17 | 1 | US-08-373-124A-2161 | Sequence 2161, App |
| C 127 | 15.4 | 0.4 | 17 | 1 | US-08-390-850-580   | Sequence 580, App  | C 200 | 14.4 | 0.3 | 17 | 1 | US-08-435-634-578   | Sequence 578, App  |
| C 128 | 15.4 | 0.4 | 17 | 1 | US-08-373-124A-2155 | Sequence 2155, App | C 201 | 14.4 | 0.3 | 17 | 1 | US-08-435-634-581   | Sequence 581, App  |
| C 129 | 15.4 | 0.4 | 17 | 1 | US-08-373-124A-2157 | Sequence 2157, App | C 202 | 14.4 | 0.3 | 17 | 1 | US-08-435-628-2153  | Sequence 2153, App |
| C 130 | 15.4 | 0.4 | 17 | 1 | US-08-435-634-579   | Sequence 579, App  | C 203 | 14.4 | 0.3 | 17 | 1 | US-08-435-628-2159  | Sequence 2159, App |
| C 131 | 15.4 | 0.4 | 17 | 1 | US-08-435-634-580   | Sequence 580, App  | C 204 | 14.4 | 0.3 | 17 | 1 | US-08-435-628-2161  | Sequence 2161, App |
| C 132 | 15.4 | 0.4 | 17 | 1 | US-08-435-628-2155  | Sequence 2155, App | C 205 | 14.4 | 0.3 | 17 | 1 | US-08-173-489C-92   | Sequence 92, Appl  |
| C 133 | 15.4 | 0.4 | 17 | 1 | US-08-435-628-2157  | Sequence 2157, App | C 206 | 14.4 | 0.3 | 17 | 1 | US-08-173-489C-95   | Sequence 95, Appl  |
| C 134 | 15.4 | 0.4 | 18 | 1 | US-08-535-249-112   | Sequence 112, App  | C 207 | 14.4 | 0.3 | 17 | 1 | US-08-584-040-4006  | Sequence 4006, App |
| C 135 | 15.4 | 0.4 | 18 | 1 | US-09-288-679-3     | Sequence 3, Appl   | C 208 | 14.4 | 0.3 | 17 | 1 | US-08-584-040-7828  | Sequence 7828, App |
| C 136 | 15.4 | 0.4 | 18 | 1 | US-09-288-679-5     | Sequence 5, Appl   | C 209 | 14.4 | 0.3 | 17 | 1 | US-09-371-772B-1773 | Sequence 1773, App |
| C 137 | 15.4 | 0.4 | 18 | 1 | US-09-725-265-18    | Sequence 18, Appl  | C 210 | 14.4 | 0.3 | 17 | 1 | US-09-371-772B-3612 | Sequence 3612, App |
| C 138 | 15.4 | 0.4 | 18 | 1 | US-09-556-127-18    | Sequence 18, Appl  | C 211 | 14.4 | 0.3 | 17 | 1 | US-09-371-772B-6425 | Sequence 6425, App |
| C 139 | 15.4 | 0.4 | 19 | 1 | US-09-316-447A-3    | Sequence 3, Appl   | C 212 | 14.4 | 0.3 | 17 | 1 | US-09-685-664B-1773 | Sequence 1773, App |
| C 140 | 15.4 | 0.4 | 19 | 1 | US-09-727-532A-3    | Sequence 3, Appl   | C 213 | 14.4 | 0.3 | 17 | 1 | US-09-685-664B-3612 | Sequence 3612, App |
| C 141 | 15.4 | 0.4 | 19 | 1 | US-09-569-193A-3    | Sequence 3, Appl   | C 214 | 14.4 | 0.3 | 18 | 1 | US-09-197-360-19    | Sequence 19, Appl  |
| C 142 | 15.4 | 0.4 | 19 | 1 | US-10-057-812A-3    | Sequence 3, Appl   | C 215 | 14.4 | 0.3 | 18 | 1 | US-09-437-076-2     | Sequence 2, Appl   |
| C 143 | 15.4 | 0.4 | 19 | 1 | US-09-865-044-3     | Sequence 3, Appl   | C 216 | 14.4 | 0.3 | 18 | 1 | US-08-679-645-1157  | Sequence 1157, App |
| C 144 | 15.4 | 0.4 | 19 | 1 | US-09-696-791-3526  | Sequence 3526, App | C 217 | 14.4 | 0.3 | 18 | 1 | US-09-637-751A-7    | Sequence 7, Appl   |
| C 145 | 15.4 | 0.4 | 19 | 1 | US-09-696-791-3529  | Sequence 3529, App | C 218 | 14.4 | 0.3 | 18 | 1 | US-09-856-074B-19   | Sequence 19, Appl  |
| C 146 | 15.4 | 0.4 | 20 | 1 | US-09-687-246B-7    | Sequence 7, Appl   | C 219 | 14.4 | 0.3 | 18 | 1 | US-09-725-265-15    | Sequence 15, Appl  |
| C 147 | 15.4 | 0.4 | 20 | 1 | US-08-087-387-5     | Sequence 5, Appl   | C 220 | 14.4 | 0.3 | 18 | 1 | US-09-725-265-16    | Sequence 16, Appl  |
| C 148 | 15   | 0.4 | 15 | 1 | US-08-455-627-5     | Sequence 5, Appl   | C 221 | 14.4 | 0.3 | 18 | 1 | US-09-725-265-17    | Sequence 17, Appl  |
| C 149 | 15   | 0.4 | 15 | 1 | US-08-461-271-5     | Sequence 5, Appl   | C 222 | 14.4 | 0.3 | 18 | 1 | US-09-725-265-19    | Sequence 19, Appl  |
| C 150 | 15   | 0.4 | 15 | 1 | US-08-713-685A-5    | Sequence 5, Appl   | C 223 | 14.4 | 0.3 | 18 | 1 | US-09-556-127-15    | Sequence 15, Appl  |
| C 151 | 15   | 0.4 | 15 | 1 | US-08-689-856-5     | Sequence 5, Appl   | C 224 | 14.4 | 0.3 | 18 | 1 | US-09-556-127-16    | Sequence 16, Appl  |
| C 152 | 15   | 0.4 | 15 | 1 | US-08-689-856-5     | Sequence 5, Appl   | C 225 | 14.4 | 0.3 | 18 | 1 | US-09-556-127-17    | Sequence 17, Appl  |
| C 153 | 15   | 0.4 | 15 | 1 | US-08-863-639A-8    | Sequence 8, Appl   | C 226 | 14.4 | 0.3 | 18 | 1 | US-09-556-127-19    | Sequence 19, Appl  |
| C 154 | 15   | 0.4 | 15 | 1 | US-08-832-021-17    | Sequence 17, Appl  | C 227 | 14.4 | 0.3 | 18 | 1 | US-09-994-311-7     | Sequence 7, Appl   |
| C 155 | 15   | 0.4 | 15 | 1 | US-08-832-021-22    | Sequence 22, Appl  | C 228 | 14.4 | 0.3 | 18 | 1 | US-09-994-311-7     | Sequence 7, Appl   |
| C 156 | 15   | 0.4 | 15 | 1 | US-09-070-477-5     | Sequence 5, Appl   | C 229 | 14   | 0.3 | 14 | 1 | US-08-832-021-5     | Sequence 5, Appl   |
| C 157 | 15   | 0.4 | 15 | 1 | US-08-787-321-5     | Sequence 5, Appl   | C 230 | 14   | 0.3 | 14 | 1 | US-08-832-021-9     | Sequence 9, Appl   |
| C 158 | 14.8 | 0.3 | 18 | 1 | US-08-145-704-42    | Sequence 42, Appl  | C 231 | 14   | 0.3 | 14 | 1 | US-08-724-466B-17   | Sequence 17, Appl  |
| C 159 | 14.8 | 0.3 | 18 | 1 | US-08-145-704-43    | Sequence 43, Appl  | C 232 | 14   | 0.3 | 14 | 1 | US-08-724-466B-21   | Sequence 21, Appl  |
| C 160 | 14.8 | 0.3 | 18 | 1 | US-08-105-168B-21   | Sequence 21, Appl  | C 233 | 14   | 0.3 | 14 | 1 | US-08-882-164D-17   | Sequence 17, Appl  |
| C 161 | 14.8 | 0.3 | 18 | 1 | US-08-698-948-21    | Sequence 21, Appl  | C 234 | 14   | 0.3 | 14 | 1 | US-08-882-164D-21   | Sequence 21, Appl  |
| C 162 | 14.8 | 0.3 | 18 | 1 | US-08-358-556A-24   | Sequence 24, Appl  | C 235 | 14   | 0.3 | 14 | 1 | US-08-535-249-57    | Sequence 57, Appl  |
| C 163 | 14.8 | 0.3 | 18 | 1 | US-08-863-639A-15   | Sequence 15, Appl  | C 236 | 14   | 0.3 | 14 | 1 | US-08-535-249-63    | Sequence 63, Appl  |
| C 164 | 14.8 | 0.3 | 18 | 1 | US-08-863-639A-16   | Sequence 16, Appl  | C 237 | 14   | 0.3 | 14 | 1 | US-08-535-249-71    | Sequence 71, Appl  |
| C 165 | 14.8 | 0.3 | 18 | 1 | US-08-887-574-42    | Sequence 42, Appl  | C 238 | 14   | 0.3 | 14 | 1 | US-08-535-249-74    | Sequence 74, Appl  |
| C 166 | 14.8 | 0.3 | 18 | 1 | US-08-987-574-43    | Sequence 43, Appl  | C 239 | 14   | 0.3 | 14 | 1 | US-08-535-249-75    | Sequence 75, Appl  |
| C 167 | 14.8 | 0.3 | 18 | 1 | US-08-535-168-42    | Sequence 42, Appl  | C 240 | 14   | 0.3 | 14 | 1 | US-08-535-249-91    | Sequence 91, Appl  |
| C 168 | 14.8 | 0.3 | 18 | 1 | US-08-535-168-43    | Sequence 43, Appl  | C 241 | 14   | 0.3 | 14 | 1 | US-08-535-249-101   | Sequence 101, App  |
| C 169 | 14.8 | 0.3 | 18 | 1 | US-09-475-316A-122  | Sequence 122, App  | C 242 | 14   | 0.3 | 14 | 1 | US-08-535-249-103   | Sequence 103, App  |
| C 170 | 14.8 | 0.3 | 18 | 1 | US-09-437-076-3     | Sequence 3, Appl   | C 243 | 14   | 0.3 | 14 | 1 | US-08-535-249-106   | Sequence 106, App  |
| C 171 | 14.8 | 0.3 | 18 | 1 | US-09-017-974-42    | Sequence 42, Appl  | C 244 | 14   | 0.3 | 14 | 1 | US-08-535-249-122   | Sequence 122, App  |
| C 172 | 14.8 | 0.3 | 18 | 1 | US-09-017-974-43    | Sequence 43, Appl  | C 245 | 14   | 0.3 | 14 | 1 | US-08-535-249-136   | Sequence 136, App  |
| C 173 | 14.8 | 0.3 | 18 | 1 | US-08-682-255A-42   | Sequence 42, Appl  | C 246 | 14   | 0.3 | 14 | 1 | US-09-475-947A-310  | Sequence 310, App  |
| C 174 | 14.8 | 0.3 | 18 | 1 | US-08-682-255A-43   | Sequence 43, Appl  | C 247 | 14   | 0.3 | 15 | 1 | US-08-182-968A-299  | Sequence 299, App  |
| C 175 | 14.8 | 0.3 | 18 | 1 | US-09-429-130-42    | Sequence 42, Appl  | C 248 | 14   | 0.3 | 15 | 1 | US-08-182-968A-300  | Sequence 300, App  |
| C 176 | 14.8 | 0.3 | 18 | 1 | US-09-429-130-43    | Sequence 43, Appl  | C 249 | 14   | 0.3 | 15 | 1 | US-08-292-620A-359  | Sequence 359, App  |
| C 177 | 14.8 | 0.3 | 18 | 1 | US-08-535-249-72    | Sequence 72, Appl  | C 250 | 14   | 0.3 | 15 | 1 | US-08-292-620A-360  | Sequence 360, App  |
| C 178 | 14.8 | 0.3 | 18 | 1 | US-08-535-249-79    | Sequence 79, Appl  | C 251 | 14   | 0.3 | 15 | 1 | US-08-292-620A-364  | Sequence 364, App  |
| C 179 | 14.8 | 0.3 | 18 | 1 | US-08-535-249-85    | Sequence 85, Appl  | C 252 | 14   | 0.3 | 15 | 1 | US-08-292-620A-365  | Sequence 365, App  |



|       |      |     |    |   |                     |                   |       |      |     |    |   |                      |                    |
|-------|------|-----|----|---|---------------------|-------------------|-------|------|-----|----|---|----------------------|--------------------|
| C 253 | 14   | 0.3 | 15 | 1 | US-08-774-306A-299  | Sequence 299, App | C 326 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-5582  | Sequence 5582, Ap  |
| C 254 | 14   | 0.3 | 15 | 1 | US-08-774-306A-300  | Sequence 300, App | C 327 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-5583  | Sequence 5583, Ap  |
| C 255 | 14   | 0.3 | 15 | 1 | US-08-886-456-1     | Sequence 1, Appli | C 328 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-6814  | Sequence 6814, Ap  |
| C 256 | 14   | 0.3 | 15 | 1 | US-08-832-021-18    | Sequence 18, Appl | C 329 | 13.8 | 0.3 | 17 | 1 | US-09-597-731-7      | Sequence 7, Appli  |
| C 257 | 14   | 0.3 | 15 | 1 | US-08-832-021-19    | Sequence 19, Appl | C 330 | 13.8 | 0.3 | 17 | 1 | US-09-476-387-756    | Sequence 756, App  |
| C 258 | 14   | 0.3 | 15 | 1 | US-08-832-021-19    | Sequence 19, Appl | C 331 | 13.8 | 0.3 | 17 | 1 | US-09-401-063-647    | Sequence 647, App  |
| C 259 | 14   | 0.3 | 15 | 1 | US-08-832-021-20    | Sequence 20, Appl | C 332 | 13.8 | 0.3 | 17 | 1 | US-09-866-108A-243   | Sequence 243, App  |
| C 260 | 14   | 0.3 | 15 | 1 | US-08-832-021-21    | Sequence 21, Appl | C 333 | 13.8 | 0.3 | 17 | 1 | US-09-866-108A-1065  | Sequence 1065, Ap  |
| C 261 | 14   | 0.3 | 15 | 1 | US-08-832-021-21    | Sequence 21, Appl | C 334 | 13.8 | 0.3 | 17 | 1 | US-09-866-108A-1066  | Sequence 1066, Ap  |
| C 262 | 14   | 0.3 | 15 | 1 | US-08-832-021-23    | Sequence 23, Appl | C 335 | 13.8 | 0.3 | 17 | 1 | US-09-866-108A-2222  | Sequence 2222, Ap  |
| C 263 | 14   | 0.3 | 15 | 1 | US-08-832-021-24    | Sequence 24, Appl | C 336 | 13.8 | 0.3 | 17 | 1 | US-09-866-108A-8557  | Sequence 8557, Ap  |
| C 264 | 14   | 0.3 | 15 | 1 | US-09-064-156A-299  | Sequence 299, App | C 337 | 13.8 | 0.3 | 17 | 1 | US-09-866-108A-9226  | Sequence 9226, Ap  |
| C 265 | 14   | 0.3 | 15 | 1 | US-09-064-156A-300  | Sequence 300, App | C 338 | 13.8 | 0.3 | 17 | 1 | US-09-866-108A-10508 | Sequence 10508, A  |
| C 266 | 14   | 0.3 | 15 | 1 | US-09-071-845-359   | Sequence 359, App | C 339 | 13.8 | 0.3 | 17 | 1 | US-09-866-108A-10509 | Sequence 10509, A  |
| C 267 | 14   | 0.3 | 15 | 1 | US-09-071-845-360   | Sequence 360, App | C 340 | 13.8 | 0.3 | 17 | 1 | US-09-129-603-4      | Sequence 4, Appli  |
| C 268 | 14   | 0.3 | 15 | 1 | US-09-071-845-364   | Sequence 364, App | C 341 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-235   | Sequence 235, App  |
| C 269 | 14   | 0.3 | 15 | 1 | US-09-071-845-365   | Sequence 365, App | C 342 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-731   | Sequence 731, App  |
| C 270 | 14   | 0.3 | 16 | 1 | US-08-242-664-30    | Sequence 30, Appl | C 343 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-860   | Sequence 860, App  |
| C 271 | 14   | 0.3 | 16 | 1 | US-08-484-138-30    | Sequence 30, Appl | C 344 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1068  | Sequence 1068, Ap  |
| C 272 | 14   | 0.3 | 16 | 1 | PCT-US95-06379-30   | Sequence 30, Appl | C 345 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1069  | Sequence 1069, Ap  |
| C 273 | 14   | 0.3 | 17 | 1 | US-09-300-958A-63   | Sequence 63, Appl | C 346 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1070  | Sequence 1070, Ap  |
| C 274 | 13.8 | 0.3 | 17 | 1 | US-09-090-672B-105  | Sequence 105, App | C 347 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1071  | Sequence 1071, Ap  |
| C 275 | 13.8 | 0.3 | 17 | 1 | US-09-300-958A-63   | Sequence 63, Appl | C 348 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1075  | Sequence 1075, Ap  |
| C 276 | 13.8 | 0.3 | 17 | 1 | US-08-281-940-54    | Sequence 54, Appl | C 349 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1076  | Sequence 1076, Ap  |
| C 277 | 13.8 | 0.3 | 17 | 1 | US-08-758-306-1333  | Sequence 1333, Ap | C 350 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1080  | Sequence 1080, Ap  |
| C 278 | 13.8 | 0.3 | 17 | 1 | US-08-710-134-54    | Sequence 54, Appl | C 351 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1251  | Sequence 1251, Ap  |
| C 279 | 13.8 | 0.3 | 17 | 1 | US-08-485-885-54    | Sequence 54, Appl | C 352 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1772  | Sequence 1772, Ap  |
| C 280 | 13.8 | 0.3 | 17 | 1 | US-08-985-162-647   | Sequence 647, App | C 353 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-1781  | Sequence 1781, Ap  |
| C 281 | 13.8 | 0.3 | 17 | 1 | US-08-998-099-52    | Sequence 52, Appl | C 354 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-2067  | Sequence 2067, Ap  |
| C 282 | 13.8 | 0.3 | 17 | 1 | US-09-135-020-7     | Sequence 7, Appli | C 355 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-2453  | Sequence 2453, Ap  |
| C 283 | 13.8 | 0.3 | 17 | 1 | US-09-444-871-7     | Sequence 7, Appli | C 356 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-2800  | Sequence 2800, Ap  |
| C 284 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-1690  | Sequence 1690, Ap | C 357 | 13.8 | 0.3 | 17 | 1 | US-09-685-664B-3418  | Sequence 3418, Ap  |
| C 285 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2186  | Sequence 2186, Ap | C 358 | 13.8 | 0.3 | 17 | 1 | US-09-090-672B-107   | Sequence 107, Appl |
| C 286 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2315  | Sequence 2315, Ap | C 359 | 13.8 | 0.3 | 33 | 1 | US-09-750-401-29     | Sequence 29, Appl  |
| C 287 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2544  | Sequence 2544, Ap | C 360 | 13.6 | 0.3 | 16 | 1 | US-08-882-649A-8     | Sequence 8, Appli  |
| C 288 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2545  | Sequence 2545, Ap | C 361 | 13.6 | 0.3 | 16 | 1 | US-09-644-827B-10    | Sequence 10, Appl  |
| C 289 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2546  | Sequence 2546, Ap | C 362 | 13.4 | 0.3 | 15 | 1 | US-08-363-240A-33    | Sequence 33, Appl  |
| C 290 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2547  | Sequence 2547, Ap | C 363 | 13.4 | 0.3 | 15 | 1 | US-08-292-620A-356   | Sequence 356, App  |
| C 291 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2551  | Sequence 2551, Ap | C 364 | 13.4 | 0.3 | 15 | 1 | US-08-292-620A-357   | Sequence 357, App  |
| C 292 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2552  | Sequence 2552, Ap | C 365 | 13.4 | 0.3 | 15 | 1 | US-08-292-620A-358   | Sequence 358, App  |
| C 293 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2556  | Sequence 2556, Ap | C 366 | 13.4 | 0.3 | 15 | 1 | US-08-292-620A-363   | Sequence 363, App  |
| C 294 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-2727  | Sequence 2727, Ap | C 367 | 13.4 | 0.3 | 15 | 1 | US-08-292-620A-366   | Sequence 366, App  |
| C 295 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-4005  | Sequence 4005, Ap | C 368 | 13.4 | 0.3 | 15 | 1 | US-08-585-684B-824   | Sequence 824, App  |
| C 296 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-4014  | Sequence 4014, Ap | C 369 | 13.4 | 0.3 | 15 | 1 | US-08-585-684B-825   | Sequence 825, App  |
| C 297 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-4300  | Sequence 4300, Ap | C 370 | 13.4 | 0.3 | 15 | 1 | US-08-585-684B-1392  | Sequence 1392, Ap  |
| C 298 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-5563  | Sequence 5563, Ap | C 371 | 13.4 | 0.3 | 15 | 1 | US-08-879-457-2      | Sequence 2, Appli  |
| C 299 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-5963  | Sequence 5963, Ap | C 372 | 13.4 | 0.3 | 15 | 1 | US-08-893-204C-2     | Sequence 2, Appli  |
| C 300 | 13.8 | 0.3 | 17 | 1 | US-08-584-040-7626  | Sequence 7626, Ap | C 373 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-25     | Sequence 25, Appl  |
| C 301 | 13.8 | 0.3 | 17 | 1 | US-08-679-645-878   | Sequence 878, App | C 374 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-26     | Sequence 26, Appl  |
| C 302 | 13.8 | 0.3 | 17 | 1 | US-09-597-735-7     | Sequence 7, Appli | C 375 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-29     | Sequence 29, Appl  |
| C 303 | 13.8 | 0.3 | 17 | 1 | US-09-444-295-7     | Sequence 7, Appli | C 376 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-34     | Sequence 34, Appl  |
| C 304 | 13.8 | 0.3 | 17 | 1 | US-09-597-732-7     | Sequence 7, Appli | C 377 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-36     | Sequence 36, Appl  |
| C 305 | 13.8 | 0.3 | 17 | 1 | US-09-475-947A-118  | Sequence 118, App | C 378 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-41     | Sequence 41, Appl  |
| C 306 | 13.8 | 0.3 | 17 | 1 | US-09-474-432B-757  | Sequence 757, App | C 379 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-43     | Sequence 43, Appl  |
| C 307 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-235  | Sequence 235, App | C 380 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-46     | Sequence 46, Appl  |
| C 308 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-731  | Sequence 731, App | C 381 | 13.4 | 0.3 | 15 | 1 | US-08-832-021-58     | Sequence 58, Appl  |
| C 309 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-860  | Sequence 860, App | C 382 | 13.4 | 0.3 | 15 | 1 | US-08-675-119-2      | Sequence 2, Appli  |
| C 310 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1068 | Sequence 1068, Ap | C 383 | 13.4 | 0.3 | 15 | 1 | US-08-851-843A-43    | Sequence 43, Appl  |
| C 311 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1069 | Sequence 1069, Ap | C 384 | 13.4 | 0.3 | 15 | 1 | US-08-851-843A-45    | Sequence 45, Appl  |
| C 312 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1071 | Sequence 1071, Ap | C 385 | 13.4 | 0.3 | 15 | 1 | US-09-071-845-356    | Sequence 356, App  |
| C 313 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1071 | Sequence 1071, Ap | C 386 | 13.4 | 0.3 | 15 | 1 | US-09-071-845-357    | Sequence 357, App  |
| C 314 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1075 | Sequence 1075, Ap | C 387 | 13.4 | 0.3 | 15 | 1 | US-09-071-845-358    | Sequence 358, App  |
| C 315 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1076 | Sequence 1076, Ap | C 388 | 13.4 | 0.3 | 15 | 1 | US-09-071-845-363    | Sequence 363, App  |
| C 316 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1080 | Sequence 1080, Ap | C 389 | 13.4 | 0.3 | 15 | 1 | US-09-071-845-366    | Sequence 366, App  |
| C 317 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1251 | Sequence 1251, Ap | C 390 | 13.4 | 0.3 | 15 | 1 | US-08-974-549A-113   | Sequence 113, App  |
| C 318 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1772 | Sequence 1772, Ap | C 391 | 13.4 | 0.3 | 15 | 1 | US-09-038-073-824    | Sequence 824, App  |
| C 319 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-1781 | Sequence 1781, Ap | C 392 | 13.4 | 0.3 | 15 | 1 | US-09-038-073-825    | Sequence 825, App  |
| C 320 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-2067 | Sequence 2067, Ap | C 393 | 13.4 | 0.3 | 15 | 1 | US-09-038-073-1392   | Sequence 1392, Ap  |
| C 321 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-2453 | Sequence 2453, Ap | C 394 | 13.4 | 0.3 | 15 | 1 | US-08-854-050-43     | Sequence 43, Appl  |
| C 322 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-2800 | Sequence 2800, Ap | C 395 | 13.4 | 0.3 | 15 | 1 | US-08-854-050-45     | Sequence 45, Appl  |
| C 323 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-3418 | Sequence 3418, Ap | C 396 | 13.4 | 0.3 | 15 | 1 | US-09-430-323-43     | Sequence 43, Appl  |
| C 324 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-5235 | Sequence 5235, Ap | C 397 | 13.4 | 0.3 | 15 | 1 | US-09-430-323-45     | Sequence 45, Appl  |
| C 325 | 13.8 | 0.3 | 17 | 1 | US-09-371-772B-5435 | Sequence 5435, Ap | C 398 | 13.4 | 0.3 | 15 | 1 |                      |                    |

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450 12.8 0.3 39 1 US-08-789-588-6 Sequence 6, Appli  
451 12.6 0.3 20 1 US-09-725-265-42 Sequence 42, Appl  
452 12.6 0.3 20 1 US-09-823-634A-13 Sequence 13, Appl  
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457 12.6 0.3 21 1 US-09-009-913-100 Sequence 100, App  
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468 12.4 0.3 15 1 US-08-832-021-41 Sequence 41, Appl  
469 12.4 0.3 15 1 US-09-071-845-366 Sequence 366, App  
470 12.4 0.3 17 1 US-08-584-040-2186 Sequence 2186, App  
471 12.4 0.3 17 1 US-09-371-772B-731 Sequence 731, App

472 12.4 0.3 17 1 US-09-685-664B-731 Sequence 731, App  
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474 12.4 0.3 18 1 US-08-965-908-1 Sequence 1, Appli  
475 12.4 0.3 18 1 US-09-725-265-17 Sequence 17, Appl  
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ALIGNMENTS

RESULT 1  
US-08-486-057B-6  
; Sequence 6, Application US/08486057B  
; Patent No. 5650494  
; GENERAL INFORMATION:  
; APPLICANT: Cerletti, Nico  
; APPLICANT: McMaster, Gary K.  
; APPLICANT: Cox, David  
; APPLICANT: Schmitz, Albert  
; APPLICANT: Meyhack, Bernd  
; TITLE OF INVENTION: Process for Refolding Recombinantly  
; TITLE OF INVENTION: Produced TGF-beta-like Proteins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry P. No. 5650494ak  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,057B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/201,703  
; FILING DATE: 25-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,309  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/621,502  
; FILING DATE: 03-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8927546.5  
; FILING DATE: 06-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5650494ak, Henry P.  
; REGISTRATION NUMBER: 33200  
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 277-5110  
; TELEFAX: (908) 277-4306  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-486-057B-6

Query Match 0.8%; Score 35.8; DB 1; Length 39;  
Best Local Similarity 94.9%; Pred. No. 0.63;  
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GCTTGGATGGCGCTATTGCTTTAGAAATGTCAGGAT 39

## RESULT 2

US-08-789-588-6

; Sequence 6, Application US/08789588

; Patent No. 5922846

; GENERAL INFORMATION:

; APPLICANT: Cerletti, Nico

; APPLICANT: McMaster, Gary K.

; APPLICANT: Cox, David

; APPLICANT: Schmitz, Albert

; APPLICANT: Meyhack, Bernd

; TITLE OF INVENTION: Process for Refolding Recombinantly

; TITLE OF INVENTION: Produced TGF-beta-like Proteins

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Henry P. No. 5922846ak

; STREET: 520 White Plains Road, P.O. Box 2005

; CITY: Tarrytown

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10591-9005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/789,588

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/486,057

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/201,703

; FILING DATE: 25-FEB-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/960,309

; FILING DATE: 13-OCT-1992

; APPLICATION NUMBER: US 07/621,502

; FILING DATE: 03-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 8927546.5

; FILING DATE: 06-DEC-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5922846ak, Henry P.

; REGISTRATION NUMBER: 33200

; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 277-5110

; TELEFAX: (908) 277-4306

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-789-588-6

Query Match 0.8%; Score 35.8; DB 1; Length 39;

Best Local Similarity 94.9%; Pred. No. 0.63;

Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GCTTGGATGCGGCTATTGCTTTAGAAATGTCAGGAT 39

## RESULT 3

US-08-486-057B-7/c

; Sequence 7, Application US/08486057B

; Patent No. 5650494

; GENERAL INFORMATION:

; APPLICANT: Cerletti, Nico

; APPLICANT: McMaster, Gary K.

; APPLICANT: Cox, David

; APPLICANT: Schmitz, Albert

; APPLICANT: Meyhack, Bernd

; TITLE OF INVENTION: Process for Refolding Recombinantly

; TITLE OF INVENTION: Produced TGF-beta-like Proteins

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Henry P. No. 5650494ak

; STREET: 520 White Plains Road, P.O. Box 2005

; CITY: Tarrytown

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10591-9005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,057B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/201,703

; FILING DATE: 25-FEB-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/960,309

; FILING DATE: 13-OCT-1992

; APPLICATION NUMBER: US 07/621,502

; FILING DATE: 03-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 8927546.5

; FILING DATE: 06-DEC-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5650494ak, Henry P.

; REGISTRATION NUMBER: 33200

; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 277-5110

; TELEFAX: (908) 277-4306

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-486-057B-7

Query Match 0.8%; Score 34.2; DB 1; Length 39;

Best Local Similarity 92.3%; Pred. No. 1.2;

Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 39 CTTTCAATATGATGTCAGTCTTGCAAAATGCAGCTAA 1

## RESULT 4

US-08-789-588-7/c

; Sequence 7, Application US/08789588

; Patent No. 5922846

; GENERAL INFORMATION:

; APPLICANT: Cerletti, Nico

; APPLICANT: McMaster, Gary K.

; APPLICANT: Cox, David

; APPLICANT: Schmitz, Albert

APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
TITLE OF INVENTION: Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Henry P. No. 5922846ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/789,588  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,057  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/621,502  
FILING DATE: 03-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5922846ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-789-588-7

Query Match 0.8%; Score 34.2; DB 1; Length 39;  
Best Local Similarity 92.3%; Pred. No. 1.2;  
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 39 CTTTCAATATGATTCGAAGTCTTTGTAATGAGCTAA 1

RESULT 5  
US-09-750-401-29  
Sequence 29, Application US/09750401  
Patent No. 6635422  
GENERAL INFORMATION:  
APPLICANT: Keene, Jack D.  
APPLICANT: Carson, Craig C.  
APPLICANT: Tenenbaum, Scott A.  
TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
TITLE OF INVENTION: complexes  
FILE REFERENCE: RBN-001  
CURRENT APPLICATION NUMBER: US/09/750,401  
CURRENT FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: US 60/173,338

PRIOR FILING DATE: 1999-12-28  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29  
LENGTH: 33  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 3'-UTR sequence of TGF beta 2  
US-09-750-401-29

Query Match 0.8%; Score 33; DB 1; Length 33;  
Best Local Similarity 33.3%; Pred. No. 1.2;  
Matches 11; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTAAATGTAATGTTCTTT 3296  
DB 1 UUUUUUUUUUUUUUUUUUUUUUUUUUUUU 33

RESULT 6  
US-09-750-401-31  
Sequence 31, Application US/09750401  
Patent No. 6635422  
GENERAL INFORMATION:  
APPLICANT: Keene, Jack D.  
APPLICANT: Tenenbaum, Scott A.  
TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
TITLE OF INVENTION: complexes  
FILE REFERENCE: RBN-001  
CURRENT APPLICATION NUMBER: US/09/750,401  
CURRENT FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: US 60/173,338  
PRIOR FILING DATE: 1999-12-28  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 31  
LENGTH: 25  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 3'-UTR sequence of TGF beta 2  
US-09-750-401-31

Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 36.0%; Pred. No. 11;  
Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 3693 TTCAATTTTTTTTATATATCTTT 3717  
DB 1 UUCAUUUUUUUUUUUUUUUUUUUUUUUUUU 25

RESULT 7  
US-09-396-196G-60887  
Sequence 60887, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Mittmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 60887  
LENGTH: 25

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; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60887

    Query Match      0.6%; Score 25; DB 1; Length 25;
    Best Local Similarity 100.0%; Pred. No. 11;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3678 GACTTGCACCTACAAATTCATTTT 3702
      |||||||||||||||||||
Db 1 GACTTGCACCTACAAATTCATTTT 25

RESULT 8
US-09-396-196G-60888
; Sequence 60888, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60888
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60888

    Query Match      0.6%; Score 25; DB 1; Length 25;
    Best Local Similarity 100.0%; Pred. No. 11;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3705 TATATACTATCTCCCTGCTGTAT 3729
      |||||||||||||||||||
Db 1 TATATACTATCTCCCTGCTGTAT 25

RESULT 9
US-09-396-196G-60889
; Sequence 60889, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60889
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60889

    Query Match      0.6%; Score 25; DB 1; Length 25;
    Best Local Similarity 100.0%; Pred. No. 11;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3966 TTAAAGAAATCTCAACTCAGAGTCTT 3990
      |||||||||||||||||||
Db 1 TTAAAGAAATCTCAACTCAGAGTCTT 25

; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60890

    Query Match      0.6%; Score 25; DB 1; Length 25;
    Best Local Similarity 100.0%; Pred. No. 11;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4026 TATTATGGACTCTCTTGGCCGTTTC 4050
      |||||||||||||||||||
Db 1 TATTATGGACTCTCTTGGCCGTTTC 25

RESULT 10
US-09-396-196G-60890
; Sequence 60890, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60890
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60890

    Query Match      0.6%; Score 25; DB 1; Length 25;
    Best Local Similarity 100.0%; Pred. No. 11;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTGGCCGTTCAAA 4053
      |||||||||||||||||||
Db 1 TTATGGACTCTCTTGGCCGTTCAAA 25

RESULT 11
US-09-396-196G-60891
; Sequence 60891, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60891
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60891

    Query Match      0.6%; Score 25; DB 1; Length 25;
    Best Local Similarity 100.0%; Pred. No. 11;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTGGCCGTTCAAA 4053
      |||||||||||||||||||
Db 1 TTATGGACTCTCTTGGCCGTTCAAA 25

RESULT 12
US-09-396-196G-60892
; Sequence 60892, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
```

102.6  
68.1/24

```

; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60892

Query Match
Best Local Similarity 100.0%; Pred. No. 11; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4038 CTCCTTGCCGTTCAAAAGCAGACAG 4062
Db 1 CTCCTTGCCGTTCAAAAGCAGACAG 25

RESULT 13
US-09-396-196G-60893
; Sequence 60893, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60893

Query Match
Best Local Similarity 100.0%; Pred. No. 11; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4158 AAAGTCCAGGCCGACACTGCTCATT 4182
Db 1 AAAGTCCAGGCCGACACTGCTCATT 25

RESULT 14
US-09-396-196G-60894
; Sequence 60894, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60896

Query Match
Best Local Similarity 100.0%; Pred. No. 11; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4173 ACTCGTCATTTTATTTCATAATTCA 4197
Db 1 ACTCGTCATTTTATTTCATAATTCA 25

RESULT 15
US-09-396-196G-60895
; Sequence 60895, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60895

Query Match
Best Local Similarity 100.0%; Pred. No. 11; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4170 AGCACTCGTCATTTTATTTCATAATT 4194
Db 1 AGCACTCGTCATTTTATTTCATAATT 25

RESULT 16
US-09-396-196G-60896
; Sequence 60896, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60896

```

```
Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4188 CATAATTCATCCATTATTTCCCTG 4212
Db 1 CATAATTCATCCATTATTTCCCTG 25

RESULT 17
US-09-396-196G-60897
; Sequence 60897, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60897
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60897

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4194 TTCATCCATTATTTCCCTGATTTC 4218
Db 1 TTCATCCATTATTTCCCTGATTTC 25

RESULT 18
US-09-396-196G-60898
; Sequence 60898, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60898

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4200 CATTATTTCCCTGATTTCATTGAAA 4224
Db 1 CATTATTTCCCTGATTTCATTGAAA 25

RESULT 19
US-09-396-196G-60899
; Sequence 60899, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60899
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60899

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3708 ATACTATCTCCCTGCCTGTTATTT 3732
Db 1 ATACTATCTCCCTGCCTGTTATTT 25

RESULT 20
US-09-396-196G-60900
; Sequence 60900, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60900
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60900

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3750 TGACATGAGCTACCTGGGTCCATTTC 3774
Db 1 TGACATGAGCTACCTGGGTCCATTTC 25

RESULT 21
US-09-396-196G-60901
; Sequence 60901, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
```

```
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60901

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3753 CATGAGCTACCTGGTCCATTCTC 3777
Db 1 CATGAGCTACCTGGTCCATTCTC 25

RESULT 22
US-09-396-196G-60902
; Sequence 60902, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60902

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3834 AGCTTTGAGCTCCACAGTGTTCAG 3858
Db 1 AGCTTTGAGCTCCACAGTGTTCAG 25

RESULT 23
US-09-396-196G-60903
; Sequence 60903, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60903

; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60901
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60901

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3840 GAGTCCACAGTGTTCAGCCTTTT 3864
Db 1 GAGTCCACAGTGTTCAGCCTTTT 25

RESULT 24
US-09-396-196G-60904
; Sequence 60904, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60904
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60904

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3858 GCCTTTTCGCTCAGTGTGAGTCA 3882
Db 1 GCCTTTTCGCTCAGTGTGAGTCA 25

RESULT 25
US-09-396-196G-60905
; Sequence 60905, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60905
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60905

Query Match          0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3861 TTTTCTGCGTCACTGTGAGTCATGT 3885
Db 1 TTTTCTGCGTCACTGTGAGTCATGT 25

RESULT 26
US-09-396-196G-60906
; Sequence 60906, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60906
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60906

Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3864 TCTGCGTCACTGTGAGTCATGTGGC 3888
Db 1 TCTGCGTCACTGTGAGTCATGTGGC 25

RESULT 27
US-09-750-401-32
; Sequence 32, Application US/09750401
; Patent No. 6635422
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE OF INVENTION: complexes
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/750,401
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-09-750-401-32

Query Match 0.5%; Score 22; DB 1; Length 22;
Best Local Similarity 22.7%; Pred. No. 24;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAATGCTTTT 4099
Db 1 UUUUUCUUAAUUGUUUUUU 22

RESULT 28
US-09-380-662-8
```

```
; Sequence 8, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-380-662-8

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 CATCTGTCCTCGGTGGCGCT 1273
Db 1 CATCTGTCCTCGGTGGCGCT 20

RESULT 29
US-09-661-753-48/c
; Sequence 48, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-48

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAAACTGCCGCGC 53
Db 20 GAGCTGCTGAAACTGCCGCGC 1

RESULT 30
US-09-661-753-49/c
; Sequence 49, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
```

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/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 49
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-49

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 AAGCTAGGGAAGGTGCGAG 278
Db 20 AAGCTAGGGAAGGTGCGAG 1

RESULT 31
US-09-661-753-50/c
/ Sequence 50, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ APPLICANT: Susan F. Murray
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 50
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-50

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 TGGCCGCGCTGGAGCAAGAA 381
Db 20 TGGCCGCGCTGGAGCAAGAA 1

RESULT 32
US-09-661-753-51/c
/ Sequence 51, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ APPLICANT: Susan F. Murray
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 51
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-51

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 TGGCCGCGCTGGAGCAAGAA 381
Db 20 TGGCCGCGCTGGAGCAAGAA 1

RESULT 33
US-09-661-753-52/c
/ Sequence 52, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ APPLICANT: Susan F. Murray
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 52
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-52

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 ACACGTGTGGAAGGAGGCGC 690
Db 20 ACACGTGTGGAAGGAGGCGC 1

RESULT 34
US-09-661-753-53/c
/ Sequence 53, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ APPLICANT: Susan F. Murray
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 53
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-53

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 830 TCAGATCAGCCACTCCGCAC 849
Db 20 TCAGATCAGCCACTCCGCAC 1

RESULT 35
US-09-661-753-54/c
```

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/ Sequence 54, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 54
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-54

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1016 TTGGGAACGCGTGCATTTT 1035
Db 20 TTGGGAACGCGTGCATTTT 1

RESULT 36
US-09-661-753-55/c
/ Sequence 55, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 55
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-55

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 GCTCTGCAATCGTCCCGG 1266
Db 20 GCTCTGCAATCGTCCCGG 1

RESULT 37
US-09-661-753-56/c
/ Sequence 56, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 56
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-56

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 GTCTTCGCTTGCAAAACCC 1687
Db 20 GTCTTCGCTTGCAAAACCC 1

RESULT 39
US-09-661-753-58/c
/ Sequence 58, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 58
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-58

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 GCAGGAGAGGCAAGCCGGA 1470
Db 20 GCAGGAGAGGCAAGCCGGA 1

RESULT 38
US-09-661-753-57/c
/ Sequence 57, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 57
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-57

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 GTCTTCGCTTGCAAAACCC 1687
Db 20 GTCTTCGCTTGCAAAACCC 1

RESULT 39
US-09-661-753-58/c
/ Sequence 58, Application US/09661753
/ Patent No. 6436909
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
/ FILE REFERENCE: ISPH-0498
/ CURRENT APPLICATION NUMBER: US/09/661,753
/ CURRENT FILING DATE: 2000-09-14
/ EARLIER APPLICATION NUMBER: 60/154,546
/ EARLIER FILING DATE: 1999-09-17
/ NUMBER OF SEQ ID NOS: 68
/ SEQ ID NO 58
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-58

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1754 TCCACCCAGCGCTACATCG 1773  
 DB 20 TCCACCCAGCGCTACATCG 1

RESULT 40  
 US-09-661-753-59/c  
 ; Sequence 59, Application US/09661753  
 ; Patent No. 6436909  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas M. Dean  
 ; APPLICANT: Susan F. Murray  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA  
 ; FILE REFERENCE: ISPH-0498  
 ; CURRENT APPLICATION NUMBER: US/09/661,753  
 ; CURRENT FILING DATE: 2000-09-14  
 ; EARLIER APPLICATION NUMBER: 60/154,546  
 ; EARLIER FILING DATE: 1999-09-17  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SEQ ID NO 59  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-661-753-59

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2032 AAAAAACAGTGGGAGACC 2051  
 DB 20 AAAAAACAGTGGGAGACC 1

RESULT 41  
 US-09-661-753-60/c  
 ; Sequence 60, Application US/09661753  
 ; Patent No. 6436909  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas M. Dean  
 ; APPLICANT: Susan F. Murray  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA  
 ; FILE REFERENCE: ISPH-0498  
 ; CURRENT APPLICATION NUMBER: US/09/661,753  
 ; CURRENT FILING DATE: 2000-09-14  
 ; EARLIER APPLICATION NUMBER: 60/154,546  
 ; EARLIER FILING DATE: 1999-09-17  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SEQ ID NO 60  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-661-753-60

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2321 CACCATTAATCCGAGCTT 2340  
 DB 20 CACCATTAATCCGAGCTT 1

RESULT 42  
 US-09-661-753-61/c  
 ; Sequence 61, Application US/09661753  
 ; Patent No. 6436909

GENERAL INFORMATION:  
 ; APPLICANT: Nicholas M. Dean  
 ; APPLICANT: Susan F. Murray  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA  
 ; FILE REFERENCE: ISPH-0498  
 ; CURRENT APPLICATION NUMBER: US/09/661,753  
 ; CURRENT FILING DATE: 2000-09-14  
 ; EARLIER APPLICATION NUMBER: 60/154,546  
 ; EARLIER FILING DATE: 1999-09-17  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SEQ ID NO 61  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-661-753-61

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2478 CAGGACACGAAATCACGGT 2497  
 DB 20 CAGGACACGAAATCACGGT 1

RESULT 43  
 US-09-661-753-62/c  
 ; Sequence 62, Application US/09661753  
 ; Patent No. 6436909  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas M. Dean  
 ; APPLICANT: Susan F. Murray  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA  
 ; FILE REFERENCE: ISPH-0498  
 ; CURRENT APPLICATION NUMBER: US/09/661,753  
 ; CURRENT FILING DATE: 2000-09-14  
 ; EARLIER APPLICATION NUMBER: 60/154,546  
 ; EARLIER FILING DATE: 1999-09-17  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SEQ ID NO 62  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Antisense Oligonucleotide  
 US-09-661-753-62

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2854 ACGTATTGTTTCCAGCCGCG 2873  
 DB 20 ACGTATTGTTTCCAGCCGCG 1

RESULT 44  
 US-09-661-753-63/c  
 ; Sequence 63, Application US/09661753  
 ; Patent No. 6436909  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nicholas M. Dean  
 ; APPLICANT: Susan F. Murray  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA  
 ; FILE REFERENCE: ISPH-0498  
 ; CURRENT APPLICATION NUMBER: US/09/661,753  
 ; CURRENT FILING DATE: 2000-09-14  
 ; EARLIER APPLICATION NUMBER: 60/154,546  
 ; EARLIER FILING DATE: 1999-09-17  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SEQ ID NO 63

```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-63

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3075 GAACCAATACCCAGGGG 3094
Db 20 GAACCAATACCCAGGGG 1

RESULT 45
US-09-661-753-64/c
; Sequence 64, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-64

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3297 GCCAGTTTAAGCAAGCCGGT 3316
Db 20 GCCAGTTTAAGCAAGCCGGT 1

RESULT 46
US-09-661-753-65/c
; Sequence 65, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-65

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3352 TTTTGACCGTGAAGTGGCTG 3371
Db 20 TTTTGACCGTGAAGTGGCTG 1

RESULT 47
US-09-661-753-66/c
; Sequence 66, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-66

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3753 CATGAGCTACCTGGGTCCAT 3772
Db 20 CATGAGCTACCTGGGTCCAT 1

RESULT 48
US-09-661-753-67/c
; Sequence 67, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498
; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-67

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3874 TGTGAGTCATGTGGCGGGTG 3893
Db 20 TGTGAGTCATGTGGCGGGTG 1

RESULT 49
US-09-661-753-68/c
; Sequence 68, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
```

| EXPERIMENTAL<br>CONDITIONS | ORIGINAL SOURCE: | INDIVIDUAL ISOLATE: | INDIVIDUAL ISOLATE: | DNA Target, Experiment 7,<br>Fig. 2 |
|----------------------------|------------------|---------------------|---------------------|-------------------------------------|
| 1                          |                  |                     |                     |                                     |
| 2                          |                  |                     |                     |                                     |
| 3                          |                  |                     |                     |                                     |
| 4                          |                  |                     |                     |                                     |
| 5                          |                  |                     |                     |                                     |
| 6                          |                  |                     |                     |                                     |
| 7                          |                  |                     |                     |                                     |
| 8                          |                  |                     |                     |                                     |
| 9                          |                  |                     |                     |                                     |
| 10                         |                  |                     |                     |                                     |
| 11                         |                  |                     |                     |                                     |
| 12                         |                  |                     |                     |                                     |
| 13                         |                  |                     |                     |                                     |
| 14                         |                  |                     |                     |                                     |
| 15                         |                  |                     |                     |                                     |
| 16                         |                  |                     |                     |                                     |
| 17                         |                  |                     |                     |                                     |
| 18                         |                  |                     |                     |                                     |
| 19                         |                  |                     |                     |                                     |
| 20                         |                  |                     |                     |                                     |
| 21                         |                  |                     |                     |                                     |
| 22                         |                  |                     |                     |                                     |
| 23                         |                  |                     |                     |                                     |
| 24                         |                  |                     |                     |                                     |
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| 98                         |                  |                     |                     |                                     |
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| 100                        |                  |                     |                     |                                     |

1. TITLE OF IN

```
/ TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
/ TITLE OF INVENTION: Properties
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: P.O. Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306-0850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/473,015
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/214,599 - 584922
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33,875
/ REFERENCE/DOCKET NUMBER: 5525-0012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
/ US-08-473-015-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 88;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTTITTTT 2754
Db 1 AAAAAAAAAACCCCTTTTITTTT 24

RESULT 53
US-08-465-368-13
/ Sequence 13, Application US/08465368
/ Patent No. 5726297
/ GENERAL INFORMATION:
/ APPLICANT: Gryaznov, Sergei
/ APPLICANT: Schultz, Ronald G.
/ APPLICANT: Chen, Jer-kang
/ TITLE OF INVENTION: OLIGODENOVIRIBONUCLEOTIDE
/ TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES: USES AND
/ TITLE OF INVENTION: COMPOSITIONS THEREOF
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: P.O. Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306-0850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,306
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/214,599
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33,875
/ REFERENCE/DOCKET NUMBER: 5525-0012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
```

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/465,368
/ FILING DATE: 05-JUN-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/210,505
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33,875
/ REFERENCE/DOCKET NUMBER: 5525-0013
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
/ US-08-465-368-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 88;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTTITTTT 2754
Db 1 AAAAAAAAAACCCCTTTTITTTT 24

RESULT 54
US-08-477-306-13
/ Sequence 13, Application US/08477306
/ Patent No. 5837835
/ GENERAL INFORMATION:
/ APPLICANT: Gryaznov, Sergei
/ TITLE OF INVENTION: Oligonucleotide N3'-P5'
/ TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
/ TITLE OF INVENTION: Properties
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: P.O. Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306-0850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/477,306
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/214,599
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33,875
/ REFERENCE/DOCKET NUMBER: 5525-0012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
```

TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2  
US-08-477-306-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 88;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTTTTTTT 2754  
DB 1 AAAA AAAA AACCCTTTTTTTTTT 24

RESULT 55  
US-08-700-448-13  
Sequence 13, Application US/08700448  
Patent No. 5965720

GENERAL INFORMATION:  
APPLICANT: Gryaznov, Sergei et al.  
TITLE OF INVENTION: Oligonucleotide N3'-p5',  
TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: P.O. Box 60850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,448  
FILING DATE: 01/10/97  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Vincent M. Powers  
REGISTRATION NUMBER: 36,246  
REFERENCE/DOCKET NUMBER: 5525-0012.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 324-0960  
TELEFAX: (650) 324-0960

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2  
US-08-700-448-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 88;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTTTTTTT 2754  
DB 1 AAAA AAAA AACCCTTTTTTTTTT 24

RESULT 56

US-08-923-386A-13  
Sequence 13, Application US/08923386A  
Patent No. 6169170  
GENERAL INFORMATION:  
APPLICANT: Gryaznov, Sergei  
TITLE OF INVENTION: Oligonucleotide N3'-p5',  
TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: P.O. Box 60850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306-0850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/923,386A  
FILING DATE:  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 5525-0012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 3  
US-08-923-386A-13

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 88;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTTTTTTT 2754  
DB 1 AAAA AAAA AACCCTTTTTTTTTT 24

RESULT 57

US-09-655-804B-67  
Sequence 67, Application US/09655804B  
Patent No. 6548251  
GENERAL INFORMATION:  
APPLICANT: KOZIYAVKIN, Sergei  
APPLICANT: MALYKH, Andrei  
APPLICANT: POLOUCHINE, Nikolai  
APPLICANT: SLESAREV, Alexei  
TITLE OF INVENTION: INHIBITION OF MOLECULAR AND BIOLOGICAL PROCESSES USING MODIFIED  
TITLE OF INVENTION: OLIGONUCLEOTIDES  
FILE REFERENCE: 107070  
CURRENT APPLICATION NUMBER: US/09/655,804B



; SOFTWARE: P  
; SEQ ID NO 27

OPERATING SYSTEM: FC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/458,367  
;/ FILING DATE: 02-Jun-1995  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/409631  
;/ FILING DATE: 22-Mar-1995  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/348284  
;/ FILING DATE: 30-No. 5783433-1994  
;/ PRIOR APPLICATION DATA: 08/116186  
;/ FILING DATE: 02-Sep-1993  
;/ APPLICATION NUMBER: 07/895300  
;/ FILING DATE: 08-Jun-1992  
;/ NAME: Johnston, Sean A.  
;/ REGISTRATION NUMBER: 35,910  
;/ REFERENCE/DOCKET NUMBER: P0747C4  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 415/225-3562  
;/ TELEFAX: 415/952-9881  
;/ TELEX: 910/371-7168  
;/ INFORMATION FOR SEQ ID NO: 18:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 22 base pairs  
;/ TYPE: Nucleic Acid  
;/ STRANDEDNESS: Single  
;/ TOPOLOGY: Linear  
;/ US-08-458-367-18

Query Match 0.4%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 81;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 615 GCGCGCGCGCACGCGCGCGC 636  
Db 1 GCGCGCGCGCGCGCGCGCGC 22

RESULT 62  
US-08-458-367-18/c  
;/ Sequence 18, Application US/08458367  
;/ Patent No. 5783433  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Frenz, John  
;/ APPLICANT: Shire, Steven J.  
;/ APPLICANT: Sliwowski, Mary B.  
;/ TITLE OF INVENTION: PURIFIED FORMS OF DNase  
;/ NUMBER OF SEQUENCES: 18  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Genentech, Inc.  
;/ STREET: 460 Point San Bruno Blvd  
;/ CITY: South San Francisco  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94080  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: WinPatIn (Genentech)  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/458,367  
;/ FILING DATE: 02-Jun-1995  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/409631  
;/ FILING DATE: 22-Mar-1995  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/348284  
;/ FILING DATE: 30-No. 5783433-1994

;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/116186  
;/ FILING DATE: 02-Sep-1993  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/895300  
;/ FILING DATE: 08-Jun-1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Johnston, Sean A.  
;/ REGISTRATION NUMBER: 35,910  
;/ REFERENCE/DOCKET NUMBER: P0747C4  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 415/225-3562  
;/ TELEFAX: 415/952-9881  
;/ TELEX: 910/371-7168  
;/ INFORMATION FOR SEQ ID NO: 18:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 22 base pairs  
;/ TYPE: Nucleic Acid  
;/ STRANDEDNESS: Single  
;/ TOPOLOGY: Linear  
;/ US-08-458-367-18  
  
Query Match 0.4%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 81;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 615 GCGCGCGCGCACGCGCGCGC 636  
Db 22 GCGCGCGCGCGCGCGCGCGC 1  
  
RESULT 63  
US-08-482-577B-34  
;/ Sequence 34, Application US/08482577B  
;/ Patent No. 5807713  
;/ GENERAL INFORMATION:  
;/ APPLICANT: HOTTEN, GERTRUD  
;/ APPLICANT: NEIDHARDT, HELGE  
;/ APPLICANT: BECHTOLD, ROLF  
;/ APPLICANT: POHL, JENS  
;/ TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
;/ TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS  
;/ NUMBER OF SEQUENCES: 49  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY, AND ORAM  
;/ STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
;/ STREET: SUITE 330  
;/ CITY: WASHINGTON  
;/ STATE: DC  
;/ COUNTRY: USA  
;/ ZIP: 20005  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/482,577B  
;/ FILING DATE:  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: KLEISNER, SHARON  
;/ REGISTRATION NUMBER: 36,335  
;/ REFERENCE/DOCKET NUMBER: P564-5010  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 202/638-5000  
;/ TELEFAX: 202/638-4810  
;/ INFORMATION FOR SEQ ID NO: 34:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 22 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear

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; MOLECULE TYPE: DNA
US-08-482-577B-34
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
|||||
Db 1 GGGATCTAGGTTGGAAATGGAT 22

RESULT 64
US-08-288-508C-25
; Sequence 25, Application US/08288508C
; Patent No. 5994094
; GENERAL INFORMATION:
; APPLICANT: H tten, Gertrud
; APPLICANT: Neidhardt, Helge
; APPLICANT: Paulista, Michael
; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
; TITLE OF INVENTION: THE TGF- FAMILY
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US/08/288,508C
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 26 829.3
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 18 222.8
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 20 157.5
; FILING DATE: 09-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JAHNS, Kristina M.
; REGISTRATION NUMBER: P-41,092
; REFERENCE/DOCKET NUMBER: P564-4019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-288-508C-25
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
|||||
Db 1 GGGATCTAGGTTGGAAATGGAT 22
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RESULT 65
US-08-289-222E-38
; Sequence 38, Application US/08289222E
; Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTIEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; TITLE OF INVENTION: FAMILY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARMELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; STREET: SUITE 330
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,222E
; FILING DATE: 25-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-9021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-289-222E-38
Query Match 0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAAATGGAT 2221
|||||
Db 1 GGGATCTAGGTTGGAAATGGAT 22

RESULT 66
US-09-218-176-17
; Sequence 17, Application US/09218176
; Patent No. 6171584
; GENERAL INFORMATION:
; APPLICANT: H ITTEN, Gertrud
; APPLICANT: NEIDHARDT, Helge
```

```
; APPLICANT: BECHTOLD, Rolf
; APPLICANT: POHL, Jens
; APPLICANT: PAULISTA, Michael
; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
; TITLE OF INVENTION: TGF- FAMILY
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARMELESTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., G Street Lobby,
; STREET: Suite 330
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/218,176
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03065
; FILING DATE: 12-JUL-1996
; APPLICATION NUMBER: 08/679,048
; FILING DATE: 12-JUL-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03065
; FILING DATE: 12-JUL-1996
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 2-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,577
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92 102 324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 01-JUL-1994
; APPLICATION NUMBER: DE 195 11 243.1
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-6010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-218-176-17
;
; Query Match 0.4%; Score 18.8; DB 1; Length 22;
; Best Local Similarity 90.9%; Pred. No. 81;
; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2200 GGGATCTTGGATGGGAATGGAT 2221
; DB 1 GGGATCTAGGTGGGAATGGAT 22
;
; RESULT 67
; US-09-054-526B-38
; Sequence 38, Application US/09054526B
```

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; Patent No. 6197550
; GENERAL INFORMATION:
; APPLICANT: H TTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARMELESTEIN, MURRAY & ORAM LLP
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; STREET: SUITE 330
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,526B
; FILING DATE: 03-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-8005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-054-526B-38
;
; Query Match 0.4%; Score 18.8; DB 1; Length 22;
; Best Local Similarity 90.9%; Pred. No. 81;
; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2200 GGGATCTTGGATGGGAATGGAT 2221
; DB 1 GGGATCTAGGTGGGAATGGAT 22
;
; RESULT 68
; US-09-386-450D-25
; Sequence 25, Application US/09386450D
; Patent No. 6764994
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, Gertrud
; APPLICANT: Neidhardt, Helge
; APPLICANT: Paulista, Michael
; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF TGF-? Family
; FILE REFERENCE: 100564-09022
; CURRENT APPLICATION NUMBER: US/09/386,450D
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; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/288,508
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: DE P 43 26 829.3
; PRIOR FILING DATE: 1993-08-10
; PRIOR APPLICATION NUMBER: DE P 44 18 222.8
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: DE P 44 20 157.5
; PRIOR FILING DATE: 1994-06-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)..(22)
; OTHER INFORMATION: portion of TGF-beta-2 corresponding to primer OD
US-09-386-450D-25

Query Match          0.4%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GGGATCTTGGATGGAATGGAT 2221
Db 1 GGGATCTAGGTTGGAATGGAT 22

RESULT 69
US-09-823-634A-15
; Sequence 15, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: MISMATCHES USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-634A-15

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGAGAAAAA 2599
Db 1 AAAAAAAAAATTGAGAAAAA 20

RESULT 70
US-09-823-647B-15
; Sequence 15, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
```

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; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-647B-15

Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGAGAAAAA 2599
Db 1 AAAAAAAAAATTGAGAAAAA 20

RESULT 71
US-09-380-662-9/c
; Sequence 9, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Oligo sapiens
US-09-380-662-9

Query Match          0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 CCCTACTTCAGAAATCGTC 1607
Db 18 CCCTACTTCAGAAATCGTC 1

RESULT 72
US-08-535-249-67/c
; Sequence 67, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: DNA (genomic)
; MOLECULE TYPE: YES
; ANTI-SENSE: YES
; US-08-535-249-67

Query Match 0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCATCTACA 1431
Db 18 AGGTGATTTCCATCTACA 1

RESULT 73
US-08-535-249-104/c
; Sequence 104, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: DNA (genomic)
; MOLECULE TYPE: YES
; ANTI-SENSE: YES
; US-08-535-249-104

Query Match 0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1

RESULT 74
US-09-009-913-100
; Sequence 100, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: AxyS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-009-913-100
```

RESULT 76  
 US-09-687-246B-7/c  
 ; Sequence 7, Application US/09687246B  
 ; Patent No. 6709818  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Johns Hopkins School of Medicine  
 ; APPLICANT: Nelson, William  
 ; APPLICANT: Tchou, Julia  
 ; APPLICANT: Bakker, Jila  
 ; APPLICANT: Lin, Xiaohui  
 ; TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DIS  
 ; FILE REFERENCE: JHU1660-1  
 ; CURRENT APPLICATION NUMBER: US/09/687,246B  
 ; CURRENT FILING DATE: 2000-10-12  
 ; PRIOR APPLICATION NUMBER: 60/159,168  
 ; PRIOR FILING DATE: 1999-10-13  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: primer N-F1  
 US-09-687-246B-7

```

RESULT 78
US-08-863-639A-51
; Sequence 51, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sheldon & Mak
;

```

RESULT 76  
 US-09-687-246B-7/c  
 ; Sequence 7, Application US/09687246B  
 ; Patent No. 6709818  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Johns Hopkins School of Medicine  
 ; APPLICANT: Nelson, William  
 ; APPLICANT: Tchou, Julia  
 ; APPLICANT: Bakker, Jila  
 ; APPLICANT: Lin, Xiaohui  
 ; TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DIS  
 ; FILE REFERENCE: JHU1660-1  
 ; CURRENT APPLICATION NUMBER: US/09/687,246B  
 ; CURRENT FILING DATE: 2000-10-12  
 ; PRIOR APPLICATION NUMBER: 60/159,168  
 ; PRIOR FILING DATE: 1999-10-13  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: primer N-F1  
 US-09-687-246B-7

```

; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-51

```

```

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

```

```

RESULT 79
US-08-863-639A-51/c
; Sequence 51, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Watson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321

```

```

; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-51
;
; Query Match 0.4%; Score 16.8; DB 1; Length 20;
; Best Local Similarity 90.0%; Pred. No. 1.3e+02;
; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 616 CGCGCGCGCACGCGCGCG 635
; Db 20 CGCGCGCGCGCGCGCGCG 1
;
; RESULT 80
; US-09-030-701-59
; Sequence 59, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; US-09-030-701-59

```

```

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

```

```

RESULT 81
US-09-030-701-59/c
; Sequence 59, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

```



```
/ FEATURE:
/ OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-59

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 82
US-09-082-649B-22
; Sequence 22, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-22

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 83
US-09-082-649B-22/c
; Sequence 22, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA

/ FEATURE:
/ OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-22

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 84
US-09-082-649B-76
; Sequence 76, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-76

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634
Db 1 GCGCGCGCGCGCGCGCGC 20

RESULT 85
US-09-082-649B-76/c
; Sequence 76, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
```

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-082-6498-76

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCGCGCGCGCG 634  
DB 20 GCGCGCGCGCGCGCGCGCG 1

RESULT 86  
US-08-535-249-99/c  
Sequence 99, Application US/08535249  
Patent No. 6455689  
GENERAL INFORMATION:  
APPLICANT: Schlengersien, Georg-Ferdinand  
APPLICANT: Brysch, Wolfgang  
APPLICANT: Schlengersien, Karl-Hermann  
APPLICANT: Schlengersien, Reimar  
APPLICANT: Bogdahn, Ulrich  
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
NUMBER OF SEQUENCES: 137  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/535,249  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 089.0  
FILING DATE: 30-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 849.7  
FILING DATE: 13-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-6666  
TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-08-535-249-99

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAGCG 1947  
DB 1 CATCATCCCGAATAAAGCG 20

DB 20 CATCATCCCGAATAAAGTG 1

RESULT 87  
US-09-725-265-42/c  
Sequence 42, Application US/09725265  
Patent No. 6492121  
GENERAL INFORMATION:  
APPLICANT: KURANE, RYUICHIRO  
APPLICANT: KANAGAWA, TAKAHIRO  
APPLICANT: KAMAGATA, YOICHI  
APPLICANT: YAMADA, KAZUTAKA  
APPLICANT: YOKOMAKU, TOYOKAZU  
APPLICANT: KOYAMA, OSAMU  
APPLICANT: FURUSHO, KENTA

TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE  
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA  
TITLE OF INVENTION: THE METHOD  
FILE REFERENCE: 199953USOXDIV  
CURRENT APPLICATION NUMBER: US/09/725,265  
CURRENT FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: US 09/556,127  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: JP 1999-111601  
PRIOR FILING DATE: 1999-04-20  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 42  
LENGTH: 20  
TYPE: DNA  
ORGANISM: ARTIFICIAL SEQUENCE  
FEATURE:  
OTHER INFORMATION: SYNTHETIC DNA  
US-09-725-265-42

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATATATTT 1171  
DB 20 TTTTATATATATATAT 1

RESULT 88  
US-09-823-634A-13  
Sequence 13, Application US/09823634A  
Patent No. 6596489  
GENERAL INFORMATION:  
APPLICANT: Applied Gene Technologies, Inc.  
APPLICANT: Dattagupta, Nanibhushan  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE  
TITLE OF INVENTION: MISMATCHES USING RNASE H  
FILE REFERENCE: 47541-20006.00  
CURRENT APPLICATION NUMBER: US/09/823,634A  
CURRENT FILING DATE: 2002-02-28  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligo AGT02020  
US-09-823-634A-13

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTCGAGAAAAA 2599  
DB 1 AAAAAAATTCGAGAAAAA 20

```

; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 92
US-09-556-127-42/c
; Sequence 42, Application US/09556127
; Patent No. 6693661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-42

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATATATTT 1171
Db 20 TTTTATATATATATATATAT 1

RESULT 93
US-09-965-101-22
; Sequence 22, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim

```

```

; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 92
US-09-556-127-42/c
; Sequence 42, Application US/09556127
; Patent No. 6693661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-42

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATATATTT 1171
Db 20 TTTTATATATATATATATAT 1

RESULT 93
US-09-965-101-22
; Sequence 22, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim

```

```
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-22
```

```
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20
|||||
```

```
RESULT 94
US-09-965-101-22/c
; Sequence 22, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-22
```

```
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1
|||||
```

```
RESULT 95
US-09-965-101-76
; Sequence 76, Application US/09965101
```

```
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-76
```

```
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 615 GCGCGCGCGCACGCGCGC 634
Db 1 GCGCGCGCGCGCGCGCGC 20
|||||
```

```
RESULT 96
US-09-965-101-76/c
; Sequence 76, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-76
```

```
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 615 GCGCGCGCGCACGCGCGC 634
Db 20 GCGCGCGCGCGCGCGCGC 1
|||||
```

RESULT 97  
5221620-13/c  
; PATENT NO. 5221620  
; APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING  
; GROWTH FACTOR BETA-2  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/446,020  
; FILING DATE: 05-DEC-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 285,140  
; FILING DATE: 16-DEC-1988  
; APPLICATION NUMBER: 234,065  
; FILING DATE: 18-AUG-1988  
; APPLICATION NUMBER: 148,267  
; FILING DATE: 25-JAN-1988  
; APPLICATION NUMBER: 106,752  
; FILING DATE: 06-OCT-1987  
; SEQ ID NO:13:  
; LENGTH: 20  
5221620-13

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2211 TGGAAATGGATCCATGAACC 2230  
DB 20 TGGAAATGGATACACGAACC 1

RESULT 98  
5221620-13/c  
; PATENT NO. 5221620  
; APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY  
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING  
; GROWTH FACTOR BETA-2  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/446,020  
; FILING DATE: 05-DEC-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 285,140  
; FILING DATE: 16-DEC-1988  
; APPLICATION NUMBER: 234,065  
; FILING DATE: 18-AUG-1988  
; APPLICATION NUMBER: 148,267  
; FILING DATE: 25-JAN-1988  
; APPLICATION NUMBER: 106,752  
; FILING DATE: 06-OCT-1987  
; SEQ ID NO:13:  
; LENGTH: 20  
5221620-13

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2211 TGGAAATGGATCCATGAACC 2230  
DB 20 TGGAAATGGATACACGAACC 1

RESULT 99  
US-09-655-804B-67/c  
; Sequence 67, Application US/09655804B  
; Patent No. 6548251  
; GENERAL INFORMATION:  
; APPLICANT: KOZYAVKIN, Sergei  
; APPLICANT: MALYKH, Andrei

; APPLICANT: POLOUCHINE, Nikolai  
; APPLICANT: SLESAREV, Alexei  
; TITLE OF INVENTION: INHIBITION OF MOLECULAR AND BIOLOGICAL PROCESSES USING MODIFIED  
; FILE REFERENCE: OLIGONUCLEOTIDES  
; FILE REFERENCE: 107070  
; CURRENT APPLICATION NUMBER: US/09/655,804B  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-655-804B-67

Query Match 0.4%; Score 16.6; DB 1; Length 24;  
Best Local Similarity 82.8%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2732 AAAAGAAACATCTTTTTTTT 2754  
DB 24 AAAAAAAGTCTTTTTTTT 2

RESULT 100  
US-08-535-249-76/c  
; Sequence 76, Application US/08535249  
; Patent No. 6455689  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdan, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; NUMBER OF SEQUENCES: 137  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,249  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 76:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown

```

RESULT 102
US-09-696-791-3527/c
; Sequence 3527, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3527
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3527

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 924 CCAGGAGAAAAAACAAC 941
|||||
DB 19 CCAGGAGAAAAACAAC 2

RESULT 103
US-09-696-791-3528/c
; Sequence 3528, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3528
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3528

Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 924 CCAGGAGAAAAAACAAC 941
|||||
DB 18 CCAGGAGAAAAACAAC 1

RESULT 104
US-09-702-251-10
; Sequence 10, Application US/09702251
; Patent No. 6372492
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0199

```

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; CURRENT APPLICATION NUMBER: US/09/702,251
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-251-10

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3393 TCCTTTGCTCTGTATAT 3410
Db 2 TCCTTCGCTCTGTATAT 19

RESULT 105
US-09-198-452A-2628
; Sequence 2628, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2628
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2628

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1055 GCCAGGACGCTTTTCTA 1072
Db 2 GCCAGGACGCTTTTCTA 19

RESULT 106
US-09-380-662-16/c
; Sequence 16, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-380-662-16

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1217 CATGCACTACTGTGTG 1232
Db 16 CATGCACTACTGTGTG 1

RESULT 107
US-09-380-662-17
; Sequence 17, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.38USWO
; CURRENT APPLICATION NUMBER: US/09/380,662
; CURRENT FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-380-662-17

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1217 CATGCACTACTGTGTG 1232
Db 1 CATGCACTACTGTGTG 16

RESULT 108
US-08-535-249-105/c
; Sequence 105, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELE: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-105

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAA 2035
Db 16 AGTCCACTAGGAAAA 1

RESULT 109
US-08-535-249-113/c
; Sequence 113, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELE: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-113

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATTGC 2168
Db 16 TGTGCAGGATAATTGC 1

RESULT 110
US-09-601-144-2
; Sequence 2, Application US/09601144
; Patent No. 6566514
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Lee, Yoon S.
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDIXIN
; TITLE OF INVENTION: AND THIOREDIXIN REDUCTASE GENES AND METHODS OF USING
; TITLE OF INVENTION: SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 683-112US-A
; CURRENT APPLICATION NUMBER: US/09/601,144
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/073,196
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Human
US-09-601-144-2

Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2209 GATGGAATGGATCCA 2224
Db 1 GATGGAATGGATCCA 16

RESULT 111
US-08-330-000-1/c
; Sequence 1, Application US/08330000
; Patent No. 5686242
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; APPLICANT: Lima, Walter F.
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5686242ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```



```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,000
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 755,485
; FILING DATE: September 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07489
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca Lynne
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1723
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-330-000-1

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAAACATC 2818
Db 17 AAAAAAAAAAACATC 2

RESULT 112
US-08-965-908-1/c
; Sequence 1, Application US/08965908
; Patent No. 6022691
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; ADDRESS: Lima, Walter F.
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 6022691ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,908
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/330,000
; FILING DATE:
; APPLICATION NUMBER: 755,485
; FILING DATE: September 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07489
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca Lynne
; REGISTRATION NUMBER: 35,152

```

```

; REFERENCE/DOCKET NUMBER: ISIS-1723
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-965-908-1

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAAACATC 2818
Db 17 AAAAAAAAAAACATC 2

RESULT 113
US-09-026-601-25
; Sequence 25, Application US/09026601
; Patent No. 6358680
; GENERAL INFORMATION:
; APPLICANT: Beck, James J.
; TITLE OF INVENTION: Detection of Wheat and Barley Fungal
; TITLE OF INVENTION: Pathogens Using the Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6358680artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6358680th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,601
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1984
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer JB659"
; US-09-026-601-25

Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3190 GAAGCTTCATGGACGC 3205
Db 1 GAAGCTTCATGGACGC 16

```

```

RESULT 114
US-08-842-079-4
; Sequence 4, Application US/08842079
; Patent No. 6133434
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/08/842,079
; CURRENT FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-08-842-079-4

Query Match          0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2102 GTCCAGCGCGCGGAAG 2117
Db 1 GTCCAGCGCGCGGAAG 16

RESULT 115
US-09-638-857-4
; Sequence 4, Application US/09638857
; Patent No. 6509163
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/09/638,857
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 08/842,079
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-638-857-4

Query Match          0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2102 GTCCAGCGCGCGGAAG 2117
Db 1 GTCCAGCGCGCGGAAG 16

RESULT 116
US-08-478-470-13/c
; Sequence 13, Application US/08478470
; Patent No. 5591607
; GENERAL INFORMATION:
; APPLICANT: GRYAZNOV, SERGEI
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: N3',P5' PHOSPHORAMIDATES:
; TITLE OF INVENTION: HYBRIDIZATION AND NUCLEASE

```

```

; TITLE OF INVENTION: RESISTANCE PROPERTIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro
; ADDRESSEE: Huddleson & Tatum
; STREET: 5 Palo Alto Square
; STREET: 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,470
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: John D. Mendlein
; REGISTRATION NUMBER: 38,770
; REFERENCE/DOCKET NUMBER: LYNX-005/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5020
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7,
; INDIVIDUAL ISOLATE: Fig. 2
US-08-478-470-13

Query Match          0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAGAAAACATCTTTTTTTT 2754
Db 24 AAAAAGAAAGGGTTTTTTTTT 1

RESULT 117
US-08-214-599-13/c
; Sequence 13, Application US/08214599
; Patent No. 5599922
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5',
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
US-08-473-015-13

Query Match          0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels

Qy  2731 AAAAAGAAACATCTTTTITTTT 2754
      ||||| ||||| ||||| |||||
Db  24 AAAAAAAAAAGGGGTTTTTTTTTT 1

RESULT 119
US-08-465-368-13/c
; Sequence 13, Application US/08465368
; Patent No. 5726297
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Schultz, Ronald G.
; APPLICANT: Chen, Jer-kang
; TITLE OF INVENTION: OLIGODEOXYRIBONUCLEOTIDE
; TITLE OF INVENTION: N3'P5'PHOSPHORAMIDATES:  US5 AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,368
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/210,505
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
US-08-465-368-13

Query Match          0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels

Qy  2731 AAAAAGAAACATCTTTTITTTT 2754

```

```
Db      24 AAAAAAAAAAGGGGTTTTTTTTTT 1
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RESULT 120
US-08-477-306-13/c
; Sequence 13, Application US/08477306
; Patent No. 5837835
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,306
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
; US-08-477-306-13

Query Match      0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2731 AAAAAAACAATCTTTT 2754
||||| ||| ||||| |||||
Db      24 AAAAAAAAAAGGGGTTTTTTTTTT 1

RESULT 121
US-08-477-306-13/c
; Sequence 13, Application US/08477306
; Patent No. 5837835
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,306
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,599
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 5525-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 2
; US-08-477-306-13

Query Match      0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2731 AAAAAAACAATCTTTT 2754
||||| ||| ||||| |||||
Db      24 AAAAAAAAAAGGGGTTTTTTTTTT 1

RESULT 122
US-08-923-386A-13/c
; Sequence 13, Application US/08923386A
; Patent No. 6163170
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; TITLE OF INVENTION: Oligonucleotide N3'-P5'
; TITLE OF INVENTION: Phosphoramidates: Hybridization and Nuclease Resistance
; TITLE OF INVENTION: Properties
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,386A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
```

REFERENCE/DOCKET NUMBER: 5525-0012  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: DNA Target, Experiment 7, Fig. 3  
US-08-923-386A-13

Query Match 0.4%; Score 16; DB 1; Length 24;  
Best Local Similarity 79.2%; Pred. No. 2.5e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAAAGAAACATCTTTTCTTTT 2754  
|||||  
Db 24 AAAAAAAGGGGTTTTTTTTT 1

RESULT 123  
US-08-999-029-1/c  
Sequence 1, Application US/08899029  
Patent No. 6143531  
GENERAL INFORMATION:  
APPLICANT: HUSE, WILLIAM D.  
TITLE OF INVENTION: IMPROVED METHOD OF DOUBLE  
TITLE OF INVENTION: STRANDED DNA SYNTHESIS  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York,  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/899, 029  
FILING DATE: 22-JUL-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/116, 049  
FILING DATE: 02-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B  
REGISTRATION NUMBER: 30,605  
REFERENCE/DOCKET NUMBER: 8142-125-999  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
US-08-999-029-1

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAATTCGAG 2594  
|||||  
Db 19 AAAAAAACTCGAG 1

RESULT 124  
US-09-696-791-4067/c  
Sequence 32, Application US/09696791  
Patent No. 6770633  
GENERAL INFORMATION:  
APPLICANT: Robbins, Joan M.  
APPLICANT: Tritz, Richard  
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
TITLE OF INVENTION: SKIN AND EYE DISEASES  
FILE REFERENCE: 480124.407  
CURRENT APPLICATION NUMBER: US/09/696,791  
CURRENT FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 4523  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4067  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: PCNA HH ribozyme binding site  
US-09-696-791-4067

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3591 TTGGACTTTTCTTTAA 3609  
|||||  
Db 19 TTGGACTTTTCTTTAA 1

RESULT 125  
US-09-750-401-32/c  
Sequence 32, Application US/09750401  
Patent No. 6635422  
GENERAL INFORMATION:  
APPLICANT: Keene, Jack D.  
APPLICANT: Carson, Craig C.  
APPLICANT: Tenenbaum, Scott A.  
TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
TITLE OF INVENTION: complexes  
FILE REFERENCE: RBN-001  
CURRENT APPLICATION NUMBER: US/09/750,401  
CURRENT FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: US 60/173,338  
PRIOR FILING DATE: 1999-12-28  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 32  
LENGTH: 22  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 3'-UTR sequence of TGF beta 2  
US-09-750-401-32

Query Match 0.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 2.4e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2578 AAAAAAATTCGAGAAAAA 2599  
|||||  
Db 22 AAAAAACCAATTAAAGAAAAA 1

RESULT 126  
US-08-390-850-579

```
; Sequence 579, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: December 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 579:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-390-850-579

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 41.2%; Pred. No. 1.4e+02;
Matches 7; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTCTTTTAAAGGA 1048
Db 1 UUUUUUUUUUAAAGGA 17

RESULT 127
US-08-390-850-580
; Sequence 580, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: December 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-390-850-580

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.4e+02;
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1033 TTTCTTTTAAAGGA 1049
Db 1 UUUUUUUUUUAAAGGA 17

RESULT 128
US-08-373-124A-2155
; Sequence 2155, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
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/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
/ SOFTWARE: Word Perfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/373,124A  
/ FILING DATE: January 13, 1995  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/245,466  
/ FILING DATE: May 18, 1994  
/ APPLICATION NUMBER: 08/192,943  
/ FILING DATE: February 7, 1994  
/ APPLICATION NUMBER: 07/987,132  
/ FILING DATE: December 7, 1992  
/ APPLICATION NUMBER: 07/936,422  
/ FILING DATE: August 26, 1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Warburg, Richard  
/ REGISTRATION NUMBER: 32,327  
/ REFERENCE/DOCKET NUMBER: 209/035  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (213) 489-1600  
/ TELEFAX: (213) 955-0440  
/ TELEX: 67-3510  
/ INFORMATION FOR SEQ ID NO: 2155:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 17 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-08-373-124A-2155

Query Match 0.4%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 23.5%; Pred. No. 1.4e+02;  
Matches 4; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATA 1168  
:::||||:|:  
Db 1 UUAUUUUUAUAUA 17

RESULT 129  
US-08-373-124A-2157  
/ Sequence 2157, Application US/08373124A  
/ Patent No. 5646042  
/ GENERAL INFORMATION:  
/ APPLICANT: Stinchcomb, Dan T.  
/ APPLICANT: Draper, Kenneth  
/ APPLICANT: McSwiggen, James  
/ APPLICANT: Jarvis, Thale  
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
/ TITLE OF INVENTION: CANCER USING RIBOZYMES  
/ NUMBER OF SEQUENCES: 2627  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Lyon & Lyon  
/ STREET: 633 West Fifth Street  
/ STREET: Suite 4700  
/ CITY: Los Angeles  
/ STATE: California  
/ COUNTRY: U.S.A.  
/ ZIP: 90071  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
/ MEDIUM TYPE: storage  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
/ SOFTWARE: Word Perfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/373,124A  
/ FILING DATE: January 13, 1995  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/245,466  
/ FILING DATE: May 18, 1994

/ APPLICATION NUMBER: 08/192,943  
/ FILING DATE: February 7, 1994  
/ APPLICATION NUMBER: 07/987,132  
/ FILING DATE: December 7, 1992  
/ APPLICATION NUMBER: 07/936,422  
/ FILING DATE: August 26, 1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Warburg, Richard  
/ REGISTRATION NUMBER: 32,327  
/ REFERENCE/DOCKET NUMBER: 209/035  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (213) 489-1600  
/ TELEFAX: (213) 955-0440  
/ TELEX: 67-3510  
/ INFORMATION FOR SEQ ID NO: 2157:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 17 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-08-373-124A-2157

Query Match 0.4%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 23.5%; Pred. No. 1.4e+02;  
Matches 4; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTCTTTTATATATA 1169  
:::||||:|:  
Db 1 UUAUUUUUAUAUA 17

RESULT 130  
US-08-435-634-579  
/ Sequence 579, Application US/08435634  
/ Patent No. 5731295  
/ GENERAL INFORMATION:  
/ APPLICANT: Draper, Kenneth G.  
/ APPLICANT: Pavco, Pamela  
/ APPLICANT: McSwiggen, James  
/ APPLICANT: Gustofson, John  
/ APPLICANT: Stinchcomb, Dan T.  
/ TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
/ TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
/ NUMBER OF SEQUENCES: 1151  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Lyon & Lyon  
/ STREET: 633 West Fifth Street  
/ STREET: Suite 4700  
/ CITY: Los Angeles  
/ STATE: California  
/ COUNTRY: U.S.A.  
/ ZIP: 90071  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
/ MEDIUM TYPE: storage  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
/ SOFTWARE: FastSeq Version 1.5  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/435,634  
/ FILING DATE: 05-MAY-1995  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/390,850  
/ FILING DATE: February 17, 1995  
/ APPLICATION NUMBER: 08/354,920  
/ FILING DATE: December 13, 1994  
/ APPLICATION NUMBER: 08/152,487  
/ FILING DATE: No. 5731295ember 12, 1993  
/ APPLICATION NUMBER: 07/989,848  
/ FILING DATE: December 7, 1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 211/084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 579:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-435-634-579

Query Match 0.4%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 41.2%; Pred. No. 1.4e+02;  
Matches 7; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTCTTTTAAAGGA 1048  
DB 1 UUUCAUUUUAAAGGA 17

## RESULT 131

US-08-435-634-580  
; Sequence 580, Application US/08435634  
; Patent No. 5731295  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,634  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/390,850  
; FILING DATE: February 17, 1995  
; APPLICATION NUMBER: 08/354,920  
; FILING DATE: December 13, 1994  
; APPLICATION NUMBER: 08/152,487  
; FILING DATE: No. 5731295ember 12, 1993  
; APPLICATION NUMBER: 07/989,848  
; FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 211/084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 580:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-435-634-580

Query Match 0.4%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 47.1%; Pred. No. 1.4e+02;  
Matches 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1033 TTTCTTTTAAAGGA 1049  
DB 1 UUUCAUUUUAAAGGA 17

## RESULT 132

US-08-435-628-2155  
; Sequence 2155, Application US/08435628  
; Patent No. 5817796  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,628  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/373,124  
; FILING DATE: January 13, 1995  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2155:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-435-628-2155





```
; APPLICANT: Cole, Douglas
; APPLICANT: Guzaev, Andrei
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric Compounds
; FILE REFERENCE: ISIS3380
; CURRENT APPLICATION NUMBER: US/09/288,679
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Phosphorothioate backbone
US-09-288-679-3

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2

RESULT 136
US-09-288-679-5/c
; Sequence 5, Application US/09288679
; Patent No. 6465628
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; APPLICANT: Manoharan, Muthia
; APPLICANT: Capaldi, Daniel
; APPLICANT: Krotz, Achim
; APPLICANT: Cole, Douglas
; APPLICANT: Guzaev, Andrei
; TITLE OF INVENTION: Improved Process for the Synthesis of Oligomeric Compounds
; FILE REFERENCE: ISIS3380
; CURRENT APPLICATION NUMBER: US/09/288,679
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/118,564
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. 6465628el Sequence
US-09-288-679-5

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2

RESULT 137
US-09-725-265-18/c
; Sequence 18, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
```

```
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-18

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1

RESULT 138
US-09-556-127-18/c
; Sequence 18, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAWAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-18

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1

RESULT 139
US-09-316-447A-3
; Sequence 3, Application US/09316447A
```

```
/ Patent No. 6287774
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Assay Methods and Systems
/ FILE REFERENCE: 09316447
/ CURRENT APPLICATION NUMBER: US/09/316,447A
/ CURRENT FILING DATE: 1999-02-21
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-316-447A-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 140
US-09-727-532A-3
/ Sequence 3, Application US/09727532A
/ Patent No. 6436646
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Kinase Assays Using Polycations
/ FILE REFERENCE: 100/07930
/ CURRENT APPLICATION NUMBER: US/09/727,532A
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/316,447
/ PRIOR FILING DATE: 1999-05-21
/ PRIOR APPLICATION NUMBER: US 60/156,366
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/139,562
/ PRIOR FILING DATE: 1999-06-16
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PNA probe
US-09-727-532A-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 141
US-09-569-193A-3
/ Sequence 3, Application US/09569193A
/ Patent No. 6472141
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Kinase Assays Using Polycations
/ FILE REFERENCE: 100/07930
/ CURRENT APPLICATION NUMBER: US/09/569,193A
/ CURRENT FILING DATE: 2000-05-11
/ PRIOR APPLICATION NUMBER: US 09/316,447

/ Patent No. 6287774
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Assay Methods and Systems
/ FILE REFERENCE: 09316447
/ CURRENT APPLICATION NUMBER: US/09/316,447A
/ CURRENT FILING DATE: 1999-02-21
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-316-447A-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 142
US-09-422-978-4619
/ Sequence 4619, Application US/09422978
/ Patent No. 6537751
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Daniel
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
/ FILE REFERENCE: GENSET-020CP1
/ CURRENT APPLICATION NUMBER: US/09/422,978
/ CURRENT FILING DATE: 1999-10-20
/ EARLIER APPLICATION NUMBER: US 09/298,850
/ EARLIER FILING DATE: 1999-04-21
/ EARLIER APPLICATION NUMBER: US 60/109,732
/ EARLIER FILING DATE: 1998-11-23
/ EARLIER APPLICATION NUMBER: US 60/082,614
/ EARLIER FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 11796
/ SEQ ID NO 4619
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: 1..19
/ OTHER INFORMATION: upstream amplification primer 99-16399 for SEQ 685,
US-09-422-978-4619

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3126 GTTGTATTAGGACTAAG 3142
Db 2 GTTGTATTAGGACTAAG 18

RESULT 143
US-10-057-812A-3
/ Sequence 3, Application US/10057812A
/ Patent No. 6689565
/ GENERAL INFORMATION:
/ APPLICANT: Nikiforov, Theo T.
/ TITLE OF INVENTION: Kinase Assays Using Polycations
/ FILE REFERENCE: 100/07930
/ CURRENT APPLICATION NUMBER: US/10/057,812A
/ CURRENT FILING DATE: 2002-01-24
/ PRIOR APPLICATION NUMBER: US/09/569,193
```

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; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 09/316,447
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/156,366
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/139,562
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-057-812A-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 144
US-09-865-044-3
; Sequence 3, Application US/09865044
; Patent No. 6699655
; GENERAL INFORMATION:
; APPLICANT: Nikiforov, Theo T.
; TITLE OF INVENTION: Assay Methods and Systems
; FILE REFERENCE: 09316447
; CURRENT APPLICATION NUMBER: US/09/865,044
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 09/316,447
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-865-044-3

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 145
US-09-696-791-3526/c
; Sequence 3526, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3526
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```

; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3526

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CAGGAGAAAAAACAAC 941
Db 19 CAGGAGAAAAAACAAC 3

RESULT 146
US-09-696-791-3529/c
; Sequence 3529, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3529
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdc25 hs ribozyme binding site
US-09-696-791-3529

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAAACA 940
Db 17 CCAGGAGAAAAAACA 1

RESULT 147
US-09-687-246B-7
; Sequence 7, Application US/09687246B
; Patent No. 6709818
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins School of Medicine
; APPLICANT: Nelson, William
; APPLICANT: Tchou, Julia
; APPLICANT: Bakker, Jila
; APPLICANT: Lin, Xiaohui
; TITLE OF INVENTION: METHODS OF DIAGNOSING AND TREATING HEPATIC CELL PROLIFERATIVE DIS
; FILE REFERENCE: JHU1660-1
; CURRENT APPLICATION NUMBER: US/09/687,246B
; CURRENT FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/159,168
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer N-F1
US-09-687-246B-7
```

```

/ STATE: California
/ COUNTRY: USA
/ ZIP: 94306-2155
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/455,627
/ FILING DATE: 31-MAY-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nakamura, Jackie N.
/ REGISTRATION NUMBER: 35,966
/ REFERENCE/DOCKET NUMBER: LYNX-003/01 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-843-5000
/ TELEFAX: 415-857-0663
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ US-08-455-627-5

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814
DB 15 GTGAAAAA 1

RESULT 150
US-08-461-271-5/c
/ Sequence 5, Application US/08461271
/ Patent No. 5741643
/ GENERAL INFORMATION:
/ APPLICANT: Sergei M. Gryaznov
/ TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
/ TITLE OF INVENTION: and therapeutic applications
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
/ STREET: 465 Lincoln Centre Drive
/ CITY: Foster City
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch diskette
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: Windows 3.1/DOS 5.0
/ SOFTWARE: Microsoft Word for Windows, vers. 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/461,271
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/087,387
/ FILING DATE: 2-Jul-93
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stephen C. Macevicz
/ REGISTRATION NUMBER: 30,285
/ REFERENCE/DOCKET NUMBER: 104
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 358-7855
/ TELEFAX: (415) 358-7794
/ INFORMATION FOR SEQ ID NO: 5:

```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-461-271-5

Query Match          0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAAAAAAAAAA 2814
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 151
US-08-713-685A-5/c
; Sequence 5, Application US/08713685A
; Patent No. 5817795
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
; TITLE OF INVENTION: and therapeutic applications
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,685A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,271
; FILING DATE:
; APPLICATION NUMBER: 08/087,387
; FILING DATE: 2-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevicz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-713-685A-5

Query Match          0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAAAAAAAAAA 2814
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 152
US-08-689-856-5/c
; Sequence 5, Application US/08689856
```

```
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-689-856-5

Query Match          0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAAAAAAAAAA 2814
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 153
US-08-863-639A-8
; Sequence 8, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C.T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/863,639A  
; FILING DATE: May 28, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph E. Mueth  
; REGISTRATION NUMBER: 20,532  
; REFERENCE/DOCKET NUMBER: 11859-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (626) 796-4000  
; TELEFAX: (626) 795-6321  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; US-08-863-639A-8

Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2587  
Db 1 TTTAAAAA 15

## RESULT 154

US-08-832-021-17/c  
; Sequence 17, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardini, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-17

Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2587  
Db 15 TTTAAAAA 1

## RESULT 155

US-08-832-021-22/c  
; Sequence 22, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardini, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-22

Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2800 GTGAAAAA 2814  
Db 15 GTGAAAAA 1

## RESULT 156

US-09-070-477-5/c  
; Sequence 5, Application US/09070477  
; Patent No. 6048974  
; GENERAL INFORMATION:  
; APPLICANT: Sergei M. Gryaznov  
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
; TITLE OF INVENTION: and therapeutic applications  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics  
; STREET: 465 Lincoln Centre Drive  
; CITY: Foster City  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94040  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Windows 3.1/DOS 5.0  
; SOFTWARE: Microsoft Word for Windows, vers. 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,477  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,685  
; FILING DATE:  
; APPLICATION NUMBER: 08/461,271  
; FILING DATE:  
; APPLICATION NUMBER: 08/087,387  
; FILING DATE: 2-Jul-93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stephen C. Macevitz  
; REGISTRATION NUMBER: 30,285  
; REFERENCE/DOCKET NUMBER: 104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 358-7855  
; TELEFAX: (415) 358-7794  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-070-477-5

Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





NAME/KEY: misc\_feature  
LOCATION: 18  
OTHER INFORMATION: /note= "Amine moiety attached to 3'  
OTHER INFORMATION: end and phosphorothioate backbone"  
US-08-145-704-43

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCGCCCC 990  
Db 1 CCCCCCCCCCCCCCCCC 18

RESULT 160  
US-08-105-168B-21/c  
Sequence 21, Application US/08105168B  
Patent No. 5589585  
GENERAL INFORMATION:  
APPLICANT: MABILAT et al.  
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION  
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETECTION OF MYCOBACTERIA  
TITLE OF INVENTION: MYCOBACTERIA  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria,  
STATE: Virginia  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" DS/HD  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS DOS 3.1  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
FILING DATE: August 12, 1993  
APPLICATION NUMBER: US/08/105,168B  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR9210094  
FILING DATE: August 8, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: William P. Berridge  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 28835  
TELEPHONE: (703) 836-6400  
TELEFAX: (703) 836-2787  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL:  
ANTI-SENSE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
FEATURE:  
NAME/KEY:  
LOCATION: 640-657  
IDENTIFICATION METHOD:  
OTHER INFORMATION:

US-08-105-168B-21

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 359 CCTTGGCCGCTTGAGCA 376  
Db 18 CCTTGGCCGCTTGAGCA 1

RESULT 161  
US-08-698-948-21/c  
Sequence 21, Application US/08698948  
Patent No. 5849901  
GENERAL INFORMATION:  
APPLICANT: MABILAT et al.  
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION  
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETECTION OF MYCOBACTERIA  
TITLE OF INVENTION: MYCOBACTERIA  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oliff & Berridge  
STREET: 700 South Washington Street, Suite 300  
CITY: Alexandria,  
STATE: Virginia  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" DS/HD  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS DOS 3.1  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/698,948  
FILING DATE: August 16, 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/105,168  
FILING DATE: August 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR9210094  
FILING DATE: August 8, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: William P. Berridge  
REGISTRATION NUMBER: 30,024  
REFERENCE/DOCKET NUMBER: WPB 28835A  
TELEPHONE: (703) 836-6400  
TELEFAX: (703) 836-2787  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL:  
ANTI-SENSE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
FEATURE:  
NAME/KEY:  
LOCATION: 640-657  
IDENTIFICATION METHOD:  
OTHER INFORMATION:

US-08-698-948-21

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      359 CCTTGGCCGCTGGAGCA 376
Db      18 CCTTGGCCGCTGGAGCA 1

RESULT 162
US-08-358-556A-24
; Sequence 24, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelein, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; NAME/KEY: CDS
; LOCATION: 1..18
; US-08-358-556A-24

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      973 CCCCCCCCCCGCCGCC 990
Db      1 CCCCCCCCCCGCCGCC 18

RESULT 163
US-08-863-639A-15
; Sequence 15, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.

```

```

; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-15

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2666 ACAGCAACCAACCAACA 2683
Db      1 ACAACAACCAACCAACA 18

RESULT 164
US-08-863-639A-16
; Sequence 16, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435

```

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Joseph E. Mueth
/ REGISTRATION NUMBER: 20,532
/ REFERENCE/DOCKET NUMBER: 11859-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (626) 796-4000
/ TELEFAX: (626) 795-6321
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Other nucleic acid
/ US-08-639A-16

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2667 CAGCAACAACAACACAA 2684
Db 1 CAACAACAACAACA 18

RESULT 165
US-08-987-574-42
/ Sequence 42, Application US/08987574
/ Patent No. 6150339
/ GENERAL INFORMATION:
/ APPLICANT: Rando, Robert F.
/ APPLICANT: Fennewald, Susan
/ APPLICANT: Zendeigui, Joseph G.
/ APPLICANT: Ojwang, Joshua O.
/ APPLICANT: Hogan, Michael E.
/ TITLE OF INVENTION: Anti-Viral Guanosine-Rich
/ TITLE OF INVENTION: Oligonucleotides
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fulbright & Jaworski
/ STREET: 1301 McKinney, Suite 5100
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.A.
/ ZIP: 77010-3095
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/987,574
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/04529
/ FILING DATE: 28-OCT-1993
/ APPLICATION NUMBER: US 08/053,027
/ FILING DATE: 23-APR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paul, Thomas D.
/ REGISTRATION NUMBER: 32,714
/ REFERENCE/DOCKET NUMBER: D-5574-CIP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/651-5151
/ TELEFAX: 713/651-5246
/ TELEX: 762829
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 18
/ OTHER INFORMATION: /note= "Amine moiety
/ OTHER INFORMATION: attached to 3' end and phosphorothioate
/ OTHER INFORMATION: backbone"
/ US-08-987-574-43

/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 18
/ OTHER INFORMATION: /note= "Amine moiety
/ OTHER INFORMATION: attached to 3' end
/ OTHER INFORMATION: attached to 3' end"
/ US-08-987-574-42

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCGCCCC 990
Db 1 CCCCCCCCCCGCCCC 18

RESULT 166
US-08-987-574-43
/ Sequence 43, Application US/08987574
/ Patent No. 6150339
/ GENERAL INFORMATION:
/ APPLICANT: Rando, Robert F.
/ APPLICANT: Fennewald, Susan
/ APPLICANT: Zendeigui, Joseph G.
/ APPLICANT: Ojwang, Joshua O.
/ APPLICANT: Hogan, Michael E.
/ TITLE OF INVENTION: Anti-Viral Guanosine-Rich
/ TITLE OF INVENTION: Oligonucleotides
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fulbright & Jaworski
/ STREET: 1301 McKinney, Suite 5100
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.A.
/ ZIP: 77010-3095
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/987,574
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/04529
/ FILING DATE: 28-OCT-1993
/ APPLICATION NUMBER: US 08/053,027
/ FILING DATE: 23-APR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paul, Thomas D.
/ REGISTRATION NUMBER: 32,714
/ REFERENCE/DOCKET NUMBER: D-5574-CIP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/651-5151
/ TELEFAX: 713/651-5246
/ TELEX: 762829
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 18
/ OTHER INFORMATION: /note= "Amine moiety
/ OTHER INFORMATION: attached to 3' end and phosphorothioate
/ OTHER INFORMATION: backbone"
/ US-08-987-574-43
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Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCGCCCC 990  
 |||||  
 Db 1 CCCCCCCCCCCCCCCC 18

RESULT 167  
 US-08-535-168-42  
 ; Sequence 42, Application US/08535168  
 ; Patent No. 6184369  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rando, Robert F.  
 ; APPLICANT: Fennwald, Susan  
 ; APPLICANT: Zendequi, Joseph G.  
 ; APPLICANT: Ojwang, Joshua O.  
 ; APPLICANT: Hogan, Michael E.  
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
 ; TITLE OF INVENTION: Oligonucleotides  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fulbright & Jaworski  
 ; STREET: 1301 McKinney, Suite 5100  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: U.S.A.  
 ; ZIP: 77010-3095  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/535,168  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/04529  
 ; FILING DATE: 28-OCT-1993  
 ; APPLICATION NUMBER: US 08/053,027  
 ; FILING DATE: 23-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Paul, Thomas D.  
 ; REGISTRATION NUMBER: 32,714  
 ; REFERENCE/DOCKET NUMBER: D-5574-CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 713/651-5151  
 ; TELEFAX: 713/651-5246  
 ; TELEX: 762829  
 ; INFORMATION FOR SEQ ID NO: 42:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 18  
 ; OTHER INFORMATION: /note= "Amine moiety  
 ; OTHER INFORMATION: attached to 3' end"  
 ; OTHER INFORMATION: attached to 3' end"

US-08-535-168-42  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 973 CCCCCCCCCACCGCCCC 990  
 |||||  
 Db 1 CCCCCCCCCCCCCCCC 18

RESULT 169  
 US-09-475-316A-122/c  
 ; Sequence 122, Application US/09475316A  
 ; Patent No. 6210942  
 ; GENERAL INFORMATION:

RESULT 168  
 US-08-535-168-43  
 ; Sequence 43, Application US/08535168  
 ; Patent No. 6184369  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rando, Robert F.  
 ; APPLICANT: Fennwald, Susan  
 ; APPLICANT: Zendequi, Joseph G.  
 ; APPLICANT: Ojwang, Joshua O.  
 ; APPLICANT: Hogan, Michael E.  
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
 ; TITLE OF INVENTION: Oligonucleotides  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fulbright & Jaworski  
 ; STREET: 1301 McKinney, Suite 5100  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: U.S.A.  
 ; ZIP: 77010-3095  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/535,168  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/04529  
 ; FILING DATE: 28-OCT-1993  
 ; APPLICATION NUMBER: US 08/053,027  
 ; FILING DATE: 23-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Paul, Thomas D.  
 ; REGISTRATION NUMBER: 32,714  
 ; REFERENCE/DOCKET NUMBER: D-5574-CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 713/651-5151  
 ; TELEFAX: 713/651-5246  
 ; TELEX: 762829  
 ; INFORMATION FOR SEQ ID NO: 43:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 18  
 ; OTHER INFORMATION: /note= "Amine moiety  
 ; OTHER INFORMATION: attached to 3' end and phosphorothioate  
 ; OTHER INFORMATION: backbone"  
 ; OTHER INFORMATION: backbone"

US-08-535-168-43  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 973 CCCCCCCCCACCGCCCC 990  
 |||||  
 Db 1 CCCCCCCCCCCCCCCC 18

RESULT 169  
 US-09-475-316A-122/c  
 ; Sequence 122, Application US/09475316A  
 ; Patent No. 6210942  
 ; GENERAL INFORMATION:

```
; APPLICANT: Lewis, No. 6210942man G.
; APPLICANT: Davin, Laurence B.
; APPLICANT: Dinkova-Kostova, Albena T.
; APPLICANT: Fujita, Masayuki
; APPLICANT: Gang, David R.
; APPLICANT: Sarkanen, Simo
; APPLICANT: Ford, Joshua D
; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASES,
; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
; FILE REFERENCE: WSUR-1-13793
; CURRENT APPLICATION NUMBER: US/09/475,316A
; CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/307,653
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/US97/20391
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/054,380
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: 60/030,522
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (1)..(18)
; OTHER INFORMATION: Linker primer
US-09-475-316A-122

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2577 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAACTCGAG 1

RESULT 170
US-09-437-076-3/c
; Sequence 3, Application US/09437076
; Patent No. 6261779
; GENERAL INFORMATION:
; APPLICANT: Barber-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; APPLICANT: Castro, Stephanie
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form
; CURRENT APPLICATION NUMBER: US/09/437,076
; CURRENT FILING DATE: 1999-11-09
; EARLIER FILING DATE:
; EARLIER APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Word for Windows
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized
US-09-437-076-3

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCCCCCCCC 990
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Db 18 CCCCCCCCCCCCCCCCC 1

RESULT 171
US-09-017-974-42
; Sequence 42, Application US/09017974
; Patent No. 6288042
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Wallace, Thomas L.
; APPLICANT: Cossum, Paul A.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1800
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,974
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,374
; FILING DATE: 04-FEB-97
; APPLICATION NUMBER:
; FILING DATE: 09-DEC-97
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end"
US-09-017-974-42

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCCCCCCCC 990
Db 1 CCCCCCCCCCCCCCCCC 18

RESULT 172
US-09-017-974-43
; Sequence 43, Application US/09017974
; Patent No. 6288042
; GENERAL INFORMATION:
```

APPLICANT: Rando, Robert F.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
APPLICANT: Wallace, Thomas L.  
APPLICANT: Cossum, Paul A.  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich  
TITLE OF INVENTION: Tetrad Forming Oligonucleotides  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1800  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77002-2912  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word 97 (saved as .txt file)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,974  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/037,374  
FILING DATE: 04-FEB-97  
APPLICATION NUMBER:  
FILING DATE: 09-DEC-97  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06223  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 18  
OTHER INFORMATION: /note= "Amine moiety  
OTHER INFORMATION: attached to 3' end and phosphorothioate  
OTHER INFORMATION: backbone"  
US-09-017-974-43

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCACCGCCCC 990  
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 173  
US-08-682-255A-42  
Sequence 42, Application US/08682255A  
Patent No. 6323185  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennewald, Susan  
APPLICANT: Zendequi, Joseph G.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
APPLICANT: Pommier, Yves  
APPLICANT: Mazumder, Abhijit  
TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Oligonucleotides  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Conley, Rose & Tayon, P.C.  
STREET: 600 Travis, Suite 1850  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77002-2912  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS Windows 95  
SOFTWARE: MS Word 97 (saved as .txt file)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,255A  
FILING DATE: 17-JULY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/535,168  
FILING DATE: 23-OCT-95  
APPLICATION NUMBER: 60/001,505  
FILING DATE: 19-JULY-95  
APPLICATION NUMBER: 60/014,007  
FILING DATE: 25-MARCH-96  
APPLICATION NUMBER: 60/013,688  
FILING DATE: 19-MARCH-96  
APPLICATION NUMBER: 60/015,714  
FILING DATE: 17-APRIL-96  
APPLICATION NUMBER: 60/016,271  
FILING DATE: 23-APRIL-96  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, C. Steven  
REGISTRATION NUMBER: 33,962  
REFERENCE/DOCKET NUMBER: 1472-06214  
TELEPHONE: 713/238-8010  
TELEFAX: 713/238-8008  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 18  
OTHER INFORMATION: /note= "Amine moiety  
OTHER INFORMATION: attached to 3' end"  
US-08-682-255A-42

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCACCGCCCC 990  
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 174  
US-08-682-255A-43  
Sequence 43, Application US/08682255A  
Patent No. 6323185  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Fennewald, Susan  
APPLICANT: Zendequi, Joseph G.  
APPLICANT: Ojwang, Joshua O.  
APPLICANT: Hogan, Michael E.  
APPLICANT: Pommier, Yves  
APPLICANT: Mazumder, Abhijit

```
;
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,255A
; FILING DATE: 17-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168
; FILING DATE: 23-OCT-95
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/015,714
; FILING DATE: 17-APRIL-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 23-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end and phosphorothioate
; OTHER INFORMATION: backbone"
; US-08-682-255A-43

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCGCCCC 990
Db 1 CCCCCCCCCCGCGCCCC 18

RESULT 175
US-09-429-130-42
; Sequence 42, Application US/09429130
; Patent No. 6355785
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; Fennewald, Susan
; Zendegui, Joseph G.
; Ojwang, Joshua E.
; Hogan, Michael E.

; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/429,130
; FILING DATE: 28-Oct-1999
; CLASSIFICATION: <Unknown>
; 19-JULY-95
; 25-MARCH-96
; 19-MARCH-96
; 17-APRIL-96
; 23-APRIL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/682,255
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end"
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
; US-09-429-130-42

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCGCCCC 990
Db 1 CCCCCCCCCCGCGCCCC 18

RESULT 176
US-09-429-130-43
; Sequence 43, Application US/09429130
; Patent No. 6355785
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Db 1 CCCCCCCCCCCCCCCCCC

RESULT 177
US-08-535-249-72/c
; Sequence 72, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of cancer
; TITLE OF INVENTION: immuno-suppressive effect of transforming growth factor- $\beta$ 
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-72

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels

QY 1527 TATAAAATCGACATGCCG 1544
18 TACAAATAGACATGCCG 1

Db

RESULT 178
US-08-535-249-79/c
; Sequence 79, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar

```



```
/ APPLICANT: Bogdahn, Ulrich
/ TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
/   TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
/ NUMBER OF SEQUENCES: 137
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jacobson, Price, Holman & Stern
/ STREET: 400 Seventh St. N.W.
/ CITY: Washington D.C
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/535,249
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 93 107 089.0
/ FILING DATE: 30-APR-1993
/ PRIOR APPLICATION DATA: EP 93 107 849.7
/ FILING DATE: 13-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Player, William E.
/ REGISTRATION NUMBER: 31,409
/ REFERENCE/DOCKET NUMBER: 10577/P58418
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-6666
/ TELEX: RCA 248593 IDEA UR
/ INFORMATION FOR SEQ ID NO: 79:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
/ US-08-535-249-79

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1636 ATGCTTCGAATCTGGTGA 1653
Db 18 ATGCTTCCAATTGGTGA 1
||||| |||||

RESULT 179
US-08-535-249-85/c
/ Sequence 85, Application US/08535249
/ Patent No. 6455689
/ GENERAL INFORMATION:
/ APPLICANT: Schlengersiepen, Georg-Ferdinand
/ APPLICANT: Brysch, Wolfgang
/ APPLICANT: Schlengersiepen, Karl-Hermann
/ APPLICANT: Schlengersiepen, Reimar
/ APPLICANT: Bogdahn, Ulrich
/ TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
/   TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
/ NUMBER OF SEQUENCES: 137
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jacobson, Price, Holman & Stern
/ STREET: 400 Seventh St. N.W.
/ CITY: Washington D.C
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/535,249
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 93 107 089.0
/ FILING DATE: 30-APR-1993
/ PRIOR APPLICATION DATA: EP 93 107 849.0
/ FILING DATE: 13-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Player, William E.
/ REGISTRATION NUMBER: 31,409
/ REFERENCE/DOCKET NUMBER: 10577/P58418
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-6666
/ TELEX: RCA 248593 IDEA UR
/ INFORMATION FOR SEQ ID NO: 79:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
/ US-08-535-249-79
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/535,249
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 93 107 089.0
/ FILING DATE: 30-APR-1993
/ PRIOR APPLICATION DATA: EP 93 107 849.7
/ FILING DATE: 13-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Player, William E.
/ REGISTRATION NUMBER: 31,409
/ REFERENCE/DOCKET NUMBER: 10577/P58418
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-6666
/ TELEX: RCA 248593 IDEA UR
/ INFORMATION FOR SEQ ID NO: 85:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
/ US-08-535-249-85

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1711 GGATTGCACTGATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1
||||| |||||

RESULT 180
US-08-535-249-96/c
/ Sequence 96, Application US/08535249
/ Patent No. 6455689
/ GENERAL INFORMATION:
/ APPLICANT: Schlengersiepen, Georg-Ferdinand
/ APPLICANT: Brysch, Wolfgang
/ APPLICANT: Schlengersiepen, Karl-Hermann
/ APPLICANT: Schlengersiepen, Reimar
/ APPLICANT: Bogdahn, Ulrich
/ TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
/   TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
/ NUMBER OF SEQUENCES: 137
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jacobson, Price, Holman & Stern
/ STREET: 400 Seventh St. N.W.
/ CITY: Washington D.C
/ COUNTRY: U.S.A.
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/535,249
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 93 107 089.0
/ FILING DATE: 30-APR-1993
/ PRIOR APPLICATION DATA: EP 93 107 849.7
/ FILING DATE: 13-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Player, William E.
/ REGISTRATION NUMBER: 31,409
/ REFERENCE/DOCKET NUMBER: 10577/P58418
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-6666
/ TELEX: RCA 248593 IDEA UR
/ INFORMATION FOR SEQ ID NO: 85:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
/ US-08-535-249-85
```

```
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-96

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1880 AATAAGCTTACACTGCCC 1897
Db 18 AATAAGCTTACACTGTC 1

RESULT 181
US-08-535-249-115/c
; Sequence 115, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; ADDRESSES: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; APPLICATION DATA:
; FILING DATE: 13-MAY-1993
; APPLICATION NUMBER: EP 93 107 849.7
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-115

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2175 CGCCCTCTTTACATTGAT 2192
Db 18 CGTCCACTTTACATTGAT 1

RESULT 182
US-08-535-249-128/c
; Sequence 128, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; ADDRESSES: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; APPLICATION DATA:
; FILING DATE: 13-MAY-1993
; APPLICATION NUMBER: EP 93 107 849.7
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-128

Query Match          0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2375 ACCACTGACCATTTCTCTA 2392
```

Db 18 ACCTCTAACCAATCTCTA 1

## RESULT 183

US-08-535-249-132/c  
; Sequence 132, Application US/08535249  
; Patent No. 6455689  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; NUMBER OF INVENTIONS: Immuno-suppressive effect of transforming-growth-factor beta  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS: 137  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/535,249  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William B.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202)393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 132:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-08-535-249-132

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2439 GTCAAGTCTTGTAAATGC 2456

Db 18 GTAAAGTCTTGCAATGC 1

## RESULT 184

US-09-725-265-20/c  
; Sequence 20, Application US/09725265  
; Patent No. 6492121  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KANAGATA, YOICHI

; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; FILE REFERENCE: 199953USOXDIV  
; CURRENT APPLICATION NUMBER: US/09/725,265  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-725-265-20

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTTAC 1179

Db 18 ATATATATTTTCTTC 1

## RESULT 185

US-09-704-640-122/c  
; Sequence 122, Application US/09704640  
; Patent No. 6635459  
; GENERAL INFORMATION:  
; APPLICANT: Lewis, No. 6635459man G.  
; APPLICANT: Davin, Laurence B.  
; APPLICANT: Dinkova-Kostova, Albena T.  
; APPLICANT: Fujita, Masayuki  
; APPLICANT: Gang, David R.  
; APPLICANT: Sarkanen, Simo  
; APPLICANT: Ford, Joshua D  
; TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICRESINOL REDUCTASE,  
; TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEIN AND METHODS OF USE  
; FILE REFERENCE: WSUR-1-16492  
; CURRENT APPLICATION NUMBER: US/09/704,640  
; CURRENT FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: 09/475,316  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: 09/307,653  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: PCT/US97/20391  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: 60/054,380  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: 60/030,522  
; PRIOR FILING DATE: 1996-11-08  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 122  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (1)..(18)  
; OTHER INFORMATION: Linker primer  
US-09-704-640-122

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;  
Matches 16; Conservative 0;

QY 2577 AAAAAAAAAAATTGGAG 2594

Db 18 AAAAAAAAAAACTCGAG 1

RESULT 186  
US-09-556-127-20/c  
; Sequence 20, Application US/09556127  
; Patent No. 669661  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KAMAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/09/556,127  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-556-127-20

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;  
Matches 16; Conservative 0;

QY 1162 ATATATATTTTCTTAC 1179

Db 18 ATATATATTTTCTTTC 1

RESULT 187  
US-10-352-704-24  
; Sequence 24, Application US/10352704  
; Patent No. 6825339  
; GENERAL INFORMATION:  
; APPLICANT: Chatelain, Francois  
; APPLICANT: Kumarev, Viktor  
; TITLE OF INVENTION: Process for Preparing Polynucleotides on  
; a Solid Support and Apparatus Permitting its  
; Implementation  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; STATE: D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/352,704  
; FILING DATE: 28-Jan-2003  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/358,556A  
; FILING DATE: 14-DEC-1994  
; APPLICATION NUMBER: FR 9315164  
; FILING DATE: 16-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..18  
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-352-704-24

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCACCCGCCCC 990

Db 1 CCCCCCCCACCCGCCCC 18

RESULT 188  
US-09-904-744-3/c  
; Sequence 3, Application US/09904744  
; Patent No. 6828142  
; GENERAL INFORMATION:  
; APPLICANT: Barbera-Guillem, Emilio  
; APPLICANT: Nelsen, M. Bud  
; APPLICANT: Castro, Stephanie  
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form  
; FILE REFERENCE: B-73  
; CURRENT APPLICATION NUMBER: US/09/904,744  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/437076  
; PRIOR FILING DATE: 1999-11-09  
; PRIOR APPLICATION NUMBER: 60/107828  
; PRIOR FILING DATE: 1998-11-10  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized  
US-09-904-744-3  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCACCCGCCCC 990

```
Db      18 CCCCCCCCCCCCCCCCC 1
||||||| ||| |||
RESULT 189
PCT-US94-05407-5/c
; Sequence 5, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-05407-5

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      254 AGGAGAAGCTAGGAGG 271
Db      18 AGGAGAAGATAGGGAGG 1
||||||| ||| |||
RESULT 190
PCT-US96-11786-42
; Sequence 42, Application PC/TUS9611786
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Byves
; APPLICANT: Mazumder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11786
; FILING DATE: 17-JULY-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96

Db      18 CCCCCCCCCCCCCCCCC 1
||||||| ||| |||
RESULT 191
PCT-US96-11786-43
; Sequence 43, Application PC/TUS9611786
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Byves
; APPLICANT: Mazumder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11786
; FILING DATE: 17-JULY-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96

QY      973 CCCCCCCCCCGCCCC 990
Db      1 CCCCCCCCCCCCCCCCC 18
||||||| ||| |||
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PCT-US96-11786-42
; APPLICATION NUMBER: PCT/US96/11786
; FILING DATE: 17-JULY-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
; APPLICATION NUMBER: 60/015,714; 60/016,271
; FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
; FILING DATE: APRIL-96; 17-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end"
PCT-US96-11786-42
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end and phosphorothioate
; OTHER INFORMATION: backbone"
;
PCT-US96-11786-43

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCCGCC 990
Db 1 CCCCCCCCCCGCCGCC 18

RESULT 192
US-08-535-249-94/c
; Sequence 94, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
;
US-08-535-249-107
Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;

```

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; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
;
US-08-535-249-94

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1851 CACCACAAAGACAGGA 1866
Db 16 CACCATAAAGACAGGA 1

RESULT 193
US-08-535-249-107/c
; Sequence 107, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
;
US-08-535-249-107
Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;

```

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2060 CCTGCTAATGTTGTTG 2075  
|||||  
Db 16 CCTGCTAATGTTATTG 1

## RESULT 194

US-08-050-073-155  
; Sequence 155, Application US/08050073  
; Patent No. 5567809  
; GENERAL INFORMATION:  
; APPLICANT: Apple, Raymond J.  
; APPLICANT: Begovich, Ann B.  
; APPLICANT: Bugawan, Teodorica L.  
; APPLICANT: Erlich, Henry A.  
; APPLICANT: Griffith, Robert L.  
; APPLICANT: Scharf, Stephen J.  
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA  
; TITLE OF INVENTION: Typing  
; NUMBER OF SEQUENCES: 315  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,073  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 8769  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 155:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA

## US-08-050-073-155

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 365 CCGCTGGAGCAAGAA 380  
|||  
Db 1 CCTCCTGGAGCAAGAA 16

## RESULT 195

US-08-390-850-578  
; Sequence 578, Application US/08390850  
; Patent No. 5612215  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT

; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: U.S.A.  
; ZIP: 90071

## COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/390,850  
; FILING DATE: February 17, 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/354,920  
; FILING DATE: December 13, 1994  
; APPLICATION NUMBER: 08/152,487  
; FILING DATE: No. 5612215ember 12, 1993  
; APPLICATION NUMBER: 07/989,848  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 211/084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 578:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-390-850-578

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 37.5%; Pred. No. 2e+02;  
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTTCTTTTAAAGG 1047  
:::| :|||  
Db 2 UUUUCAUUUUAAGG 17

## RESULT 196

US-08-390-850-581  
; Sequence 581, Application US/08390850  
; Patent No. 5612215  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:

/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
/ MEDIUM TYPE: storage  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
/ SOFTWARE: FastSeq Version 1.5  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/390,850  
/ FILING DATE: February 17, 1995  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/354,920  
/ FILING DATE: December 13, 1994  
/ APPLICATION NUMBER: 08/152,487  
/ FILING DATE: No. 5612215ember 12, 1993  
/ APPLICATION NUMBER: 07/989,848  
/ FILING DATE: December 7, 1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Warburg, Richard  
/ REGISTRATION NUMBER: 32,327  
/ REFERENCE/DOCKET NUMBER: 211/084  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (213) 489-1600  
/ TELEFAX: (213) 955-0440  
/ TELEX: 67-3510  
/ INFORMATION FOR SEQ ID NO: 581:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 17 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-08-390-850-581

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1034 TTCTTTTAAAGGAA 1049  
Db 1 UUCAUUUUUAAGGAA 16

RESULT 197  
US-08-373-124A-2153  
/ Sequence 2153, Application US/08373124A  
/ Patent No. 5646042  
/ GENERAL INFORMATION:  
/ APPLICANT: Stinchcomb, Dan T.  
/ APPLICANT: Draper, Kenneth  
/ APPLICANT: McSwiggen, James  
/ APPLICANT: Jarvis, Thale  
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
/ TITLE OF INVENTION: CANCER USING RIBOZYMES  
/ NUMBER OF SEQUENCES: 2627  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Lyon & Lyon  
/ STREET: 633 West Fifth Street  
/ STREET: Suite 4700  
/ CITY: Los Angeles  
/ STATE: California  
/ COUNTRY: U.S.A.  
/ ZIP: 90071  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
/ MEDIUM TYPE: storage  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
/ SOFTWARE: Word Perfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/373,124A  
/ FILING DATE: January 13, 1995  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/245,466  
/ FILING DATE: May 18, 1994

/ APPLICATION NUMBER: 08/192,943  
/ FILING DATE: February 7, 1994  
/ APPLICATION NUMBER: 07/987,132  
/ FILING DATE: December 7, 1992  
/ APPLICATION NUMBER: 07/936,422  
/ FILING DATE: August 26, 1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Warburg, Richard  
/ REGISTRATION NUMBER: 32,327  
/ REFERENCE/DOCKET NUMBER: 209/035  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (213) 489-1600  
/ TELEFAX: (213) 955-0440  
/ TELEX: 67-3510  
/ INFORMATION FOR SEQ ID NO: 2153:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 17 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-08-373-124A-2153

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 18.8%; Pred. No. 2e+02;  
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATAT 1167  
Db 2 UUUUUUUUUUAU 17

RESULT 198  
US-08-373-124A-2159  
/ Sequence 2159, Application US/08373124A  
/ Patent No. 5646042  
/ GENERAL INFORMATION:  
/ APPLICANT: Stinchcomb, Dan T.  
/ APPLICANT: Draper, Kenneth  
/ APPLICANT: McSwiggen, James  
/ APPLICANT: Jarvis, Thale  
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
/ TITLE OF INVENTION: CANCER USING RIBOZYMES  
/ NUMBER OF SEQUENCES: 2627  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Lyon & Lyon  
/ STREET: 633 West Fifth Street  
/ STREET: Suite 4700  
/ CITY: Los Angeles  
/ STATE: California  
/ COUNTRY: U.S.A.  
/ ZIP: 90071  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
/ MEDIUM TYPE: storage  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
/ SOFTWARE: Word Perfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/373,124A  
/ FILING DATE: January 13, 1995  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/245,466  
/ FILING DATE: May 18, 1994  
/ APPLICATION NUMBER: 08/192,943  
/ FILING DATE: February 7, 1994  
/ APPLICATION NUMBER: 07/987,132  
/ FILING DATE: December 7, 1992  
/ APPLICATION NUMBER: 07/936,422  
/ FILING DATE: August 26, 1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Warburg, Richard  
/ REGISTRATION NUMBER: 32,327



; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2159:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-373-124A-2159

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 25.0%; Pred. No. 2e+02;  
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 1154 TCCTTTTATATATAT 1169  
Db 1 UAUUUUAUAUAU 16

## RESULT 199

US-08-373-124A-2161  
; Sequence 2161, Application US/08373124A  
; Patent No. 5646042

; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/373,124A  
; FILING DATE: January 13, 1995  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992

; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2161:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-373-124A-2161

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 25.0%; Pred. No. 2e+02;  
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 1156 TTTTATATATATTT 1171  
Db 1 UUUUUUAUAUAUGU 16

## RESULT 200

US-08-435-634-578  
; Sequence 578, Application US/08435634  
; Patent No. 5731295

; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,634  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514

; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/390,850  
; FILING DATE: February 17, 1995  
; APPLICATION NUMBER: 08/354,920  
; FILING DATE: December 13, 1994  
; APPLICATION NUMBER: 08/152,487  
; FILING DATE: No. 5731295ember 12, 1993  
; APPLICATION NUMBER: 07/989,848  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 211/084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 578:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-435-634-578

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 37.5%; Pred. No. 2e+02;  
Matches 6; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTTCTTTTAAAGG 1047  
: : : : :  
Db 2 UUUUUAUUUUAAGG 17

RESULT 201  
US-08-435-634-581  
; Sequence 581, Application US/08435634  
; Patent No. 5731295  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,634  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/390,850  
; FILING DATE: February 17, 1995  
; APPLICATION NUMBER: 08/354,920  
; FILING DATE: December 13, 1994  
; APPLICATION NUMBER: 08/152,487  
; FILING DATE: No. 5731295 September 12, 1993  
; APPLICATION NUMBER: 07/989,848  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 211/084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 581:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-435-634-581

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1034 TTTCTTTTAAAGGAA 1049  
: : : : :  
Db 1 UUCAUUUUAAGGAA 16

RESULT 202  
US-08-435-628-2153  
; Sequence 2153, Application US/08435628

; Patent No. 5817796  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,628  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/373,124  
; FILING DATE: January 13, 1995  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2153:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-435-628-2153

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 18.8%; Pred. No. 2e+02;  
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTTCTTTTATATAT 1167  
: : : : :  
Db 2 UUUUUUUUUUAUAU 17

RESULT 203  
US-08-435-628-2159  
; Sequence 2159, Application US/08435628  
; Patent No. 5817796  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale

```
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
/ TITLE OF INVENTION: CANCER USING RIBOZYMES
/ NUMBER OF SEQUENCES: 2627
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/435,628
/ FILING DATE: 05-MAY-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/373,124
/ FILING DATE: January 13, 1995
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994
/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2159:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-435-628-2159

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 2e+02;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

Qy 1154 TCTTTTATATATAT 1169
Db 1 UAUUUUUUAUAUAU 16

RESULT 204
US-08-435-628-2161
; Sequence 2161, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
```

```
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/435,628
/ FILING DATE: 05-MAY-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/373,124
/ FILING DATE: January 13, 1995
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994
/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2161:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-435-628-2161

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 25.0%; Pred. No. 2e+02;
Matches 4; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

Qy 1156 TTTTATATATATTT 1171
Db 1 UUUUUUAUAUAU 16

RESULT 205
US-08-173-489C-92
; Sequence 92, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
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; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from superoxide
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 92 :FROM 1 TO 17
;
US-08-173-489C-92

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2930 CCCCCTCCCTCTCC 2945
|||||
DB 1 CCCCCTCCCTCTCC 16

RESULT 206
US-08-173-489C-95
; Sequence 95, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: superoxide dismutase gene (accession #
; DESCRIPTION: J02947) nucleotides 1212 to 1228
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: chromosome 21
; MAP POSITION: 21q22.1
; PUBLICATION INFORMATION:
; AUTHORS: Hjalmarsson, K, Marklund, S L,
; AUTHORS: Engstroem, A, Edlund, T.
; TITLE: Isolation and sequence of
; TITLE: complementary dna encoding human extracellular-
; TITLE: superoxide dismutase
; JOURNAL: Proceedings of the National Academy of
; JOURNAL: Sciences, USA
; VOLUME: 84
; PAGES: 6340-6344
; DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 95 :FROM 1 TO 17
;
US-08-173-489C-95

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 975 CCCCCACCCCGCCCC 990
|||||
DB 2 CCCCCACCCCTCCCC 17

RESULT 207
US-08-584-040-4006
; Sequence 4006, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
```

```
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 4006:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-4006

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 2 UCUCUCCUCCACGUGAC 17

RESULT 208
US-08-584-040-7828/c
; Sequence 7828, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
```

```
/ INFORMATION FOR SEQ ID NO: 7828:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-7828

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 ACAGCAACAACAACCA 2681
Db 17 ACAGCAACAACAACA 2

RESULT 209
US-09-371-772B-1773
; Sequence 1773, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1773
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-371-772B-1773

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 2 UCUCUCCUCCACGUGAC 17

RESULT 210
US-09-371-772B-3612/c
; Sequence 3612, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3612
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3612

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 ACAGCAACAAACCAACCA 2681
Db 17 ACAGCAACAAACAAACA 2

RESULT 211
US-09-371-772B-6425
; Sequence 6425, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6425
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6425

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 1 UCUCUCCACGUGAC 16

RESULT 212
US-09-685-664B-1773
; Sequence 1773, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
```

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; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1773
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1773

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828
Db 2 UCUCUCCACGUGAC 17

RESULT 213
US-09-685-664B-3612/c
; Sequence 3612, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3612
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3612

Query Match          0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 ACAGCAACAAACCAACCA 2681
Db 17 ACAGCAACAAACAAACA 2

RESULT 214
US-09-197-360-19
; Sequence 19, Application US/09197360
; Patent No. 5962673
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0018
; CURRENT APPLICATION NUMBER: US/09/197,360
; CURRENT FILING DATE: 1998-11-28
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

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; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-679-645-1157

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. NO. 2.2e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 586 CTCCTCCGCGGCTCGCC 601
DB 2 CUCCCCGCCGUCGCC 17
|:||||| |:|||||
|:||||| |:|||||

RESULT 217
US-09-637-751A-7/c
; Sequence 7, Application US/09637751A
; Patent No. 6383754
; GENERAL INFORMATION:
; APPLICANT: Kaufman, Joseph C.
; APPLICANT: Roth, Matthew E.
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Feng, Li
; APPLICANT: Latimer, Darin R.
; TITLE OF INVENTION: Binary Encoded Sequence Tags
; Patent No. 6383754
; FILE REFERENCE: AGL 100
; CURRENT APPLICATION NUMBER: US/09/637,751A
; CURRENT FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-637-751A-7

Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. NO. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAAACA 2816
DB 18 TGAATAAAAAAAAAAAA 3
|||||||
|||||||

RESULT 218

```

```
US-09-856-074B-19
; Sequence 19, Application US/09856074B
; Patent No. 6395545
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-ALPHA EXPRESSION
; FILE REFERENCE: RTSP-0117
; CURRENT APPLICATION NUMBER: US/09/856,074B
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US/09/197,360
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US/09/856,074
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-856-074B-19

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3727 TATTTTATGTATGTC 3742
Db 1 TATTTTATGTATTC 16

RESULT 219
US-09-725-265-15/c
; Sequence 15, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-15

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 221
US-09-725-265-17/c
; Sequence 17, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17
```

```
RESULT 220
US-09-725-265-16/c
; Sequence 16, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-16

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 221
US-09-725-265-17/c
; Sequence 17, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17
```



```
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 222
US-09-725-265-19/c
; Sequence 19, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199933USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-19

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 223
US-09-556-127-15/c
; Sequence 15, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-15

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 224
US-09-556-127-16/c
; Sequence 16, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-556-127-16

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTTTTT 3

RESULT 225
US-09-556-127-17/c
; Sequence 17, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
```

; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-556-127-17

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
|||||  
Db 18 ATATATATTTTCTT 3

RESULT 226  
US-09-556-127-19/c  
; Sequence 19, Application US/09556127  
; Patent No. 6699661  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, YUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KANAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOKAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; FILE OF INVENTION: THE METHOD  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/09/556,127  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-556-127-19

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
|||||  
Db 18 ATATATATTTTCTT 3

RESULT 227  
US-09-994-311-7/c  
; Sequence 7, Application US/09994311  
; Patent No. 6773886  
; GENERAL INFORMATION:  
; APPLICANT: Kaufman, Joseph C.  
; APPLICANT: Roth, Matthew B.  
; APPLICANT: Lizardi, Paul M.  
; APPLICANT: Peng, Li  
; APPLICANT: Latimer, Darin R.  
; TITLE OF INVENTION: Binary Encoded Sequence Tags  
; Patent No. 6773886  
; FILE REFERENCE: AGL 100

; CURRENT APPLICATION NUMBER: US/09/994,311  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: US/09/637,751  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-994-311-7

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACA 2816  
|||||  
Db 18 TGAATAAAAAAAAAACA 3

RESULT 228  
US-09-904-744-2/c  
; Sequence 2, Application US/09904744  
; Patent No. 6828142  
; GENERAL INFORMATION:  
; APPLICANT: Barbera-Guillem, Emilio  
; APPLICANT: Nelson, M. Bud  
; APPLICANT: Castro, Stephanie  
; TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form  
; TITLE OF INVENTION: dendrimers in a signal amplification system  
; FILE REFERENCE: B-73  
; CURRENT APPLICATION NUMBER: US/09/904,744  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/437076  
; PRIOR FILING DATE: 1999-11-09  
; PRIOR APPLICATION NUMBER: 60/107828  
; PRIOR FILING DATE: 1998-11-10  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthesized  
US-09-904-744-2

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACCAACC 946  
|||||  
Db 17 AAAAAAAAAACCAACC 2

RESULT 229  
US-08-832-021-5/c  
; Sequence 5, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardini, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02

NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5  
LENGTH: 14  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-5

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAA 2587

DB 14 TTAAAAA 1

## RESULT 230

US-08-832-021-9/c  
Sequence 9, Application US/08832021

Patent No. 6045998

GENERAL INFORMATION:

APPLICANT: Combates, N.

APPLICANT: Pardini, J.

APPLICANT: Parimoo, S.

APPLICANT: Prouty, S.

APPLICANT: Stenn, K.

TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

FILE REFERENCE: JBP-382

CURRENT APPLICATION NUMBER: US/08/832,021

CURRENT FILING DATE: 1997-04-02

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 14

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-9

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGA 2814

DB 14 TGA 1

## RESULT 231

US-08-724-466B-17/c

Sequence 17, Application US/08724466B

Patent No. 6063606

GENERAL INFORMATION:

APPLICANT: Petkovich, P. Martin, White, Jay A.

APPLICANT: Beckett, Barbara R., Jones, Glenville

TITLE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Blake, Cassels & Graydon

STREET: Box 25, Commerce Court West

CITY: Toronto

ZIP: M5L 1A9

COUNTRY: Canada

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: WORD PERFECT

CURRENT APPLICATION DATA:

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: US/08/724,466B  
FILING DATE: October 1, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/667,546

FILING DATE: June 21, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Hunt, John C.

REGISTRATION NUMBER: 36,424

REFERENCE/DOCKET NUMBER: 50767/00004

TELEPHONE: (416) 863-4344

TELEFAX: (416) 863-2653

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-724-466B-17

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAA 2587

DB 14 TTAAAAA 1

## RESULT 232

US-08-724-466B-21/c

Sequence 21, Application US/08724466B

Patent No. 6063606

GENERAL INFORMATION:

APPLICANT: Petkovich, P. Martin, White, Jay A.

APPLICANT: Beckett, Barbara R., Jones, Glenville

TITLE OF INVENTION: Retinoid Metabolizing Protein

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Blake, Cassels & Graydon

STREET: Box 25, Commerce Court West

CITY: Toronto

ZIP: M5L 1A9

COUNTRY: Canada

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

COMPUTER: COMPAQ, IBM PC compatible

OPERATING SYSTEM: MS-DOS 5.1

SOFTWARE: WORD PERFECT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,466B

FILING DATE: October 1, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/667,546

FILING DATE: June 21, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Hunt, John C.

REGISTRATION NUMBER: 36,424

REFERENCE/DOCKET NUMBER: 50767/00004

TELEPHONE: (416) 863-4344

TELEFAX: (416) 863-2653

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-724-466B-21

QY 2801 TGAIAAAAAAAAAA 2814  
Db 14 TGAIAAAAAAAAAA 1

RESULT 233  
US-08-882-164D-17/c  
; Sequence 17, Application US/08882164D  
; Patent No. 6306624  
; GENERAL INFORMATION:  
; APPLICANT: Petkovich, P. Martin, White, Jay A.,  
; APPLICANT: Beckett, Barbara R., Jones, Glenville  
; TITLE OF INVENTION: Retinoid Metabolizing Protein  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Blake, Cassels & Graydon  
; STREET: Box 25, Commerce Court West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5L 1A9  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
; COMPUTER: COMPAQ, IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 5.1  
; SOFTWARE: WORD PERFECT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/882,164D  
; FILING DATE: June 25, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/667,546  
; FILING DATE: June 21, 1996  
; APPLICATION NUMBER: 08/724,466  
; FILING DATE: October 1, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunt, John C.  
; REGISTRATION NUMBER: 36,424  
; REFERENCE/DOCKET NUMBER: 50767/00010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 863-4344  
; TELEFAX: (416) 863-2653  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-882-164D-17

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAIAAAAAAAAAA 2587  
Db 14 TTAIAAAAAAAAAA 1

RESULT 234  
US-08-882-164D-21/c  
; Sequence 21, Application US/08882164D  
; Patent No. 6306624  
; GENERAL INFORMATION:  
; APPLICANT: Petkovich, P. Martin, White, Jay A.,  
; APPLICANT: Beckett, Barbara R., Jones, Glenville  
; TITLE OF INVENTION: Retinoid Metabolizing Protein  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Blake, Cassels & Graydon  
; STREET: Box 25, Commerce Court West  
; CITY: Toronto  
; STATE: Ontario

; COUNTRY: Canada  
; ZIP: M5L 1A9  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
; COMPUTER: COMPAQ, IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 5.1  
; SOFTWARE: WORD PERFECT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/882,164D  
; FILING DATE: June 25, 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/667,546  
; FILING DATE: June 21, 1996  
; APPLICATION NUMBER: 08/724,466  
; FILING DATE: October 1, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunt, John C.  
; REGISTRATION NUMBER: 36,424  
; REFERENCE/DOCKET NUMBER: 50767/00010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 863-4344  
; TELEFAX: (416) 863-2653  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-882-164D-21

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAIAAAAAAAAAA 2814  
Db 14 TGAIAAAAAAAAAA 1

RESULT 235  
US-08-535-249-57/c  
; Sequence 57, Application US/08535249  
; Patent No. 6455689  
; GENERAL INFORMATION:  
; APPLICANT: Schlengersiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlengersiepen, Karl-Hermann  
; APPLICANT: Schlengersiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta (1  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,249  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Player, William E.
/ REGISTRATION NUMBER: 31,409
/ REFERENCE/DOCKET NUMBER: 10577/P58418
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-6666
/ TELEFAX: (202) 393-5350
/ TELEX: RCA 248593 IDEA UR
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
US-08-535-249-57

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACACTGTGTG 1232
Db 14 TGCACACTGTGTG 1

RESULT 236
US-08-535-249-63/c
Sequence 63, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-71

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAG 1520
Db 14 CAGATCCTGAGCAA 1
```

```
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
US-08-535-249-63

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAA 1357
Db 14 CAGATCCTGAGCAA 1

RESULT 237
US-08-535-249-71/c
Sequence 71, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-535-249-71

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAG 1520
Db 14 CAGATCCTGAGCAA 1
```

Db 14 AGTACTACGCAAG 1

## RESULT 238

US-08-535-249-74/c

; Sequence 74, Application US/08535249

; Patent No. 6455689

; GENERAL INFORMATION:

; APPLICANT: Schlengersiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlengersiepen, Karl-Hermann

; APPLICANT: Schlengersiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/535,249

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666

; TELEFAX: (202) 393-5350

; TELEX: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-08-535-249-74

Query Match 0.3%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AAAATGCCATCCCG 1574

Db 14 AAAATGCCATCCCG 1

## RESULT 239

US-08-535-249-75/c

; Sequence 75, Application US/08535249

; Patent No. 6455689

; GENERAL INFORMATION:

; APPLICANT: Schlengersiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlengersiepen, Karl-Hermann

; APPLICANT: Schlengersiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/535,249

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 089.0

; FILING DATE: 30-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93 107 849.7

; FILING DATE: 13-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10577/P58418

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666

; TELEFAX: (202) 393-5350

; TELEX: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 75:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-08-535-249-75

Query Match 0.3%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCCACTTTCTACAG 1588

Db 14 CCCACTTTCTACAG 1

## RESULT 240

US-08-535-249-91/c

; Sequence 91, Application US/08535249

; Patent No. 6455689

; GENERAL INFORMATION:

; APPLICANT: Schlengersiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlengersiepen, Karl-Hermann

; APPLICANT: Schlengersiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; transforming-growth-factor beta

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,249  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION/DOCKET NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-08-535-249-91

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1807 AATGGCTCTCCTTC 1820  
Db 14 AATGGCTCTCCTTC 1

RESULT 241  
US-08-535-249-101/c  
; Sequence 101, Application US/08535249  
; Patent No. 6455689  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,249  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs

; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION/DOCKET NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: YES  
US-08-535-249-101

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGGCAC 1984  
Db 14 GGTATTGATGGCAC 1

RESULT 242  
US-08-535-249-103/c  
; Sequence 103, Application US/08535249  
; Patent No. 6455689  
; GENERAL INFORMATION:  
; APPLICANT: Schlingensiepen, Georg-Ferdinand  
; APPLICANT: Brysch, Wolfgang  
; APPLICANT: Schlingensiepen, Karl-Hermann  
; APPLICANT: Schlingensiepen, Reimar  
; APPLICANT: Bogdahn, Ulrich  
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/535,249  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 93 107 089.0  
; FILING DATE: 30-APR-1993  
; APPLICATION NUMBER: EP 93 107 849.7  
; FILING DATE: 13-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION/DOCKET NUMBER: 10577/P58418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)638-6666  
; TELEFAX: (202) 393-5350  
; TELEX: RCA 248593 IDEA UR  
; INFORMATION FOR SEQ ID NO: 103:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-103

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 CAGTGGTGATCAGA 2010
DB 14 CAGTGGTGATCAGA 1

RESULT 243
US-08-535-249-106/c
; Sequence 106, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-106

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AAGACCCCATCT 2059
DB 14 AAGACCCCATCT 2059

```

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DB 14 AAGACCCCATCT 1

RESULT 244
US-08-535-249-122/c
; Sequence 122, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-122

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACACT 2291
DB 14 GGAGTTCAGACACT 1

RESULT 245
US-08-535-249-136/c
; Sequence 136, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann

```



APPLICANT: Schlingensiepen, Reimar  
APPLICANT: Bogdahn, Ulrich  
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta  
NUMBER OF SEQUENCES: 137  
CORRESPONDENCE ADDRESS: 137  
ADDRESSEE: Jacobson, Price, Holman & Stern  
STREET: 400 Seventh St. N.W.  
CITY: Washington D.C  
COUNTRY: U.S.A.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/535,249  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93 107 089.0  
FILING DATE: 30-APR-1993  
PRIOR APPLICATION DATA: EP 93 107 849.7  
FILING DATE: 13-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William E.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELEPHONE: (202)638-6666  
TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 136:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-08-535-249-136

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235  
DB 14 ACTACTGTGTGCTG 1

RESULT 246  
US-09-475-947A-310  
Sequence 310, Application US/09475947A  
Patent No. 6472154  
GENERAL INFORMATION:  
APPLICANT: Garner, Harold R.  
APPLICANT: Wren, Jonathan D.  
APPLICANT: Minna, John D.  
TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
FILE REFERENCE: UTS00667  
CURRENT APPLICATION NUMBER: US/09/475,947A  
CURRENT FILING DATE: 1999-12-31  
NUMBER OF SEQ ID NOS: 346  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 310  
LENGTH: 14  
TYPE: DNA  
ORGANISM: human  
US-09-475-947A-310

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACAAA 944  
DB 1 AAAAAAAAAACAAA 14

RESULT 247  
US-08-182-968A-299/c  
Sequence 299, Application US/08182968A  
Patent No. 5610054  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 299:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-299

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCGAGAGGCGCT 3223  
DB 15 TGCCGAGAGGCGCT 2

RESULT 248  
US-08-182-968A-300/c  
Sequence 300, Application US/08182968A  
Patent No. 5610054  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION

; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/182,968A  
; FILING DATE: 13-JANUARY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: 14-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 205/277  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 300:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-182-968A-300

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCGAGAGGCT 3223  
Db 14 TGCCGAGAGGCT 1

RESULT 249  
US-08-292-620A-359/c  
; Sequence 359, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwigen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620A  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 359:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-292-620A-359

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAT 2589  
Db 15 AAAAAAAAAAAAT 2

RESULT 250  
US-08-292-620A-360/c  
; Sequence 360, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwigen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620A  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 360:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

two

US-08-292-620A-360  
Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 2576 AAAAAAAAAAAT 2589  
DB 14 AAAAAAAAAAAT 1

US-08-292-620A-364/C  
Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 2576 AAAAAAAAAAAT 2589  
DB 14 AAAAAAAAAAAT 1

RESULT 251  
US-08-292-620A-364/C  
Sequence 364, Application US/08292620A  
Patent No. 5837542  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
FILING DATE: December 7, 1992

two

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 364:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-364

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 2801 TGAIAAAAAAAAAA 2814  
DB 15 TGAIAAAAAAAAAA 2

RESULT 252  
US-08-292-620A-365/C  
Sequence 365, Application US/08292620A  
Patent No. 5837542  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

two

; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 365:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-292-620A-365

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TCAAAAAAAAAA 2814  
Db 14 TCAAAAAAAAAA 1

RESULT 253  
US-08-774-306A-299/c  
; Sequence 299, Application US/08774306A  
; Patent No. 5869253  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774.306A  
FILING DATE: December 26, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 299:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-306A-299

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGGCCT 3223  
Db 15 TGCCCAAGGCCT 2

RESULT 254  
US-08-774-306A-300/c  
; Sequence 300, Application US/08774306A  
; Patent No. 5869253  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774.306A  
FILING DATE: December 26, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 300:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-306A-300

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGGCCT 3223  
Db 14 TGCCCAAGGCCT 1

RESULT 255  
US-08-886-456-1/c  
; Sequence 1, Application US/08886456  
; Patent No. 5959090  
; GENERAL INFORMATION:  
; APPLICANT: Guzaev, Andrei  
; APPLICANT: Azhayev, Alex

APPLICANT: Lomborg, Harri  
TITLE OF INVENTION: Chemical Phosphorylation of Oligonucleotides and  
FILE OF INVENTION: Reactants Used Therefor  
FILE REFERENCE: 05566.0009-00  
CURRENT APPLICATION NUMBER: US/08/886,456  
CURRENT FILING DATE: 1997-07-01  
EARLIER APPLICATION NUMBER: 60/021,099

;  
; EARLIER FILING DATE: 1996-07-02  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Rattus rattus  
US-08-886-456-1

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2524 ACGACCATGATGTT 2537  
Db 15 ACGACCATGATGTT 2

RESULT 256  
US-08-832-021-18/c  
; Sequence 18, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardini, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-18

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2587  
Db 14 TTAATAAAAAAAAAA 1

RESULT 257  
US-08-832-021-19  
; Sequence 19, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardini, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-19

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAAAG 2758  
Db 2 TTTTNTTTTAAAG 15

RESULT 258  
US-08-832-021-19/c  
; Sequence 19, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardini, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-19

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2587  
Db 14 TTAATAAAAAAAAAA 1

RESULT 259  
US-08-832-021-20/c  
; Sequence 20, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardini, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-20

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2587

Db 14 TTAATAAAAAAAAAA 1

RESULT 260

US-08-832-021-21/c  
; Sequence 21, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-21

Query Match

Best Local Similarity 0.3%; Score 14; DB 1; Length 15;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814

Db 14 TGAATAAAAAAAAAA 1

RESULT 261

US-08-832-021-23/c  
; Sequence 23, Application US/08832021

; Patent No. 6045998

; GENERAL INFORMATION:

; APPLICANT: Combates, N.

; APPLICANT: Pardinas, J.

; APPLICANT: Parimoo, S.

; APPLICANT: Prouty, S.

; APPLICANT: Stenn, K.

; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 23

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-23

Query Match

Best Local Similarity 0.3%; Score 14; DB 1; Length 15;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814

Db 14 TGAATAAAAAAAAAA 1

RESULT 262

US-08-832-021-24/c  
; Sequence 24, Application US/08832021

; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardinas, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY

; FILE REFERENCE: JBP-382

; CURRENT APPLICATION NUMBER: US/08/832,021

; CURRENT FILING DATE: 1997-04-02

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-24

Query Match

Best Local Similarity 0.3%; Score 14; DB 1; Length 15;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814

Db 14 TGAATAAAAAAAAAA 1

RESULT 263

US-09-064-156A-299/c

; Sequence 299, Application US/09064156A

; Patent No. 6132966

; GENERAL INFORMATION:

; APPLICANT: Draper, Kenneth G.

; TITLE OF INVENTION: METHOD AND REAGENT FOR

; TITLE OF INVENTION: INHIBITING HEPATITIS C

; TITLE OF INVENTION: VIRUS REPLICATION

; NUMBER OF SEQUENCES: 498

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/064,156A

; FILING DATE: April 21, 1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/774,306

; FILING DATE: December 26, 1996

; APPLICATION NUMBER: 08/182,968

; FILING DATE: January 13, 1994

; APPLICATION NUMBER: 07/882,888

; FILING DATE: May 14, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 234/083

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 299:

/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
US-09-064-156A-299

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGGCCT 3223  
Db 15 TGCCCAAGGCCT 2

RESULT 264  
US-09-064-156A-300/c  
; Sequence 300, Application US/09064156A  
; Patent No. 6132966  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 498  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/064,156A  
; FILING DATE: April 21, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/774,306  
; FILING DATE: December 26, 1996  
; APPLICATION NUMBER: 08/182,968  
; FILING DATE: January 13, 1994  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: May 14, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 234/083  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 300:

/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
US-09-064-156A-300

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGGCCT 3223  
Db 14 TGCCCAAGGCCT 1

RESULT 265  
US-09-071-845-359/c  
; Sequence 359, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620  
; FILING DATE: August 17, 1994  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 359:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-071-845-359

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAT 2589  
Db 15 AAAAAAAAAAAT 2

RESULT 266  
US-09-071-845-360/c  
; Sequence 360, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:

```

; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-360

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAT 2589
Db 14 AAAAAAAAAAAAT 1

RESULT 267
US-09-071-845-364/c
; Sequence 364, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS

```

```

; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 364:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-364

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAIAAAAAAAAAA 2814
Db 15 TGAIAAAAAAAAAA 2

RESULT 268
US-09-071-845-365/c
; Sequence 365, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

```



STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/009,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 365:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-365

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2801 TGAIAAAAAAAAAA 2814  
Db 14 TGAIAAAAAAAAAA 1

RESULT 269  
US-08-242-664-30/c  
Sequence 30, Application US/08242664  
Patent No. 5571937  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA: US/08/242,664  
FILING DATE: May 12, 1994  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 44683  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-242-664-30

Query Match 0.3%; Score 14; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1169 TTTTCTTACTTT 1182  
Db 15 TTTTCTTACTTT 2

RESULT 270  
US-08-484-138-30/c  
Sequence 30, Application US/08484138  
Patent No. 5652350  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA: US/08/484,138  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 44683-2/JPM/WJG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-484-138-30

Query Match 0.3%; Score 14; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1169 TTTTCTTACTTT 1182  
Db 15 TTTTCTTACTTT 2

```

Db      15 TTTTCTTACTTT 2

RESULT 271
PCT-US95-06379-30/c
; Sequence 30, Application PC/TUS9506379
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-Yun
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-30

Query Match      0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1169 TTTTCTTACTTT 1182
Db      15 TTTTCTTACTTT 2

RESULT 272
US-09-300-958A-63/c
; Sequence 63, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85

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```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-63

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2575 TAAAAAAAAAAAAA 2588
Db      17 TAAAAAAAAAAAAA 4

RESULT 273
US-09-090-672B-105/c
; Sequence 105, Application US/09090672B
; Patent No. 6828428
; GENERAL INFORMATION:
; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigemasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
US-09-090-672B-105

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2575 TAAAAAAAAAAAAA 2588
Db      17 TAAAAAAAAAAAAA 4

```

```
RESULT 274
US-09-300-958A-63
; Sequence 63, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-300-958A-63

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3263 ATTTTTCCTTTTA 3279
Db 1 ATTTTTCCTTTTA 17

RESULT 275
US-08-281-940-54
; Sequence 54, Application US/08281940
; Patent No. 5589330
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: METHOD FOR MULTIPLE ALLELE-SPECIFIC
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY P.C.
; STREET: 805 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,940
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUDWIG, S. PETER
; REGISTRATION NUMBER: 25351
; REFERENCE/DOCKET NUMBER: 0372/09696
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/527-7700
; TELEFAX: 212/753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-281-940-54

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.4e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
;
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; IMMEDIATE SOURCE:
; CLONE: 2184dAN
; US-08-281-940-54

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATTTGTTTC 3636
Db 1 GATTGTATTTGTTTC 17

RESULT 276
US-08-758-306-1333
; Sequence 1333, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1333:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-1333

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.4e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3761 ACCTGGGTCCATTCCTC 3777
|||:|||||:|:|
Db 1 ACCUGGCUCCAUGCUC 17

RESULT 277
US-08-710-134-54
; Sequence 54, Application US/08710134
; Patent No. 5834181
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: US/08/710,134
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-8.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotides"
US-08-710-134-54

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
|||:|||||:|:|
Db 1 GATTGTTTTTTGTTTC 17

RESULT 278
US-08-485-885-54
; Sequence 54, Application US/08485885
; Patent No. 5849483
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/485,885
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-12.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotides"
US-08-485-885-54

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
|||:|||||:|:|
Db 1 GATTGTTTTTTGTTTC 17

RESULT 279
US-08-985-162-647/c
; Sequence 647, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McGswiggen, James
; TITLE OF INVENTION: ENZYMIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
```

APPLICANT: SPILAWSKI, 1901

TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH

```
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: KCNE1 AS AN LQT GENE
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22
; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-871-7

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAGCT 1360
Db 1 CAGATCCTGAGGATGCT 17

RESULT 284
US-08-584-040-1690/c
; Sequence 1690, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 974
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-1690
```

```
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1690:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-1690

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4228 AGGTTTTGAAGACATT 4244
Db 17 AGGTTTTTAACACATT 1

RESULT 285
US-08-584-040-2186/c
; Sequence 2186, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-2186

Query Match      0.3%; Score 13.8; DB 1; Length 17;
```

```
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2800 GTGAAAAAATAAACA 2816
DB 17 GTCAAAAAATAAGCA 1

RESULT 286
US-08-584-040-2315
; Sequence 2315, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2315:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2315

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 862 ACTGAACCTCATTTCTT 878
DB 1 ACUUAACUCAAUUCUU 17

RESULT 287
US-08-584-040-2544/c
; Sequence 2544, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2544:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2544/c

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2579 AAAAAAATTCGAGA 2595
DB 17 AAAAAAATAGTAGAGA 1

RESULT 288
US-08-584-040-2545/c
; Sequence 2545, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2544:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2544
```

```

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2545:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2545

```

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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QY 2578 AAAAAAAAAAATTGGAG 2594
||| ||| ||| ||| ||| ||| ||| |||
DB 17 AAAAAAAAAAAGTAGAG 1

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RESULT 289
US-08-584-040-2546/c
; Sequence 2546, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

```

```

; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2546:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2546

```

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2577 AAAAAAAAAAATTGGA 2593
||| ||| ||| ||| ||| ||| ||| |||
DB 17 AAAAAAAAAAAGTAGA 1

```

```

RESULT 290
US-08-584-040-2547/c
; Sequence 2547, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064

```



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2547:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-2547

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAATTGG 2592  
DB 17 AAAAAAAAAAAGTAG 1

RESULT 291  
US-08-584-040-2551/c  
; Sequence 2551, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: Storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,040  
; FILING DATE: January 11, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/005,974  
; FILING DATE: October 26, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 218/064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2551:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-584-040-2551

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 GAGAAAAAAACAA 944  
DB 17 GAAAAAAACAAAA 1

RESULT 292  
US-08-584-040-2552/c  
; Sequence 2552, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: Storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,040  
; FILING DATE: January 11, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/005,974  
; FILING DATE: October 26, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 218/064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2552:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-584-040-2552

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGAGAAAAAAACAA 943  
DB 17 GAAAAAAACAAAA 1

RESULT 293  
US-08-584-040-2556/c  
; Sequence 2556, Application US/08584040

```

; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2556:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2556

```

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2798 ATGTGAAAAA 2814
Db 17 ATTTGAAAAA 1

```

```

RESULT 294
US-08-584-040-2727
; Sequence 2727, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2727:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2727

```

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 2.4e+02;
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 3702 TTTTATATCTTC 3718
Db 1 UUUUGUACCAUUC 17

```

```

RESULT 295
US-08-584-040-4005
; Sequence 4005, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible

```

```

; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4005:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4005

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.4e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY   1811 GCTCTCCTTCGACGTGA 1827
DB   1 GAUCUCCUCCAGCGUGA 17

RESULT 296
US-08-584-040-4014/c
; Sequence 4014, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4300

REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4014:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4014

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   1849 TTCACCACAAGACAGG 1865
DB   17 TGCACCACAAGACACG 1

RESULT 297
US-08-584-040-4300
; Sequence 4300, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4300

```

```

; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4005:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4005

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.4e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY   1811 GCTCTCCTTCGACGTGA 1827
DB   1 GAUCUCCUCCAGCGUGA 17

RESULT 296
US-08-584-040-4014/c
; Sequence 4014, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4300

REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4014:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4014

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   1849 TTCACCACAAGACAGG 1865
DB   17 TGCACCACAAGACACG 1

RESULT 297
US-08-584-040-4300
; Sequence 4300, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4300

```

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Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.4e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4030 TATGGACTCTTTGCC 4046
    :|||||:|:|
Db 1 UCUGGACUCUCUGCC 17

RESULT 298
US-08-584-040-5563
; Sequence 5563, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5563:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-5563
Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 246 TCGAAGCTAGGAGAAGC 262
    :|||||:|:|
Db 1 UGGCAGCUAGAAGC 17

RESULT 299
US-08-584-040-5963
; Sequence 5963, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5963:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-5963
Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTGGCGTTCA 4051
    :|:|:|:|:|:|:|
Db 1 ACUCUCUUUCCAUA 17

RESULT 300
US-08-584-040-7626/c
; Sequence 7626, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5963:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-584-040-5963

```

NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7626:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-7626

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 GAGCTGCTGAACTGCC 50  
|||||  
Db 17 GAGCTGCTGACACTGTC 1

RESULT 301  
US-08-679-645-878/c  
Sequence 878, Application US/08679645  
Patent No. 6350934  
GENERAL INFORMATION:  
APPLICANT: Zwick, Michael G.  
APPLICANT: Edington, Brent E.  
APPLICANT: McSwiggen, James A.  
APPLICANT: Merlo, Patricia Ann Owens  
APPLICANT: Guo, Lining  
APPLICANT: Skokut, Thomas A.  
APPLICANT: Young, Scott A.  
APPLICANT: Folkerts, Otto  
APPLICANT: Merlo, Donald J.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
MODULATION OF GENE EXPRESSION  
TITLE OF INVENTION: IN PLANTS  
NUMBER OF SEQUENCES: 1263  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/679,645  
FILING DATE: July 12, 1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/001,135  
FILING DATE: July 13, 1995  
APPLICATION NUMBER: 08/300,726  
FILING DATE: September 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 878:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-679-645-878

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 931 AAAAAAAAAACCACT 947  
|||||  
Db 17 AAAAAACCAAGCT 1

RESULT 302  
US-09-597-735-7  
Sequence 7, Application US/09597735  
Patent No. 6420124  
GENERAL INFORMATION:  
APPLICANT: Keating, Mark T.  
APPLICANT: Sanguinetti, Michael C.  
APPLICANT: Curran, Mark E.  
APPLICANT: Landes, Gregory M.  
APPLICANT: Connors, Timothy D.  
APPLICANT: Burn, Timothy C.  
APPLICANT: Splawski, Igor  
TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE  
FILE REFERENCE: 2323-133  
CURRENT APPLICATION NUMBER: US/09/597,735  
CURRENT FILING DATE: 2000-06-19  
EARLIER APPLICATION NUMBER: 09/135,010  
EARLIER FILING DATE: 1998-08-17  
EARLIER APPLICATION NUMBER: 60/094,477  
EARLIER FILING DATE: 1998-07-29  
EARLIER APPLICATION NUMBER: 08/921,068  
EARLIER FILING DATE: 1997-08-29  
EARLIER APPLICATION NUMBER: 08/739,383  
EARLIER FILING DATE: 1996-10-29  
EARLIER APPLICATION NUMBER: 60/019,014  
EARLIER FILING DATE: 1995-12-22  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-597-735-7

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360  
|||||  
Db 1 CAGATCCTGAGGATGCT 17

RESULT 303  
US-09-444-295-7  
; Sequence 7, Application US/09444295  
; Patent No. 6432644  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN mink WHICH  
; TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING  
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE  
; FILE REFERENCE: 2323-133  
; CURRENT APPLICATION NUMBER: US/09/444,295  
; CURRENT FILING DATE: 1999-11-22  
; PRIOR APPLICATION NUMBER: 09/135,020  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 08/921,068  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; PRIOR APPLICATION NUMBER: 60/094,477  
; PRIOR FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-444-295-7

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360  
|||||  
Db 1 CAGATCCTGAGGATGCT 17

RESULT 304  
US-09-597-732-7  
; Sequence 7, Application US/09597732  
; Patent No. 6451534  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Curran, Mark E.  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Connors, Timothy D.  
; APPLICANT: Burn, Timothy C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE  
; FILE REFERENCE: 2323-133  
; CURRENT APPLICATION NUMBER: US/09/597,732  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 09/135,010  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 60/094,477  
; PRIOR FILING DATE: 1998-07-29  
; PRIOR APPLICATION NUMBER: 08/921,068  
; PRIOR FILING DATE: 1997-08-29

; PRIOR APPLICATION NUMBER: 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-597-732-7

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360  
|||||  
Db 1 CAGATCCTGAGGATGCT 17

RESULT 305  
US-09-475-947A-118/c  
; Sequence 118, Application US/09475947A  
; Patent No. 6472154  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Wren, Jonathan D.  
; APPLICANT: Minna, John D.  
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
; FILE REFERENCE: UTSD0667  
; CURRENT APPLICATION NUMBER: US/09/475,947A  
; CURRENT FILING DATE: 1999-12-31  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 118  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: human  
US-09-475-947A-118

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 CGAGAAACAAAAACAA 943  
|||||  
Db 17 GAAAAAAGAAAAAAA 1

RESULT 306  
US-09-474-432B-757/c  
; Sequence 757, Application US/09474432B  
; Patent No. 6528640  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Burgin, Alex  
; APPLICANT: Beaudry, Amber  
; APPLICANT: Karpeisky, Alex  
; APPLICANT: Adamic, Jasenka  
; APPLICANT: Sweedler, David  
; APPLICANT: Zinnen, Shawn  
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot  
; FILE REFERENCE: MBHB00-831-B (247/276)  
; CURRENT APPLICATION NUMBER: US/09/474,432B  
; CURRENT FILING DATE: 1999-12-19  
; PRIOR APPLICATION NUMBER: US 60/064,866  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/084,727  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: US 09/186,675  
; PRIOR FILING DATE: 1998-11-04

;  
; PRIOR APPLICATION NUMBER: US 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 1526  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 757  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-474-432B-757

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3204 GCCATATGCCCGAAGG 3220  
||| |||||  
Db 17 GGCAGATGCCCGAAGG 1

RESULT 307  
US-09-371-772B-235/c  
; Sequence 235, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 235  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-235

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4228 AGGTTTGAAGACATT 4244  
||||| |||||  
Db 17 AGGTTTAAACACATT 1

RESULT 308  
US-09-371-772B-731/c  
; Sequence 731, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040

;  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 731  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-731

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2800 GTGAAAAAACA 2816  
||| |||||  
Db 17 GTCAAAAAAGCA 1

RESULT 309  
US-09-371-772B-860  
; Sequence 860, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 860  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-860

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 47.1%; Pred. No. 2.4e+02;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 862 ACTGAACCTCATTCTT 878  
||: |||: |||: |||:  
Db 1 ACUUAACUAUUUCU 17

RESULT 310  
US-09-371-772B-1068/c  
; Sequence 1068, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08

```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1068
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1068

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2579 AAAAAAAAAAATTGGAGA 2595
    |||||
Db 17 AAAAAAAAAAAGTAGAGA 1

RESULT 311
US-09-371-772B-1069/c
; Sequence 1069, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1069
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1069

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATTGGAG 2594
    |||||
Db 17 AAAAAAAAAAAGTAGAG 1

RESULT 312
US-09-371-772B-1070/c
; Sequence 1070, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225

```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1070
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1070

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAAAAAATTGGA 2593
    |||||
Db 17 AAAAAAAAAAAGTAGA 1

RESULT 313
US-09-371-772B-1071/c
; Sequence 1071, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1071

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAATTGG 2592
    |||||
Db 17 AAAAAAAAAAAGTAG 1

RESULT 314
US-09-371-772B-1075/c
; Sequence 1075, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0

```



```

; SEQ ID NO 1075
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 928 GAGAAAAAACA AAA 944  
||| ||| ||| ||| |||  
**Db** 17 GAAAAAAAAAAAAAAA 1

RESULT 315

US-09-371-772B-1076/C  
; Sequence 1076, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: MCSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re-  
 ; sulting from Abnormalities in the Regulation of Vascular Endothelial Growth Factor Receptor  
 ; FILE OF INVENTION: 876-J  
 ; FILE REFERENCE: MBHB00, MBHB00, 876-J (237/198)

```

1 CURRENT APPLICATION NUMBER: US/09/371,772.23
2 CURRENT FILING DATE: 1999-08-10
3 PRIOR APPLICATION NUMBER: US 66/005,974
4 PRIOR FILING DATE: 1995-10-26
5 PRIOR APPLICATION NUMBER: US 08/584,040
6 PRIOR FILING DATE: 1996-01-08
7 NUMBER OF SEQ ID NOS: 14225
8 SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 10

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;
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

```

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15: Conservative 0; Mismatches 2; Indels

**Qy** 927 GGAGAAAAA AAAACAA 943  
||| ||| ||| ||| ||| |||  
**Dp** 17 GGA AAAAAAAAAA 1

## RESULT 316

RESOL 310  
US-09-371-772B-1080/c  
; Sequence 1080, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime

```

; AFFILIATION: ESCORCADO, DAIME
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00.876-J (237/198)
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; DOCTRINE. FACT  
; SEO ID NO 1080

; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM:  
 US-09-371-772B

```

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 2798 ATGTGAAAAAAAAAAAAA 2814  
 Db 17 ATTTGAAAAAAAAAAAAA 1

RESULT 317

US-09-371-772B-1251  
; Sequence 1251, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: MCSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime

```

;
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
;
; FILE REFERENCE: MBHB00_876-J (237/198)
;
; FILE REFERENCE: MBHB00_876-J (237/198)
;

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,
, CURRENT APPLICATION NUMBER: US/09/371,772S
,
, CURRENT FILING DATE: 1999-08-10
,
, PRIOR APPLICATION NUMBER: US 60/005,974
,
, PRIOR FILING DATE: 1995-10-26
,
, PRIOR APPLICATION NUMBER: US 08/584,040
,
, PRIOR FILING DATE: 1996-01-08
,
, NUMBER OF SEQ ID NOS: 14225
,
, SOFTWARE: PatentIn version 3.0
,
, SEQ ID NO: 1251
,
```

; LENGTH: 17

; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-1251

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 35.3%; Pred. No. 2.4e+02;  
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 3702 TTTTATATCTTTC 3718  
::: :|:|:|:|:|:  
Db 1 UUUGUUAUACCAUUC 17

RESULT 318

```

US-09-371-772B-1772
; Sequence 1772, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

```

```

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Res
;
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00_876-J (237/198)
;
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Res

```

, CURRENT APPLICATION NUMBER: US/09/371,772Z  
 ,  
 , CURRENT FILING DATE: 1999-08-10  
 ,  
 , PRIORITY APPLICATION NUMBER: US 60/005,974  
 ,  
 , PRIORITY FILING DATE: 1995-10-26  
 ,  
 , PRIORITY APPLICATION NUMBER: US 08/584,040  
 ,  
 , PRIORITY FILING DATE: 1996-01-08  
 ,  
 , NUMBER OF SEQ ID NOS: 14225  
 , SOFTWARE: PatentIn version 3.0  
 , SEQ ID NO 1772

; LENGTH: 17

; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-1772

Query Match      0.3%    Score 13.8; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 2.4e+02;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY    1811 GCTCTCCTTCGACGTGA 1827  
      | : ||| : ||| : ||  
Db     1 GAUCUCCUCCAGCGUGA 17

RESULT 319  
US-09-371-772B-1781/c  
; Sequence 1781, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Growth Factor Receptor  
; FILE REFERENCE: MBH00.876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1781  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-1781

Query Match      0.3%    Score 13.8; DB 1; Length 17;  
Best Local Similarity 89.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY    1849 TTCACCACAAGAAGACAGG 1865  
      | ||||| ||||| |||||  
Db     17 TGCACCACAAGAAGACAG 1.

RESULT 320  
US-09-371-772B-2067  
; Sequence 2067, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Growth Factor Receptor  
; FILE REFERENCE: MBH00.876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2067  
; LENGTH: 17  
; TYPE: RNA

## US-09-371-772B-2800

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 47.1%; Pred. No. 2.4e+02;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTTGCCGTTCA 4051  
||:|::|:|:|:  
Db 1 ACUCUCUUUCAUCA 17

## RESULT 323

US-09-371-772B-3418/c  
; Sequence 3418, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371.772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3418  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus sp.  
US-09-371-772B-3418

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAACTGCC 50  
|||||||  
Db 17 GAGCTGCTGACTGTC 1

## RESULT 324

US-09-371-772B-5235  
; Sequence 5235, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371.772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5235  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-5235

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 52.9%; Pred. No. 2.4e+02;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 861 CACTGAATCCATTTC 877  
||:|:|:|:|:  
Db 1 CACUUAACUAAUUCU 17

## RESULT 325

US-09-371-772B-5435/c  
; Sequence 5435, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371.772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5435  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-5435

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTTGGAGAA 2596  
|||||||  
Db 17 AAAAAAATTTGGAGAA 1

## RESULT 326

US-09-371-772B-5582/c  
; Sequence 5582, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371.772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5582  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-5582

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2750 TTTTAAAGGAAAAA 2766  
DB 17 TTTATTTAGGAAAAA 1

RESULT 327  
US-09-371-772B-5583/c  
; Sequence 5583, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5583  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-5583

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.3%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2749 TTTTAAAGGAAAAA 2765  
DB 17 TTTATTTAGGAAAAA 1

RESULT 328  
US-09-371-772B-6814  
; Sequence 6814, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6814  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-6814

Best Local Similarity 47.1%; Pred. No. 2.4e+02;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTGC 4045  
DB 1 UUCUGACUCUCUGC 17

RESULT 329  
US-09-597-731-7  
; Sequence 7, Application US/09597731  
; Patent No. 6582913  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Sanguinetti, Michael C.  
; APPLICANT: Curran, Mark E.  
; APPLICANT: Landes, Gregory M.  
; APPLICANT: Commors, Timothy D.  
; APPLICANT: Burn, Timothy C.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE  
; FILE REFERENCE: 2323-133  
; CURRENT APPLICATION NUMBER: US/09/597,731  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 09/135,010  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: 08/921,068  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 08/739,383  
; PRIOR FILING DATE: 1996-10-29  
; PRIOR APPLICATION NUMBER: 60/019,014  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-597-731-7

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360  
DB 1 CAGATCCTGAGGATGCT 17

RESULT 330  
US-09-476-387-756/c  
; Sequence 756, Application US/09476387  
; Patent No. 6617438  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Beaudry, Amber  
; APPLICANT: Karpeisky, Alex  
; APPLICANT: Adamic, Jasenka Matulic  
; APPLICANT: Sweedler, Dave  
; APPLICANT: Zinnen, Shawn  
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti  
; FILE REFERENCE: MHB00-831-C (249/073)  
; CURRENT APPLICATION NUMBER: US/09/476,387  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 09/474,432  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 09/186,675  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: 60/083,727  
; PRIOR FILING DATE: 1998-04-29

;; PRIOR APPLICATION NUMBER: 60/064,866  
;; PRIOR FILING DATE: 1997-11-05  
;; NUMBER OF SEQ ID NOS: 1524  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 756  
;; LENGTH: 17  
;; TYPE: RNA  
;; ORGANISM: Homo sapiens  
US-09-476-387-756

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3204 GCCATATGCCAGAAG 3220  
Db 17 GGCAGATGCCAGAAG 1

RESULT 331  
US-09-401-063-647/c  
;; Sequence 647, Application US/09401063  
;; Patent No. 6623962  
;; GENERAL INFORMATION:  
;; APPLICANT: Akhtar, Saghir  
;; APPLICANT: Fell, Patricia  
;; APPLICANT: McSwiggan, James  
;; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT  
;; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
;; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
;; TITLE OF INVENTION: FACTOR RECEPTORS  
;; NUMBER OF SEQUENCES: 1877  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; STREET: Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071-2066  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: FastSeq for Windows 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/401,063  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/985,162  
;; FILING DATE: 04 December 1997  
;; APPLICATION NUMBER: 60/036,476  
;; FILING DATE: 31 January 1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 230/107  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 647:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-09-401-063-647

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3058 GATGGCTTAAGGAGTTT 3074  
Db 17 GATGGCTTAAGGAGATT 1

RESULT 332  
US-09-866-108A-243  
;; Sequence 243, Application US/09866108A  
;; Patent No. 6686188  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharron G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng  
;; APPLICANT: SHANNON, Mark  
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
;; FILE REFERENCE: AEOMICA-7  
;; CURRENT APPLICATION NUMBER: US/09/866,108A  
;; CURRENT FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aeomica Sequence Listing Engine  
;; Patent No. 6686188  
;; SEQ ID NO 243  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108A-243  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 496 ATCCTCGCCGCTGTC 512  
Db 1 ATCCTCGCCGCTGTC 17

RESULT 333  
US-09-866-108A-1065/c  
;; Sequence 1065, Application US/09866108A  
;; Patent No. 6686188  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharron G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng

```
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 1065
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-1065

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2713 CTACTTCCTTAGAGACA 2729
DB 17 CTACGTCCTTAGAGACA 1

RESULT 334
US-09-866-108A-1066/c
/ Sequence 1066, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 1065
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-1065
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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 1066
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-1066

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2712 CCTACTTCCTTAGAGAC 2728
DB 17 CCTACGTCCTTAGAGAC 1

RESULT 335
US-09-866-108A-2222
/ Sequence 2222, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108A
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ Patent No. 6686188
/ SEQ ID NO 2222
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108A-2222

Query Match      0.3%; Score 13.8; DB 1; Length 17;
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```
Best Local Similarity 88.2%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2;

QY 675 GTGTGAAGCAGGGCC 691
Db 1 GTGTGATGCGCAGGTC 17

RESULT 336
US-09-866-108A-8557
; Sequence 8557, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/236,359
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8557
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8557

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1462 CAAGCCGAGGGCAGCC 1478
Db 1 CCAGCCAGAGGGCAGCC 17

RESULT 338
US-09-866-108A-10508/c
; Sequence 10508, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/236,359
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8557
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8557

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2519 CGATGAGCAGCATGATG 2535
Db 1 CGATGAGCAGCATGATG 17

RESULT 337
US-09-866-108A-9226
; Sequence 9226, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
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/ PRIOR APPLICATION NUMBER: PCT/US01/00669  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00665  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00668  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00663  
/ PRIOR FILING DATE: 2001-01-30  
/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 15755  
/ SOFTWARE: Aecomica Sequence Listing Engine  
/ Patent No. 6686188  
/ SEQ ID NO 10508  
/ LENGTH: 17  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-09-866-108A-10508

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2928 CTCCCGCTCCCTCCTC 2944  
DB 17 CTCCCGCTCCCTGCTC 1

RESULT 339  
US-09-866-108A-10509/c  
/ Sequence 10509, Application US/09866108A  
/ Patent No. 6686188  
/ GENERAL INFORMATION:  
/ APPLICANT: GU, Yizhong  
/ APPLICANT: JI, Yonggang  
/ APPLICANT: PENN, Sharon G.  
/ APPLICANT: HANZEL, David K.  
/ APPLICANT: RANK, David R.  
/ APPLICANT: CHEN, Wensheng  
/ APPLICANT: SHANNON, Mark  
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
/ FILE REFERENCE: AECOMICA-7  
/ CURRENT APPLICATION NUMBER: US/09/866,108A  
/ CURRENT FILING DATE: 2001-05-25  
/ PRIOR APPLICATION NUMBER: US 60/207,456  
/ PRIOR FILING DATE: 2000-05-26  
/ PRIOR APPLICATION NUMBER: GB 24263.6  
/ PRIOR FILING DATE: 2000-10-04  
/ PRIOR APPLICATION NUMBER: US 60/236,359  
/ PRIOR FILING DATE: 2000-09-27  
/ PRIOR APPLICATION NUMBER: PCT/US01/00666  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00667  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00664  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00669  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00665  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00668  
/ PRIOR FILING DATE: 2001-01-30  
/ PRIOR APPLICATION NUMBER: PCT/US01/00663  
/ PRIOR FILING DATE: 2001-01-30  
/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 15755  
/ SOFTWARE: Aecomica Sequence Listing Engine  
/ Patent No. 6686188  
/ SEQ ID NO 10509  
/ LENGTH: 17  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-09-866-108A-10509

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2927 CTCCCGCTCCCTCCTC 2943  
DB 17 CTCCCGCTCCCTGCTC 1

RESULT 340  
US-09-129-603-4/c  
/ Sequence 4, Application US/09129603A  
/ Patent No. 6790944  
/ GENERAL INFORMATION:  
/ APPLICANT: Ishiwata, Tetsuyoshi  
/ APPLICANT: Sakurada, Mikiko  
/ APPLICANT: Nishimura, Ayako  
/ APPLICANT: Nakagawa, Satoshi  
/ APPLICANT: Kuga, Tetsuro  
/ APPLICANT: Nishi, Tatsunari  
/ APPLICANT: No. 6790944ura, No. 6790944uo  
/ APPLICANT: Sawada, Shigemasa  
/ APPLICANT: Nagase, Takahiro  
/ APPLICANT: Takei, Masami  
/ TITLE OF INVENTION: No. 6790944el Protein  
/ FILE REFERENCE: 766.25  
/ CURRENT APPLICATION NUMBER: US/09/129,603A  
/ CURRENT FILING DATE: 1998-08-05  
/ EARLIER APPLICATION NUMBER: PCT/JP97/04469  
/ EARLIER FILING DATE: 1997-12-05  
/ NUMBER OF SEQ ID NOS: 9  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 4  
/ LENGTH: 17  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: other nucleic acid from homo sapiens, synthesized  
/ OTHER INFORMATION: DNA  
US-09-129-603-4

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 GAAAAAACAACAAACC 946  
DB 17 GAAAAAACAACAAAC 1

RESULT 341  
US-09-685-664B-235/c  
/ Sequence 235, Application US/09685664B  
/ Patent No. 6818447  
/ GENERAL INFORMATION:  
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.  
/ APPLICANT: Pavco, Pam  
/ APPLICANT: McSwiggen, Jim  
/ APPLICANT: Stinchcomb, Dan  
/ APPLICANT: Escobedo, Jaime  
/ TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related  
/ FILE REFERENCE: MBH00-876-K (400/021)  
/ CURRENT APPLICATION NUMBER: US/09/685,664B  
/ CURRENT FILING DATE: 2000-10-10  
/ PRIOR APPLICATION NUMBER: US 60/005,974  
/ PRIOR FILING DATE: 1995-10-26  
/ PRIOR APPLICATION NUMBER: US 08/584,040  
/ PRIOR FILING DATE: 1996-01-08  
/ PRIOR APPLICATION NUMBER: US 09/371,772  
/ PRIOR FILING DATE: 1999-08-10  
/ NUMBER OF SEQ ID NOS: 8231  
/ SOFTWARE: PatentIn version 3.0





; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1069  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-1069

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATTGGAG 2594  
|||||  
Db 17 AAAAAAAAAAAGTAGAG 1

RESULT 346  
US-09-685-664B-1070/c  
; Sequence 1070, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1070  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-1070

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAAAAAATTGGA 2593  
|||||  
Db 17 AAAAAAAAAAAGTAGA 1

RESULT 347  
US-09-685-664B-1071/c  
; Sequence 1071, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B

; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1071  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-1071

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAATTGG 2592  
|||||  
Db 17 AAAAAAAAAAAGTAG 1

RESULT 348  
US-09-685-664B-1075/c  
; Sequence 1075, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1075  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-1075

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 GAGAAAAAAACAAA 944  
|||||  
Db 17 GAAAAAAACAAA 1

RESULT 349  
US-09-685-664B-1076/c  
; Sequence 1076, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

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; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1076
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1076

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGNAGAAAAAACA 943
DB 17 GGNAAAAA 1

RESULT 350
US-09-685-664B-1080/c
; Sequence 1080, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1080
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1080

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2798 ATGTGAAAAA 2814
DB 17 ATTTGAAAAA 1

RESULT 351
US-09-685-664B-1251
; Sequence 1251, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```

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; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1251
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1251

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 2.4e+02;
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 3702 TTTTATATCTTC 3718
DB 1 UUUUGUACCAUUC 17

RESULT 352
US-09-685-664B-1772
; Sequence 1772, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1772
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-1772

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.4e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GCTCTCTTCGACGTGA 1827
DB 1 GAUCCUCCUCCGUGA 17

RESULT 353
US-09-685-664B-1781/c
; Sequence 1781, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
```

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1781  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-1781

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1849 TTCACCAACAAAGACAGG 1865  
Db 17 TGCACCACAAAGACAGC 1

RESULT 354  
US-09-685-664B-2067  
; Sequence 2067, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2067  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-685-664B-2067

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 52.9%; Pred. No. 2.4e+02;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 4030 TATGGACTCTCTTTGCC 4046  
Db 1 UCUGGACUCUCUCUGCC 17

RESULT 355  
US-09-685-664B-2453

; Sequence 2453, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2453  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-09-685-664B-2453

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 2.4e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 246 TCGAAGCTAGGAGAGC 262  
Db 1 UGGCAGCUAGAGAGC 17

RESULT 356  
US-09-685-664B-2800  
; Sequence 2800, Application US/09685664B  
; Patent No. 6818447  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00-876-K (400/021)  
; CURRENT APPLICATION NUMBER: US/09/685,664B  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8231  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2800  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-09-685-664B-2800

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 47.1%; Pred. No. 2.4e+02;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 4035 ACTCTCTTTGCCGTCA 4051  
Db 1 ACUCUCUUUCAUCA 17

```
RESULT 357
US-09-685-664B-3418/c
; Sequence 3418, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3418
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3418

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 GAGCTGCTGAACTGCC 50
Db 17 GAGCTGCTGACATGTC 1

RESULT 358
US-09-090-672B-107/c
; Sequence 107, Application US/09090672B
; Patent No. 6828428
; GENERAL INFORMATION:
; APPLICANT: Ishiwata, Tetsuoyoshi; Sakurada, Mikiko; Nishimura,
; APPLICANT: Ayako; Nakagawa, Satoehi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
; APPLICANT: Shigemasa; Takei, Masami
; TITLE OF INVENTION: Iga Nephropathy-Related Genes
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
US-09-090-672B-107

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 GAAAAAACAACCC 946
Db 17 GAAAAAACAACCC 1

RESULT 359
US-09-750-401-29/c
; Sequence 29, Application US/09750401
; Patent No. 6635422
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/750,401
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 33
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of TGF beta 2
US-09-750-401-29

Query Match          0.3%; Score 13.8; DB 1; Length 33;
Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2737 AAAACATCTTTTAAAGGAAAAATAA 2769
Db 33 AAAGAACATTTACAATTAAAGGAAAAATAA 1

RESULT 360
US-08-882-649A-8/c
; Sequence 8, Application US/08882649A
; Patent No. 6344316
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; APPLICANT: Chee, Mark
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chaoqiang, Lai
; APPLICANT: Wodicka, Lisa
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Lee, Danny
; APPLICANT: Tran, Huu M.
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: McCall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Joe Liebeschuetz  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,649A  
FILING DATE: 25-Jun-1997  
CLASSIFICATION: 435-006.000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/010,471  
FILING DATE: 23-JAN-1996  
APPLICATION NUMBER: US 60/035,170  
FILING DATE: 09-JAN-1997  
APPLICATION NUMBER: PCT/US97/01603  
FILING DATE: 22-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joe  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 018547-019410US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: YES  
(ix) Features:  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-08-882-649A-8

Query Match 0.3%; Score 13.6; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACRACC 946  
Db 16 AAAAAAAAAAAAAABC 1

RESULT 361  
US-09-644-827B-10/G  
Sequence 10, Application US/09644827B  
Patent No. 6762283  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: SCHUCHMANN, Marcus  
APPLICANT: GONCHAROV, Tanya  
TITLE OF INVENTION: Caspase-8 Interacting Proteins  
FILE REFERENCE: WALLACH=26  
CURRENT APPLICATION NUMBER: US/09/644, 827B  
CURRENT FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: 132105  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: 127721  
PRIOR FILING DATE: 1998-12-24  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:

OTHER INFORMATION: synthetic  
US-09-644-827B-10  
Query Match 0.3%; Score 13.6; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 2.2e+02;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 975 CCCCCCCCCCCCCC 990  
Db 16 CCCCCCCCCCCCCC 1  
RESULT 362  
US-08-363-240A-33  
Sequence 33, Application US/08363240A  
Patent No. 5705388  
GENERAL INFORMATION:  
APPLICANT: Couture, Larry  
APPLICANT: McSwiggen, James  
APPLICANT: Bisgaier, Charles  
APPLICANT: Pape, Michael  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: PREVENTION, INHIBITION OF  
TITLE OF INVENTION: PROGRESSION AND REGRESSION  
TITLE OF INVENTION: OF VASCULAR DISEASES  
NUMBER OF SEQUENCES: 1243  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,240A  
FILING DATE: December 23, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/096  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-240A-33  
Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 73.3%; Pred. No. 2e+02;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 829 TTCAGATCAGCCACT 843  
Db 1 UCCAGAUCCAGCCACU 15

RESULT 363  
US-08-292-620A-356/C

; Sequence 356, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620A  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 356:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-292-620A-356

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2807 AAAAAAAAACTCAAA 2821  
Db 15 AAAAAAAAAATCAAA 1

RESULT 364  
US-08-292-620A-357/c  
; Sequence 357, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620A  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 357:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-292-620A-357

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2806 AAAAAAAAACTCAA 2820  
Db 15 AAAAAAAAAATCAA 1

RESULT 365  
US-08-292-620A-358/c  
; Sequence 358, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390

;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Lyon & Lyon  
;/ STREET: 633 West Fifth Street  
;/ STREET: Suite 4700  
;/ CITY: Los Angeles  
;/ STATE: California  
;/ COUNTRY: U.S.A.  
;/ ZIP: 90071-2066  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;/ MEDIUM TYPE: storage  
;/ COMPUTER: IBM Compatible  
;/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
;/ SOFTWARE: Word Perfect 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/292,620A  
;/ FILING DATE: August 17, 1994  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ PRIOR APPLICATION DATA: including application  
;/ PRIOR APPLICATION DATA: described below:  
;/ APPLICATION NUMBER: 08/008,895  
;/ FILING DATE: January 19, 1993  
;/ FILING DATE: December 7, 1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Warburg, Richard J.  
;/ REGISTRATION NUMBER: 32,327  
;/ REFERENCE/DOCKET NUMBER: 208/149  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (213) 489-1600  
;/ TELEFAX: (213) 955-0440  
;/ TELEX: 67-3510  
;/ INFORMATION FOR SEQ ID NO: 358:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 15 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ US-08-292-620A-358

two

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2805 AAAAAAAAAACATCA 2819  
Db 15 AAAAAAAAAATCA 1

RESULT 366  
US-08-292-620A-363/c  
; Sequence 363, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.

;/ ZIP: 90071-2066  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;/ MEDIUM TYPE: storage  
;/ COMPUTER: IBM Compatible  
;/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
;/ SOFTWARE: Word Perfect 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/292,620A  
;/ FILING DATE: August 17, 1994  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ PRIOR APPLICATION DATA: including application  
;/ PRIOR APPLICATION DATA: described below:  
;/ APPLICATION NUMBER: 08/008,895  
;/ FILING DATE: January 19, 1993  
;/ FILING DATE: December 7, 1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Warburg, Richard J.  
;/ REGISTRATION NUMBER: 32,327  
;/ REFERENCE/DOCKET NUMBER: 208/149  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (213) 489-1600  
;/ TELEFAX: (213) 955-0440  
;/ TELEX: 67-3510  
;/ INFORMATION FOR SEQ ID NO: 363:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 15 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ US-08-292-620A-363

two

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 930 GAAAAAAAAACAAA 944  
Db 15 GAAAAAAAAAAAA 1

RESULT 367  
US-08-292-620A-366/c  
; Sequence 366, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;/ MEDIUM TYPE: storage  
;/ COMPUTER: IBM Compatible  
;/ OPERATING SYSTEM: IBM P.C. DOS 5.0  
;/ SOFTWARE: Word Perfect 5.1



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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620A
/ FILING DATE: August 17, 1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA: including application
/ PRIOR APPLICATION DATA: described below:
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 366:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-292-620A-366

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2799 TGTGAAAAAAAAAAAA 2813
Db 15 TCTGAAAAAAAAAAAA 1

RESULT 368
US-08-585-684B-824/c
; Sequence 824, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 825:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-825

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2510 TAATGACACGATGA 2524
Db 15 CAACGATGACGACGA 1
```

```
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 824:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-585-684B-824

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2516 CAACGATGACGACCA 2530
Db 15 CAACGATGACGACGA 1

RESULT 369
US-08-585-684B-825/c
; Sequence 825, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 825:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-825

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2510 TAATGACACGATGA 2524
Db 15 CAACGATGACGACGA 1
```



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; APPLICATION NUMBER: US/08/893.204C
; FILING DATE: 7/15/97
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenberg Morton
; REGISTRATION NUMBER: 26,049
; REFERENCE/DOCKET NUMBER: MR2493-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (410) 465-6678
; TELEFAX: (410) 461-3067
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHEICAL: yes
; ANTI-SENSE: no
; ORIGINAL SOURCE: synthetic
; PUBLICATION INFORMATION:
; AUTHORS: Katherine Meyer-Siegler
; AUTHORS: Perry Hudson
; TITLE: Enhanced Expression of Macrophage Migration
; TITLE: Inhibitory Factor in Prostatic Adenocarcinoma Metastases
; JOURNAL: Urology
; VOLUME: 48
; ISSUE: 3
; PAGES: 448-452
; DATE: 1996
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 15
; US-08-893-204C-2

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 929 AGAAAAAACAACAA 943
Db 15 AGAAAAAACAACAA 1

RESULT 373
US-08-832-021-25/c
; Sequence 25, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832.021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-25

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2573 TTTAAAAAACAACAA 2587
Db 15 TTTAAAAAACAACAA 1

RESULT 376
US-08-832-021-34/c
; Sequence 34, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
```

```
RESULT 374
US-08-832-021-26/c
; Sequence 26, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832.021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-26

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2800 GTCAAAAAAACAACAA 2814
Db 15 GTCAAAAAAACAACAA 1

RESULT 375
US-08-832-021-29/c
; Sequence 29, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832.021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-29

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2573 TTTAAAAAACAACAA 2587
Db 15 TTTAAAAAACAACAA 1

RESULT 376
US-08-832-021-34/c
; Sequence 34, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
```

```
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-34
```

```
Query Match          0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2800 GTGAAAAAATAAAAAA 2814
Db       15 GCGAAAAAATAAAAAA 1
```

```
RESULT 377
US-08-832-021-36/c
; Sequence 36, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-36
```

```
Query Match          0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      926 AGGAGAAAAAATAAAA 940
Db       15 AGGAAAAAATAAAAAA 1
```

```
RESULT 378
US-08-832-021-41/c
; Sequence 41, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
```

```
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-41
```

```
Query Match          0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2573 TTTAAAAAATAAAAAA 2587
Db       15 TCTAAAAAATAAAAAA 1
```

```
RESULT 379
US-08-832-021-43
; Sequence 43, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-43
```

```
Query Match          0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2745 TTTTAAAAAAGG 2759
Db       1 TTTTAAAAAAGG 15
```

```
RESULT 380
US-08-832-021-46/c
; Sequence 46, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 15
; TYPE: DNA
```

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-46

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814  
| | | | | | | | | | | | | | | | | |  
Db 15 GCGAAAAAAAAAAAAA 1

RESULT 381  
US-08-832-021-53/c  
; Sequence 53, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardinas, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 53  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-53

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2573 TTTAAAAAAAAAAAAA 2587  
| | | | | | | | | | | | | | | | | |  
Db 15 TATAAAAAAAAAAAAA 1

RESULT 382  
US-08-832-021-58/c  
; Sequence 58, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardinas, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-58

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 928 GAGAAAAAAAAAACCA 942  
| | | | | | | | | | | | | | | | | |  
Db 15 GAGAAAAAAAAAAAAA 1

RESULT 383  
US-08-675-119-2  
; Sequence 2, Application US/08675119  
; Patent No. 6054442  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Shih-Pong  
; APPLICANT: Maine, Ira  
; APPLICANT: Kerwin, Sean M.  
; APPLICANT: Fletcher, Terace  
; APPLICANT: Salazar, Miguel  
; APPLICANT: Mamiya, Blain  
; APPLICANT: Wajima, Makoto  
; APPLICANT: Windle, Bradford E.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: MODULATION AND INHIBITION OF HUMAN  
; TITLE OF INVENTION: TELOMERASE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675,119  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: CTCR:028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-675-119-2

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1680 CAAAACCCCAACCC 1694  
| | | | | | | | | | | | | | | | | |  
Db 1 CAAAACCCCAACCC 15

RESULT 384  
US-08-851-843A-43  
; Sequence 43, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "RNA"  
US-08-851-843A-43

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694  
Db 1 CAAACCCCAAGCC 15

RESULT 385  
US-08-851-843A-45  
Sequence 45, Application US/08851843A  
Patent No. 6093809  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809el Telomerase  
NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "RNA"  
US-08-851-843A-45

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694  
Db 1 CAAACCCCAAGCC 15

RESULT 386  
US-09-071-845-356/c  
Sequence 356, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street

STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 356:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-356

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2807 AAAAAAACATCAAA 2821  
Db 15 AAAAAAACATCAAA 1

RESULT 387  
US-09-071-845-357/c  
Sequence 357, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 357:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-357

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2806 AAAAAAACATCAAA 2820  
Db 15 AAAAAAACATCAAA 1

RESULT 388  
US-09-071-845-358/c  
Sequence 358, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:

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/
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 358:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-09-071-845-358
/
/ Query Match 0.3%; Score 13.4; DB 1; Length 15;
/ Best Local Similarity 93.3%; Pred. No. 2e+02;
/ Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
/
/ Qy 2805 AAAAAAAAAACATCA 2819
/ Db 15 AAAAAAAAAAAATCA 1
/
/ RESULT 389
/ US-09-071-845-363/C
/ Sequence 363, Application US/09071845
/ Patent No. 6132967
/ GENERAL INFORMATION:
/ APPLICANT: Susan Grimm
/ APPLICANT: Dan T. Stinchcomb
/ APPLICANT: James McSwiggen
/ APPLICANT: Sean Sullivan
/ APPLICANT: Kenneth G. Draper
/ TITLE OF INVENTION: RIBOZYME TREATMENT OF
/ TITLE OF INVENTION: DISEASES OR CONDITIONS
/ TITLE OF INVENTION: RELATED TO LEVELS OF
/ TITLE OF INVENTION: INTRACELLULAR ADHESION
/ TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
/ NUMBER OF SEQUENCES: 2390
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,845
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELEPHONE: (213) 489-1600
/
/ Qy 930 GAAAAAAAAACAAA 944
/ Db 15 GAAAAAAAAAAAAA 1
/
/ RESULT 390
/ US-09-071-845-366/C
/ Sequence 366, Application US/09071845
/ Patent No. 6132967
/ GENERAL INFORMATION:
/ APPLICANT: Susan Grimm
/ APPLICANT: Dan T. Stinchcomb
/ APPLICANT: James McSwiggen
/ APPLICANT: Sean Sullivan
/ APPLICANT: Kenneth G. Draper
/ TITLE OF INVENTION: RIBOZYME TREATMENT OF
/ TITLE OF INVENTION: DISEASES OR CONDITIONS
/ TITLE OF INVENTION: RELATED TO LEVELS OF
/ TITLE OF INVENTION: INTRACELLULAR ADHESION
/ TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
/ NUMBER OF SEQUENCES: 2390
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,845
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELEPHONE: (213) 489-1600
/
```



```
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 366:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-071-845-366

Query Match          0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2799 TGTGAAAAA 2813
Db 15 TCTGAAAAA 1

RESULT 391
US-08-974-549A-113
; Sequence 113, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 366:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-071-845-366

Query Match          0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2799 TGTGAAAAA 2813
Db 15 TCTGAAAAA 1

RESULT 392
US-09-038-073-824/c
; Sequence 824, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 824:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-824
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2516 CAACGATGACGACCA 2530
Db 15 CAACGATGACGACGA 1

RESULT 393
US-09-038-073-825/c
; Sequence 825, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 825:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-825
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2510 TAATGACACGATGA 2524
Db 15 TGATGACACGATGA 1

RESULT 394
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US-09-038-073-1392/c
; Sequence 1392, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1392:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-1392
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1207 CTTTAAAAAACATGC 1221
Db 15 CTTTAAAAACACGC 1

RESULT 395
US-08-854-050-43
; Sequence 43, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
```

```

CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "RNA"
US-08-854-050-43

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Query Match          0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1680 CAAACCCCAAGCC 1694  
Db 1 CAAACCCCAAAACC 15

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RESULT 396
US-08-854-050-45
; Sequence 45, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Cathin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco

```

```

1 STATE: California
2 COUNTRY: United States of America
3 ZIP: 94111
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: PatentIn Release #1.0, Version #1.30
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/854,050
12 FILING DATE: 09-MAY-1997
13 CLASSIFICATION: 536
14
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 08/846,017
17 FILING DATE: 25-APR-1997
18 CLASSIFICATION: 536
19
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 08/851,843
22 FILING DATE: 06-MAY-1997
23 CLASSIFICATION: 536
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/844,419
27 FILING DATE: 18-APR-1997
28 CLASSIFICATION: 536
29
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 08/724,643
32 FILING DATE: 01-OCT-1996
33 CLASSIFICATION: 536
34
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Apple, Randolph T.
37 REGISTRATION NUMBER: 36,429
38 REFERENCE/DOCKET NUMBER: 015389-00293005
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: (415) 576-0200
41 TELEFAX: (415) 576-0300
42 INFORMATION FOR SEQ ID NO: 45:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 15 base pairs
45 TYPE: nucleic acid
46 STRANDEDNESS: single
47 TOPOLOGY: linear
48
49 MOLECULE TYPE: other nucleic acid
50 DESCRIPTION: /desc = "RNA"
51
52 US-08-854-050-45

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Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. NO. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels

Qy 1680 CAAACCCCAAAGCC 1694  
db 1 CAAACCCCAAAGCC 15

```

RESULT 397
US-09-430-323-43
; Sequence 43, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California

```

```

; COUNTRY: United States of America
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "RNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-430-323-43
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15
|||||
RESULT 398
US-09-430-323-45
; Sequence 45, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "RNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-430-323-45
Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15
|||||
RESULT 399
US-09-467-932-2
; Sequence 2, Application US/09467932
; Patent No. 6593306
; GENERAL INFORMATION:
; APPLICANT: Chen, Shih-Fong
; APPLICANT: Maine, Ira
; APPLICANT: Kerwin, Sean M.
; APPLICANT: Fletcher, Terace
; APPLICANT: Salazar, Miguel
; APPLICANT: Mamiya, Blain
; APPLICANT: Wajima, Makoto
; APPLICANT: Windle, Bradford E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATION
; TITLE OF INVENTION: AND INHIBITION OF HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/09/467,932
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/879,457
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kitchell, Barbara S.
/ REGISTRATION NUMBER: 33,928
/ REFERENCE/DOCKET NUMBER: CTCR:030
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (713) 789-2679
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-467-932-2

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15

RESULT 400
US-09-402-181B-113
/ Sequence 113, Application US/09402181B
/ Patent No. 6610839
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181B
/ FILING DATE: 29-Sep-1997
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
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/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ausehus, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015389-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 113:
/
US-09-402-181B-113

Query Match 0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1680 CAAACCCCAAGCC 1694
Db 1 CAAACCCCAAGCC 15

RESULT 401
US-09-721-456-113
/ Sequence 113, Application US/09721456
/ Patent No. 6617110
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/721,456
/ FILING DATE: 22-No. 6617110-2000
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,549A
/ FILING DATE: 19-NOV-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
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/ APPLICATION NUMBER: US 08/854,050  
/ FILING DATE: 09-MAY-1997  
/ APPLICATION NUMBER: US 08/911,312  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: US 08/912,951  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: US 08/915,503  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: WO PCT/US97/17618  
/ FILING DATE: 01-OCT-1997  
/ APPLICATION NUMBER: WO PCT/US97/17885  
/ FILING DATE: 01-OCT-1997  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph Ted  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002610US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 113:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 113:  
US-09-721-456-113  
  
Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1680 CAAACCCCAAGCC 1694  
Db 1 CAAACCCCAAGCC 15  
|||||  
RESULT 402  
US-09-766-253-43  
/ Sequence 43, Application US/09766253  
/ Patent No. 680880  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin  
/ Andrews, William H.  
/ TITLE OF INVENTION: No. 680880el Telomerase  
/ NUMBER OF SEQUENCES: 171  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/766,253  
/ FILING DATE: 19-Jan-2001  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/846,017  
/ FILING DATE: 1997-04-25  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002920US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 45:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 base pairs  
/ TYPE: nucleic acid

/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002920US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 43:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "RNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-09-766-253-43  
  
Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1680 CAAACCCCAAGCC 1694  
Db 1 CAAACCCCAAGCC 15  
|||||  
RESULT 403  
US-09-766-253-45  
/ Sequence 45, Application US/09766253  
/ Patent No. 680880  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin  
/ Andrews, William H.  
/ TITLE OF INVENTION: No. 680880el Telomerase  
/ NUMBER OF SEQUENCES: 171  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/766,253  
/ FILING DATE: 19-Jan-2001  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/846,017  
/ FILING DATE: 1997-04-25  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002920US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 45:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 15 base pairs  
/ TYPE: nucleic acid

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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "RNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-766-253-45

Query Match      0.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1680 CAAAACCCCAAGCC 1694
Db 1 CAAAACCCCAAAACC 15

RESULT 404
US-08-087-387-6/c
; Sequence 6, Application US/08087387
; Patent No. 5473060
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic and therapeutic applic
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/087,387
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-087-387-6

Query Match      0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAATT 2590
Db 15 AAAAAAAAAAAAGT 1

RESULT 405
US-08-455-627-6/c
; Sequence 6, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
```

```
;
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-627-6

Query Match      0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAATT 2590
Db 15 AAAAAAAAAAAAGT 1

RESULT 406
US-08-311-760A-375
; Sequence 375, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [Lp(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/311,760A  
 ; FILING DATE: September 23, 1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 208/155  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 375:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-311-760A-375

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
 Best Local Similarity 73.3%; Pred. No. 2.4e+02;  
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1540 TGCCGTCCACCTCC 1554  
 :||||:||||:  
 Db 2 UGCCGUGCACCUC 16

RESULT 407  
 US-08-311-760A-383  
 ; Sequence 383, Application US/08311760A  
 ; Patent No. 5599706  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; APPLICANT: McSwiggan, James  
 ; APPLICANT: Newton, Roger S.  
 ; APPLICANT: Ramharack, Randy  
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
 ; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF  
 ; TITLE OF INVENTION: PHASMA LIPOPROTEIN (a) [LP(a)] BY  
 ; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN  
 ; NUMBER OF SEQUENCES: 392  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/311,760A  
 ; FILING DATE: September 23, 1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 208/155  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440

; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 383:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-311-760A-383

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
 Best Local Similarity 73.3%; Pred. No. 2.4e+02;  
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1540 TGCCGTCCACCTCC 1554  
 :||||:||||:  
 Db 2 UGCCGUGCACCUC 16

RESULT 408  
 US-08-461-271-6/c  
 ; Sequence 6, Application US/08461271  
 ; Patent No. 5741643  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sergei M. Gryaznov  
 ; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
 ; TITLE OF INVENTION: and therapeutic applications  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics  
 ; STREET: 465 Lincoln Centre Drive  
 ; CITY: Foster City  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94404

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch diskette  
 ; COMPUTER: IBM compatible  
 ; OPERATING SYSTEM: Windows 3.1/DOS 5.0  
 ; SOFTWARE: Microsoft Word for Windows, vers. 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/461,271  
 ; FILING DATE:  
 ; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/087,387  
 ; FILING DATE: 2-Jul-93  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Stephen C. Macevitz  
 ; REGISTRATION NUMBER: 30,285  
 ; REFERENCE/DOCKET NUMBER: 104  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 358-7855  
 ; TELEFAX: (415) 358-7794  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 nucleotides  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-461-271-6

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
 Best Local Similarity 93.3%; Pred. No. 2.4e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAATT 2590  
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 Db 15 AAAAAAAAAAAGT 1

RESULT 409  
 US-08-713-685A-6/c  
 ; Sequence 6, Application US/08713685A



; Patent No. 5817795  
; GENERAL INFORMATION:  
; APPLICANT: Sergei M. Gryaznov  
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
; TITLE OF INVENTION: and therapeutic applications  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics  
; STREET: 465 Lincoln Centre Drive  
; CITY: Foster City  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Windows 3.1/DOS 5.0  
; SOFTWARE: Microsoft Word for Windows, vers. 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,685A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/461,271  
; FILING DATE:  
; APPLICATION NUMBER: 08/087,387  
; FILING DATE: 2-Jul-93  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stephen C. Macevitz  
; REGISTRATION NUMBER: 30,285  
; REFERENCE/DOCKET NUMBER: 104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 358-7855  
; TELEFAX: (415) 358-7794  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-713-685A-6

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2576 AAAAAAAAAAAATT 2590  
Db 15 AAAAAAAAAAAAGT 1

RESULT 410  
US-08-856-6/c  
; Sequence 6, Application US/08689856  
; Patent No. 5830658  
; GENERAL INFORMATION:  
; APPLICANT: Sergei M. Gryaznov  
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply  
; TITLE OF INVENTION: Connected Macromolecular Structures  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward LLP  
; STREET: Five Palo Alto Square, 3000 El Camino Real  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/689,856  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,627  
; FILING DATE: 31-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nakamura, Jackie N.  
; REGISTRATION NUMBER: 35,966  
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5000  
; TELEFAX: 415-857-0663  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-689-856-6

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATT 2590  
Db 15 AAAAAAAAAAAAGT 1

RESULT 411  
US-08-774-310-375  
; Sequence 375, Application US/08774310  
; Patent No. 5877022  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Daniel T.  
; APPLICANT: McSwiggen, James  
; APPLICANT: Newton, Roger S.  
; APPLICANT: Rambarack, Randy  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF  
; TITLE OF INVENTION: PHASMA LIPOPROTEIN (a) [LP(a)] BY  
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 392  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774,310  
; FILING DATE: December 23, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/311,760  
; FILING DATE: September 23, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 223/229  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440

TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 375:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-310-375

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 73.3%; Pred. No. 2.4e+02;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1540 TGCCGTCCTCCACCTCC 1554  
:||||:|||||  
Db 2 UGCCGUGGACCUCC 16

RESULT 412  
US-08-774-310-383  
Sequence 383, Application US/08774310  
Patent No. 5877022  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: McSwiggen, James  
APPLICANT: Newton, Roger S.  
APPLICANT: Ranharack, Randy  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF  
TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY  
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 392  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,310  
FILING DATE: December 23, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/311,760  
FILING DATE: September 23, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 223/229  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 383:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-310-383

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 73.3%; Pred. No. 2.4e+02;  
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1540 TGCCGTCCTCCACCTCC 1554  
:||||:|||||  
Db 2 UGCCGUGGACCUCC 16

RESULT 413  
US-08-947-317-4  
Sequence 4, Application US/08947317  
Patent No. 5972610  
GENERAL INFORMATION:  
APPLICANT: BUCHARDT, Ole  
APPLICANT: EGHOLM, Michael  
APPLICANT: NIELSEN, Peter Eigil  
APPLICANT: BERG, Rolf H  
APPLICANT: STANLEY, Christopher J  
TITLE OF INVENTION: USE OF NUCLEIC ACID ANALOGUES IN THE INHIBITION OF  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION  
FILE REFERENCE: 1614-7062  
CURRENT APPLICATION NUMBER: US/08/947,317  
CURRENT FILING DATE: 1997-10-08  
EARLIER APPLICATION NUMBER: PCT/EP93/01435  
EARLIER FILING DATE: 1993-06-07  
EARLIER APPLICATION NUMBER: GB/9211979.1  
EARLIER FILING DATE: 1992-06-05  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer.  
US-08-947-317-4

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2741 CATCTTTTITTTTTT 2755  
|||||  
Db 1 CATCTTTTITTTTTT 15

RESULT 414  
US-09-070-477-6/c  
Sequence 6, Application US/09070477  
Patent No. 6048974  
GENERAL INFORMATION:  
APPLICANT: Sergei M. Gryaznov  
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
TITLE OF INVENTION: and therapeutic applications  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics  
STREET: 465 Lincoln Centre Drive  
CITY: Foster City  
STATE: California  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 3.1/DOS 5.0  
SOFTWARE: Microsoft Word for Windows, vers. 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,477  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION NUMBER: US/08/713,685  
FILING DATE:  
APPLICATION NUMBER: 08/461,271  
FILING DATE:

/ APPLICATION NUMBER: 08/087,387  
/ FILING DATE: 2-Jul-93  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Stephen C. Macevitz  
/ REGISTRATION NUMBER: 30,285  
/ REFERENCE/DOCKET NUMBER: 104  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 358-7855  
/ TELEFAX: (415) 358-7794  
/ INFORMATION FOR SEQ ID NO: 6:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 16 nucleotides  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-09-070-477-6

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATT 2590  
Db 15 AAAAAAAAAAAAGT 1

RESULT 415  
US-09-411-628-1  
/ Sequence 1, Application US/09411628  
/ Patent No. 6428994  
/ GENERAL INFORMATION:  
/ APPLICANT: University of Southern California  
/ TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN  
/ FILE REFERENCE: 13761-707  
/ CURRENT APPLICATION NUMBER: US/09/411,628  
/ CURRENT FILING DATE: 1999-10-01  
/ EARLIER APPLICATION NUMBER: US 60/102,906  
/ EARLIER FILING DATE: 1998-10-02  
/ NUMBER OF SEQ ID NOS: 16  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 1  
/ LENGTH: 16  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Anchored primer  
/ US-09-411-628-1

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTATTTT 2756  
Db 2 AGCTTTTATTTT 16

RESULT 416  
US-08-535-249-109/c  
/ Sequence 109, Application US/08535249  
/ Patent No. 6455689  
/ GENERAL INFORMATION:  
/ APPLICANT: Schlingsiepen, Georg-Ferdinand  
/ APPLICANT: Brysch, Wolfgang  
/ APPLICANT: Schlingsiepen, Karl-Hermann  
/ APPLICANT: Schlingsiepen, Reimar  
/ APPLICANT: Bogdahn, Ulrich  
/ TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
/ NUMBER OF SEQUENCES: 137  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Jacobson, Price, Holman & Stern

/ STREET: 400 Seventh St. N.W.  
/ CITY: Washington D.C  
/ COUNTRY: U.S.A.  
/ ZIP: 20004  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/535,249  
/ FILING DATE:  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: EP 93 107 089.0  
/ FILING DATE: 30-APR-1993  
/ PRIOR APPLICATION DATA: EP 93 107 849.7  
/ APPLICATION NUMBER:  
/ FILING DATE: 13-MAY-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Player, William E.  
/ REGISTRATION NUMBER: 31,409  
/ REFERENCE/DOCKET NUMBER: 10577/P58418  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (202)638-6666  
/ TELEFAX: (202) 393-5350  
/ TELEX: RCA 248593 IDEA UR  
/ INFORMATION FOR SEQ ID NO: 109:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 16 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: unknown  
/ TOPOLOGY: unknown  
/ MOLECULE TYPE: DNA (genomic)  
/ ANTI-SENSE: YES  
/ US-08-535-249-109

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2088 CTGGAGTCACACAG 2102  
Db 16 CTTGAGTCACACAG 2

RESULT 417  
US-08-535-249-131/c  
/ Sequence 131, Application US/08535249  
/ Patent No. 6455689  
/ GENERAL INFORMATION:  
/ APPLICANT: Schlingsiepen, Georg-Ferdinand  
/ APPLICANT: Brysch, Wolfgang  
/ APPLICANT: Schlingsiepen, Karl-Hermann  
/ APPLICANT: Schlingsiepen, Reimar  
/ APPLICANT: Bogdahn, Ulrich  
/ TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of  
/ NUMBER OF SEQUENCES: 137  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Jacobson, Price, Holman & Stern  
/ STREET: 400 Seventh St. N.W.  
/ CITY: Washington D.C  
/ COUNTRY: U.S.A.  
/ ZIP: 20004  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/535,249  
/ FILING DATE:

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/
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 93 107 089.0
/ FILING DATE: 30-APR-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 93 107 849.7
/ FILING DATE: 13-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Player, William E.
/ REGISTRATION NUMBER: 31,409
/ REFERENCE/DOCKET NUMBER: 10577/P58418
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-6666
/ TELEFAX: (202) 393-5350
/ TELEX: RCA 248593 IDEA UR
/ INFORMATION FOR SEQ ID NO: 131:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ ANTI-SENSE: YES
/ US-08-535-249-131

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2435 GATTGCAAGTCTTG 2449
Db 16 GATTGTAAGTCTTG 2

RESULT 418
US-09-300-958A-57
/ Sequence 57, Application US/09300958A
/ Patent No. 6495319
/ GENERAL INFORMATION:
/ APPLICANT: McClelland, Michael
/ APPLICANT: Welsh, John
/ APPLICANT: Trenkle, Thomas
/ TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
/ FILE REFERENCE: P-PH 3457
/ CURRENT APPLICATION NUMBER: US/09/300,958A
/ PRIOR FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: 60/083,331
/ PRIOR FILING DATE: 1998-04-27
/ PRIOR FILING DATE: 1998-08-27
/ PRIOR FILING DATE: 1998-02-04
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 57
/ LENGTH: 16
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
/ US-09-300-958A-57

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2742 ATCTTTTCTTTT 2756
Db 2 AGCTTTTCTTTT 16

RESULT 419
US-09-300-958A-57
/ Sequence 57, Application US/09300958A
/ Patent No. 6495319
/ GENERAL INFORMATION:
/ APPLICANT: McClelland, Michael
/ APPLICANT: Welsh, John
/ APPLICANT: Trenkle, Thomas
/ TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
/ FILE REFERENCE: P-PH 3457
/ CURRENT APPLICATION NUMBER: US/09/300,958A
/ PRIOR FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: 60/083,331
/ PRIOR FILING DATE: 1998-04-27
/ PRIOR FILING DATE: 1998-08-27
/ PRIOR FILING DATE: 1998-02-04
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 57
/ LENGTH: 16
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
/ US-09-300-958A-57

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2742 ATCTTTTCTTTT 2756
Db 2 AGCTTTTCTTTT 16

RESULT 420
US-09-527-972-16
/ Sequence 16, Application US/09527972
/ Patent No. 6642438
/ GENERAL INFORMATION:
/ APPLICANT: Clendennen, Stephanie K.
/ APPLICANT: Kellogg, Jill A.
/ APPLICANT: Phan, Chau B.
/ APPLICANT: Mathews, Helena V.
/ APPLICANT: Webb, Nancy M.
/ TITLE OF INVENTION: Banana and Melon Promoters for
/ FILE REFERENCE: 4257-0019.30
/ CURRENT APPLICATION NUMBER: US/09/527,972
/ PRIOR FILING DATE: 2000-03-17
/ EARLIER APPLICATION NUMBER: US 60/125,310
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16
/ LENGTH: 16
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: oligonucleotide primer
/ US-09-527-972-16

Query Match 0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2742 ATCTTTTCTTTT 2756
Db 2 AGCTTTTCTTTT 16
```

```
RESULT 421
US-09-479-005A-395/c
; Sequence 395, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH800-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 395
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-479-005A-395

Query Match      0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1212 AAAAAATGCACTAC 1226
    |||||
Db 16 AAAAAATGCACTAC 2

RESULT 422
US-10-174-794-1
; Sequence 1, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: cDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Anchored primer
US-10-174-794-1

Query Match      0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTITTTT 2756
    |||||
Db 2 AGCTTTTITTTT 16

RESULT 423
5262177-6
; Patent No. 5262177
; APPLICANT: BROWN, J OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELLMSTROM, KARL E.; ROSE, TIMOTHY M.; HELLMSTROM, INGERGERD;
; PURCHIO, ANTHONY F.; HU, SHIU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 6
; LENGTH: 16
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60889
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; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 6
; LENGTH: 16
5262177-6

Query Match      0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 970 ATTCCCCCCCCACCC 984
    |||||
Db 2 ATTCCCCCCCCACCC 16

RESULT 424
5262177-6
; Patent No. 5262177
; APPLICANT: BROWN, J OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELLMSTROM, KARL E.; ROSE, TIMOTHY M.; HELLMSTROM, INGERGERD;
; PURCHIO, ANTHONY F.; HU, SHIU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 6
; LENGTH: 16
5262177-6

Query Match      0.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 970 ATTCCCCCCCCACCC 984
    |||||
Db 2 ATTCCCCCCCCACCC 16

RESULT 425
US-09-396-196G-60889/c
; Sequence 60889, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60889
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60889
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Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2e+02;

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QY      2745 TTTTTTTTTTAA 2757
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          |||||
DB       2   TTTTTTTTTTAA 14

RESULT 429
US-08-882-164D-17
; Sequence 17, Application US/08892164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9

```

/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
/ COMPUTER: COMPAQ, IBM PC compatible  
/ OPERATING SYSTEM: MS-DOS 5.1  
/ SOFTWARE: WORD PERFECT  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/892,164D  
/ FILING DATE: June 25, 1997  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/667,546  
/ FILING DATE: June 21, 1996  
/ APPLICATION NUMBER: 08/724,466  
/ FILING DATE: October 1, 1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Hunt, John C.  
/ REGISTRATION NUMBER: 36,424  
/ REFERENCE/DOCKET NUMBER: 50767/00010  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (416) 863-4344  
/ TELEFAX: (416) 863-2653  
/ INFORMATION FOR SEQ ID NO: 17:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 14 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-08-882-164D-17

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 28+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTITTTTTTAA 2757  
Db 2 TTTTITTTTTTAA 14

RESULT 430  
US-08-863-639A-8/c  
/ Sequence 8, Application US/08863639A  
/ Patent No. 5981185  
/ GENERAL INFORMATION:  
/ APPLICANT: Matson, Robert S.  
/ APPLICANT: Coassin, Peter J.  
/ APPLICANT: Rampal, Jang B.  
/ APPLICANT: Caskey, C. T.  
/ TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
/ NUMBER OF SEQUENCES: 95  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Sheldon & Mak  
/ STREET: 225 South Lake Avenue, 9th Floor  
/ CITY: Pasadena  
/ STATE: CA  
/ COUNTRY: USA  
/ ZIP: 91101  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
/ COMPUTER: IBM compatible  
/ OPERATING SYSTEM: Windows 95  
/ SOFTWARE: Corel WordPerfect 8 version  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/863,639A  
/ FILING DATE: May 28, 1997  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Joseph E. Mueth  
/ REGISTRATION NUMBER: 20,532  
/ REFERENCE/DOCKET NUMBER: 11859-1  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (626) 796-4000  
/ TELEFAX: (626) 795-6321  
/ INFORMATION FOR SEQ ID NO: 8:  
/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 15 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: Other nucleic acid  
/ US-08-863-639A-8  
Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2745 TTTTITTTTTTAA 2757  
Db 14 TTTTITTTTTTAA 2  
RESULT 431  
US-08-832-021-17  
/ Sequence 17, Application US/08832021  
/ Patent No. 6045998  
/ GENERAL INFORMATION:  
/ APPLICANT: Combates, N.  
/ APPLICANT: Pardinas, J.  
/ APPLICANT: Parimoo, S.  
/ APPLICANT: Prouty, S.  
/ APPLICANT: Stenn, K.  
/ TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
/ FILE REFERENCE: JBP-382  
/ CURRENT APPLICATION NUMBER: US/08/832,021  
/ CURRENT FILING DATE: 1997-04-02  
/ NUMBER OF SEQ ID NOS: 64  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 17  
/ LENGTH: 15  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: primer  
/ US-08-832-021-17  
Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2745 TTTTITTTTTTAA 2757  
Db 2 TTTTITTTTTTAA 14  
RESULT 432  
US-08-832-021-18  
/ Sequence 18, Application US/08832021  
/ Patent No. 6045998  
/ GENERAL INFORMATION:  
/ APPLICANT: Combates, N.  
/ APPLICANT: Pardinas, J.  
/ APPLICANT: Parimoo, S.  
/ APPLICANT: Prouty, S.  
/ APPLICANT: Stenn, K.  
/ TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
/ FILE REFERENCE: JBP-382  
/ CURRENT APPLICATION NUMBER: US/08/832,021  
/ CURRENT FILING DATE: 1997-04-02  
/ NUMBER OF SEQ ID NOS: 64  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 18  
/ LENGTH: 15  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: primer  
/ US-08-832-021-18

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAA 2757  
Db 2 TTTTNTTTTAA 14

## RESULT 433

US-08-832-021-20  
; Sequence 20, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardinas, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-20

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAA 2757  
Db 2 TTTTNTTTTAA 14

## RESULT 434

US-08-832-021-43/c  
; Sequence 43, Application US/08832021  
; Patent No. 6045998  
; GENERAL INFORMATION:  
; APPLICANT: Combates, N.  
; APPLICANT: Pardinas, J.  
; APPLICANT: Parimoo, S.  
; APPLICANT: Prouty, S.  
; APPLICANT: Stenn, K.  
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY  
; FILE REFERENCE: JBP-382  
; CURRENT APPLICATION NUMBER: US/08/832,021  
; CURRENT FILING DATE: 1997-04-02  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-08-832-021-43

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAATAA 2587  
Db 13 TAAAAAATAA 1

0;

Gaps

Indels

Mismatches

Conservative

Length

Score

DB

Indels

Gaps

Mismatches

Conservative

Length

Score

DB

Indels

Gaps

Mismatches

Conservative

Length

Score

DB

Indels

Gaps

Mismatches

Conservative

Length

Score

DB

Indels

Gaps

Mismatches

Conservative

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Indels

Gaps

Mismatches

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Conservative

Length

Score

DB

Indels



;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/455,627  
;/ FILING DATE: 31-MAY-1995  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Nakamura, Jackie N.  
;/ REGISTRATION NUMBER: 35,966  
;/ REFERENCE/DOCKET NUMBER: LYNX-003/01 US  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 415-843-5000  
;/ TELEFAX: 415-857-0663  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 16 nucleotides  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA  
US-08-455-627-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2740 ACATCTTTTTTTTTT 2755  
Db 1 ACTTTTTTTTTTTT 16

RESULT 437  
US-08-461-271-6  
;/ Sequence 6, Application US/08461271  
;/ Patent No. 5741643  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Sergei M. Gryaznov  
;/ TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
;/ NUMBER OF SEQUENCES: 6  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics  
;/ STREET: 465 Lincoln Centre Drive  
;/ CITY: Foster City  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94404  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 5.25 inch diskette  
;/ COMPUTER: IBM compatible  
;/ OPERATING SYSTEM: Windows 3.1/DOS 5.0  
;/ SOFTWARE: Microsoft Word for Windows, vers. 2.0  
;/ CURRENT APPLICATION DATA:  
;/ FILING DATE: 2-Jul-93  
;/ PRIOR APPLICATION NUMBER: US/08/461,271  
;/ CLASSIFICATION: 435  
;/ APPLICATION DATA:  
;/ FILING DATE: 2-Jul-93  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Stephen C. Macevicz  
;/ REGISTRATION NUMBER: 30,285  
;/ REFERENCE/DOCKET NUMBER: 104  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 358-7855  
;/ TELEFAX: (415) 358-7794  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 16 nucleotides  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
US-08-461-271-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2740 ACATCTTTTTTTTTT 2755  
Db 1 ACTTTTTTTTTTTT 16  
RESULT 438  
US-08-713-685A-6  
;/ Sequence 6, Application US/08713685A  
;/ Patent No. 5817795  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Sergei M. Gryaznov  
;/ TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
;/ NUMBER OF SEQUENCES: 6  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics  
;/ STREET: 465 Lincoln Centre Drive  
;/ CITY: Foster City  
;/ STATE: California  
;/ COUNTRY: USA  
;/ ZIP: 94404  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: 5.25 inch diskette  
;/ COMPUTER: IBM compatible  
;/ OPERATING SYSTEM: Windows 3.1/DOS 5.0  
;/ SOFTWARE: Microsoft Word for Windows, vers. 2.0  
;/ CURRENT APPLICATION DATA:  
;/ FILING DATE: 2-Jul-93  
;/ PRIOR APPLICATION NUMBER: US/08/713,685A  
;/ CLASSIFICATION: 435  
;/ APPLICATION DATA:  
;/ FILING DATE: 2-Jul-93  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Stephen C. Macevicz  
;/ REGISTRATION NUMBER: 30,285  
;/ REFERENCE/DOCKET NUMBER: 104  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 358-7855  
;/ TELEFAX: (415) 358-7794  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 16 nucleotides  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
US-08-713-685A-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2740 ACATCTTTTTTTTTT 2755  
Db 1 ACTTTTTTTTTTTT 16

RESULT 439  
US-08-689-856-6  
;/ Sequence 6, Application US/08689856  
;/ Patent No. 5830658  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Sergei M. Gryaznov  
;/ TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply  
;/ NUMBER OF SEQUENCES: 26  
;/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Cooley Godward LLP  
/ STREET: Five Palo Alto Square, 3000 El Camino Real  
/ CITY: Palo Alto  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 94306-2155  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/689,856  
/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA: US/08/455,627  
/ APPLICATION NUMBER: US/08/455,627  
/ FILING DATE: 31-MAY-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Nakamura, Jackie N.  
/ REGISTRATION NUMBER: 35,966  
/ REFERENCE/DOCKET NUMBER: LYNX-003/01 US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 415-843-5000  
/ TELEFAX: 415-857-0663  
/ INFORMATION FOR SEQ ID NO: 6:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 16 nucleotides  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA  
/ US-08-689-856-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2740 ACATCTTTTTTTTTTTT 2755  
Db 1 ACTTTTTTTTTTTT 16

RESULT 440  
US-09-070-477-6  
/ Sequence 6, Application US/09070477  
/ Patent No. 6048974  
/ GENERAL INFORMATION:  
/ APPLICANT: Sergei M. Gryaznov  
/ TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
/ TITLE OF INVENTION: and therapeutic applications  
/ NUMBER OF SEQUENCES: 6  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics  
/ STREET: 465 Lincoln Centre Drive  
/ CITY: Foster City  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 94404  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 5.25 inch diskette  
/ COMPUTER: IBM compatible  
/ OPERATING SYSTEM: Windows 3.1/DOS 5.0  
/ SOFTWARE: Microsoft Word for Windows, vers. 2.0  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/070,477  
/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/713,685  
/ FILING DATE:  
/ APPLICATION NUMBER: 08/461,271  
/ FILING DATE:

/ APPLICATION NUMBER: 08/087,387  
/ FILING DATE: 2-Jul-93  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Stephen C. Macevitz  
/ REGISTRATION NUMBER: 30,285  
/ REFERENCE/DOCKET NUMBER: 104  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 358-7855  
/ TELEFAX: (415) 358-7794  
/ INFORMATION FOR SEQ ID NO: 6:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 16 nucleotides  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ US-09-070-477-6

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2740 ACATCTTTTTTTTTTTT 2755  
Db 1 ACTTTTTTTTTTTT 16

RESULT 441  
US-09-411-628-1/c  
/ Sequence 1, Application US/09411628  
/ Patent No. 6428994  
/ GENERAL INFORMATION:  
/ APPLICANT: University of Southern California  
/ TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN  
/ TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES  
/ FILE REFERENCE: 13761-707  
/ CURRENT APPLICATION NUMBER: US/09/411,628  
/ CURRENT FILING DATE: 1999-10-01  
/ EARLIER APPLICATION NUMBER: US 60/102,906  
/ NUMBER OF SEQ ID NOS: 16  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 1  
/ LENGTH: 16  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Anchored primer  
/ US-09-411-628-1

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2575 TAAAAAATAAAAAATT 2590  
Db 16 TAAAAAATAAAAAAGCTT 1

RESULT 442  
US-09-300-958A-57/c  
/ Sequence 57, Application US/09300958A  
/ Patent No. 6495319  
/ GENERAL INFORMATION:  
/ APPLICANT: McClelland, Michael  
/ APPLICANT: Welsh, John  
/ APPLICANT: Trenkle, Thomas  
/ TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
/ FILE REFERENCE: P-PH 3457  
/ CURRENT APPLICATION NUMBER: US/09/300,958A  
/ CURRENT FILING DATE: 1999-04-27  
/ PRIOR APPLICATION NUMBER: 60/083,331  
/ PRIOR FILING DATE: 1998-04-27

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; FILE REFERENCE: 4257-0019.30
; CURRENT APPLICATION NUMBER: US/09/527,972
; CURRENT FILING DATE: 2000-03-17
; EARLIER APPLICATION NUMBER: US 60/125,310
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-09-527-972-16

```

|                       |                |                    |          |           |
|-----------------------|----------------|--------------------|----------|-----------|
| Query Match           | 0.3%           | Score 12.8         | DB 1     | Length 16 |
| Best Local Similarity | 87.5%          | Pred. No. 2.9e+02  |          |           |
| Matches 14            | Conservative 0 | Mismatches 2       | Indels 0 | Gaps 0    |
| Qy                    | 2575           | TAATAAAAAAAAAATT   | 2590     |           |
|                       |                |                    |          |           |
| Db                    | 16             | TAATAAAAAAAAAAGCTT | 1        |           |

```

RESULT 445
US-10-174-794-1/c
; Sequence 1, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: cDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Anchored primer
US-10-174-794-1

```

|                       |              |                    |               |            |
|-----------------------|--------------|--------------------|---------------|------------|
| Query Match           | 0.3%         | Score 12.8;        | DB 1;         | Length 16; |
| Best Local Similarity | 87.5%;       | Pred. No. 2.9e+02; |               |            |
| Matches 14;           | Conservative | 0;                 | Mismatches 2; | Indels 0;  |
| Gaps                  | 0;           |                    |               |            |

|    |         |                    |      |            |    |        |    |      |   |
|----|---------|--------------------|------|------------|----|--------|----|------|---|
|    | Matches | 1's; conservative  | v;   | mismatches | z; | indels | v, | gaps | v |
| Qy | 2575    | TAATAAAAAAAAAATT   | 2590 |            |    |        |    |      |   |
|    |         |                    |      |            |    |        |    |      |   |
| Db | 16      | TAATAAAAAAAAAAGCTT | 1    |            |    |        |    |      |   |

;  
 ; Patent No. 6828428  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,  
 ; APPLICANT: Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,  
 ; APPLICANT: Shigenasa; Takei, Masami  
 ; TITLE OF INVENTION: IGA Nephropathy-Related Genes  
 ; NUMBER OF SEQUENCES: 111  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto  
 ; STREET: 30 Rockefeller Plaza  
 ; CITY: New York  
 ; STATE: New York  
 ;

```

;
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,672B
; FILING DATE: 04-JUNE-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04468
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: JP-8-325763
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
;
; US-09-090-672B-105

```

```

Query Match 0.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 3264 TTTTTCCTTTT 3279
DB 2 TTTTTCCTTTT 17

```

```

RESULT 447
US-09-725-265-20
; Sequence 20, Application US/09725265
; Patent No. 6492121
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
;
; US-09-725-265-20

```

```

Query Match 0.3%; Score 12.8; DB 1; Length 18;

```

```

Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2802 GAAAAAAAAAACAT 2817
DB 1 GAAAAAAAAATATAT 16

```

```

RESULT 448
US-09-556-127-20
; Sequence 20, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/09/556,127
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
;
; US-09-556-127-20

```

```

Query Match 0.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2802 GAAAAAAAAAACAT 2817
DB 1 GAAAAAAAAATATAT 16

```

```

RESULT 449
US-08-486-057B-6/c
; Sequence 6, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

, APPLICATION NUMBER: US/08/486,057B
, FILING DATE: 07-JUN-1995
, CLASSIFICATION: 514
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/201,703
, FILING DATE: 25-FEB-1994
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/960,309
, FILING DATE: 13-OCT-1992
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/621,502
, FILING DATE: 03-DEC-1990
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: GB 8927546.5
, FILING DATE: 06-DEC-1989
, ATTORNEY/AGENT INFORMATION:
, NAME: NO. 550494ak, Henry P.
, REGISTRATION NUMBER: 33200
, REFERENCE/DOCKET NUMBER: 4-17861/+
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (908) 277-5110
, TELEFAX: (908) 277-4306
, INFORMATION FOR SEQ ID NO: 6:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 39 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
US-08-486-057B-6

```

|                          |       |                    |        |            |
|--------------------------|-------|--------------------|--------|------------|
| Query Match              | 0.3%  | Score 12.8;        | DB 1;  | Length 39; |
| Best Local Similarity    | 62.5% | Pred. No. 3.7e+02; |        |            |
| Matches 20; Conservative | 0;    | Mismatches 12;     | Indels |            |

**Qy** 2131 ATCTGCTACTGCTTTAGAAATGTGCAGGAT 2162  
||| ||| ||| ||| ||| ||| ||| |||  
**Dδ** 39 ATCTTGACATTTCATAAGCAATAGCGCGCAT 8

```

RESULT 450
US-08-789-580-6/c
; Sequence 6, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005

```

```

/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/789,598
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/486,057
/ FILING DATE: 07-JUN-1995
/ APPLICATION NUMBER: US 08/201,703
/

```

FILING DATE: 25-FEB-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/960,309  
 FILING DATE: 13-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/621,502  
 FILING DATE: 03-DEC-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 8927546.5  
 FILING DATE: 06-DEC-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: NO. 5922846ak, Henry P.  
 REGISTRATION NUMBER: 33200  
 REFERENCE/DOCKET NUMBER: 4-17861+/  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 277-5110  
 TELEFAX: (908) 277-4306  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 39 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

```

Query Match          0.3%; Score 12.8; DB 1; Length 39;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

**Qy**      2131 ATGTCCTACTGCCTTTAGAAATGTGCAGGAT 2162  
             |||||     |    |    |    |    |    |  
**Dδ**      39 ATCCTGCACATTCTTAAAGCAATAGGCCCGCAT 8  
             |||||     |    |    |    |    |    |

RESULT 451  
US-09-725-265-42  
; Sequence 42, Application US/09725265  
; Patent No. 6492121

```

: GENERAL INFORMATION:
: APPLICANT: KURANE, RYUICHIRO
: APPLICANT: KANAGAWA, TAKAHIRO
: APPLICANT: KAWAGATA, YOICHI
: APPLICANT: YAMADA, KAZUTAKA
: APPLICANT: YOKOMAKU, TOYOKAZU
: APPLICANT: KOYAMA, OSAMU
: APPLICANT: FURUSHO, KENTA
: TITLE OF INVENTION: METHOD FOR DETERMINING
: TITLE OF INVENTION: NUCLEIC ACID PROBES
: TITLE OF INVENTION: THE METHOD
: FILE REFERENCE: 199953USOXDIV
: CURRENT APPLICATION NUMBER: US/09/725,265
: CURRENT FILING DATE: 2000-11-29
: PRIOR APPLICATION NUMBER: US 09/556,127
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: JP 1999-111601
: PRIOR FILING DATE: 1999-04-20
: NUMBER OF SEQ ID NOS: 70
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 42
: LENGTH: 20
: TYPE: DNA
: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-42

```

|                          |       |                    |        |            |
|--------------------------|-------|--------------------|--------|------------|
| Query Match              | 0.3%  | Score 12.6;        | DB 1;  | Length 20; |
| Best Local Similarity    | 78.9% | Pred. No. 4.6e+02; |        |            |
| Matches 15; Conservative | 0;    | Mismatches 4;      | Indels |            |

Qy 2793 TAATTATGTGAAAAAAA 2811

```

Db      2 TATATATATAAAAAAAAA 20

RESULT 452
US-09-823-634A-13/c
; Sequence 13, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13

Query Match      0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1156 TTTTATATATATATTTT 1174
Db      20 TTTTTCACAAATTTT 2

RESULT 453
US-09-823-634A-14/c
; Sequence 14, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-634A-14

Query Match      0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1156 TTTTATATATATATTTT 1174
Db      19 TTTTTCACAAATTTT 1

RESULT 454
US-09-823-647B-13/c
; Sequence 13, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES

```

```

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

Query Match      0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1156 TTTTATATATATATTTT 1174
Db      20 TTTTTCACAAATTTT 2

RESULT 455
US-09-823-647B-14/c
; Sequence 14, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

Query Match      0.3%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1156 TTTTATATATATATTTT 1174
Db      19 TTTTTCACAAATTTT 1

RESULT 456
US-09-556-127-42
; Sequence 42, Application US/09556127
; Patent No. 6699661
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD

```



GENERAL INFORMATION:  
APPLICANT: Cerletti, Nico  
APPLICANT: McMaster, Gary K.  
APPLICANT: Cox, David  
APPLICANT: Schmitz, Albert  
APPLICANT: Meyhack, Bernd  
TITLE OF INVENTION: Process for Refolding Recombinantly  
TITLE OF INVENTION: Produced TGF-beta-like Proteins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry P. No. 5922846ak  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/789,588  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,057  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/201,703  
FILING DATE: 25-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,309  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA: US 07/621,502  
FILING DATE: 03-DEC-1990  
APPLICATION NUMBER: GB 8927546.5  
FILING DATE: 06-DEC-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5922846ak, Henry P.  
REGISTRATION NUMBER: 33200  
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 277-5110  
TELEFAX: (908) 277-4306  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-789-588-7

Query Match 0.3%; Score 12.6; DB 1; Length 39;  
Best Local Similarity 60.0%; Pred. No. 3.7e+02;  
Matches 21; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1987 CTACATATGCCAGTGTGATCGAATACTATAAG 2021  
DB 5 CTGCAATTGCAGACTTTACAATCATATTAGGAAG 39

RESULT 460  
US-08-292-620A-359  
Sequence 359, Application US/08292620A  
Patent No. 5837542  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 359:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-359

Query Match 0.3%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 7.1%; Pred. No. 2.8e+02;  
Matches 1; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTITTTTTT 2755  
DB 2 AUUUUUUUUUUU 15

RESULT 461  
US-08-292-620A-360  
Sequence 360, Application US/08292620A  
Patent No. 5837542  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-360

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 7.1%; Pred. No. 2.8e+02;
Matches 1; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTCCTT 2755
DB 1 AUUUUUUUUUUUU 14

RESULT 462
US-08-292-620A-365
Sequence 365, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

```

```

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 365:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-365

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTTCCTTTCCTT 2758
DB 2 UUUUUUUUUUUCAG 15

RESULT 463
US-08-832-021-23
Sequence 23, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
APPLICANT: Combates, N.
APPLICANT: Pardinias, J.
APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-23

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTTCCTTTCCTT 2758

```

Db 2 TTTTTTTTTTTCAG 15

RESULT 464  
US-09-071-845-359  
; Sequence 359, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620  
; FILING DATE: August 17, 1994  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 359:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-071-845-359

Query Match 0.3%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 7.1%; Pred. NO. 2.8e+02;  
Matches 1; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTCAG 15

Db 2 AUUUUUUUUUUUU 15

RESULT 465  
US-09-071-845-360  
; Sequence 360, Application US/09071845  
; Patent No. 6132967

; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620  
; FILING DATE: August 17, 1994  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 360:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-071-845-360

Query Match 0.3%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 7.1%; Pred. NO. 2.8e+02;  
Matches 1; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTCAG 15

Db 1 AUUUUUUUUUUUU 14

RESULT 466  
US-09-071-845-365  
; Sequence 365, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF

```

/ TITLE OF INVENTION: DISEASES OR CONDITIONS
/ TITLE OF INVENTION: RELATED TO LEVELS OF
/ TITLE OF INVENTION: INTRACELLULAR ADHESION
/ TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
/ NUMBER OF SEQUENCES: 2390
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,845
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 365:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-071-845-365

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTITTTTAAAG 2758
Db 2 UUUUUUUUUUUCAG 15

RESULT 467
US-08-292-620A-366
/ Sequence 366, Application US/08292620A
/ Patent No. 5837542
/ GENERAL INFORMATION:
/ APPLICANT: Susan Grimm
/ APPLICANT: Dan T. Stinchcomb
/ APPLICANT: James McSwiggen
/ APPLICANT: Sean Sullivan
/ APPLICANT: Kenneth G. Draper
/ TITLE OF INVENTION: RIBOZYME TREATMENT OF
/ TITLE OF INVENTION: DISEASES OR CONDITIONS
/ TITLE OF INVENTION: RELATED TO LEVELS OF
/ TITLE OF INVENTION: INTRACELLULAR ADHESION
/ TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
/ NUMBER OF SEQUENCES: 2390
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon

```

```

/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,620A
/ FILING DATE: August 17, 1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ PRIOR APPLICATION DATA: including application
/ PRIOR APPLICATION DATA: described below:
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 366:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-292-620A-366

Query Match 0.3%; Score 12.4; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.8e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTITTTTAAAG 2758
Db 1 UUUUUUUUUUUCAG 14

RESULT 468
US-08-832-021-41
/ Sequence 41, Application US/08832021
/ Patent No. 6045998
/ GENERAL INFORMATION:
/ APPLICANT: Combates, N.
/ APPLICANT: Pardini, J.
/ APPLICANT: Parimoo, S.
/ APPLICANT: Prouty, S.
/ APPLICANT: Stenn, K.
/ TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
/ FILE REFERENCE: JBP-382
/ CURRENT APPLICATION NUMBER: US/08/832,021
/ CURRENT FILING DATE: 1997-04-02
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 41
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: primer
/ US-08-832-021-41

Query Match 0.3%; Score 12.4; DB 1; Length 15;

```

two

Best Local Similarity 92.9%; Pred. No. 2.8e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAAAG 2758  
Db 1 TTTTNTTTTAAAG 14

## RESULT 469

US-09-071-845-366  
; Sequence 366, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620  
; FILING DATE: August 17, 1994  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 366:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-09-071-845-366

Query Match 0.3%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 14.3%; Pred. No. 2.8e+02;  
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTNTTTTAAAG 2758  
Db 1 UUUUUUUUUUCAG 14

## RESULT 470

US-08-584-040-2186  
; Sequence 2186, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,040  
; FILING DATE: January 11, 1996  
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/005,974  
; FILING DATE: October 26, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 218/064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2186:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-584-040-2186

Query Match 0.3%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 14.3%; Pred. No. 3.7e+02;  
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2744 CTTTNTTTTAA 2757

Db 3 CUUUUUUUUUUGA 16

## RESULT 471

US-09-371-772B-731  
; Sequence 731, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel.

```

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH000,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 731
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-731

Query Match          0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 14.3%; Pred. No. 3.7e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2744 CTTTTTTTTTAA 2757
Db 3 CUUUUUUUUUUGA 16

RESULT 472
US-09-685-664B-731
; Sequence 731, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggan, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Methods and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH000-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 731
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-731

Query Match          0.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 14.3%; Pred. No. 3.7e+02;
Matches 2; Conservative 11; Mismatches 1; Indels 0; Gaps 0;

QY 2744 CTTTTTTTTTAA 2757
Db 3 CUUUUUUUUUUGA 16

RESULT 473
US-08-330-000-1
; Sequence 1, Application US/08330000
; Patent No. 5686242
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; APPLICANT: Lima, Walter F.
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES AND RESEARCH REAGENTS
; NUMBER OF SEQUENCES: 18

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5686242ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,000
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 755,485
; FILING DATE: September 5, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07489
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca Lynne
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1723
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-330-000-1

Query Match          0.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTTTTTT 2755
Db 3 ATGTTTTTTTTTT 16

RESULT 474
US-08-965-908-1
; Sequence 1, Application US/08965908
; Patent No. 6022691
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas W.
; APPLICANT: Lima, Walter F.
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES AND RESEARCH REAGENTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 6022691ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,908

```

;  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/330,000  
; FILING DATE:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-965-908-1

Query Match 0.3%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 4.1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2742 ATCTTTTTCCTTTT 2755  
||| ||||| |||||  
Db 3 ATGTTTTCCTTTT 16

RESULT 475  
US-09-725-265-17  
; Sequence 17, Application US/09725265  
; Patent No. 6492121  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KAMAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; FILE REFERENCE: 1999S3USOXDIV  
; CURRENT APPLICATION NUMBER: US/09/725,265  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-725-265-17

Query Match 0.3%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 4.1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAT 2589  
||||| ||||| ||

Db 1 AAAAAAAAAAATAT 14

RESULT 476  
US-09-556-127-17  
; Sequence 17, Application US/09556127  
; Patent No. 6695661  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KAMAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/09/556,127  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-09-556-127-17

Query Match 0.3%; Score 12.4; DB 1; Length 18;  
Best Local Similarity 92.9%; Pred. No. 4.1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAT 2589  
||||| ||||| ||  
Db 1 AAAAAAAAAAATAT 14

Search completed: February 25, 2005, 09:40:33  
Job time : 20 secs



|       |    |     |    |   |          |                    |       |    |     |    |   |          |                    |
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| C 107 | 13 | 0.3 | 13 | 1 | CF280757 | ACCESSION:CF280757 | C 180 | 13 | 0.3 | 13 | 1 | CF329946 | ACCESSION:CF329946 |
| C 108 | 13 | 0.3 | 13 | 1 | CF282369 | ACCESSION:CF282369 | C 181 | 13 | 0.3 | 13 | 1 | CF329988 | ACCESSION:CF329988 |
| C 109 | 13 | 0.3 | 13 | 1 | CF290970 | ACCESSION:CF290970 | C 182 | 13 | 0.3 | 13 | 1 | CF330023 | ACCESSION:CF330023 |
| C 110 | 13 | 0.3 | 13 | 1 | CF290971 | ACCESSION:CF290971 | C 183 | 13 | 0.3 | 13 | 1 | CF330725 | ACCESSION:CF330725 |
| C 111 | 13 | 0.3 | 13 | 1 | CF291011 | ACCESSION:CF291011 | C 184 | 13 | 0.3 | 13 | 1 | CF331041 | ACCESSION:CF331041 |
| C 112 | 13 | 0.3 | 13 | 1 | CF291060 | ACCESSION:CF291060 | C 185 | 13 | 0.3 | 13 | 1 | CF331266 | ACCESSION:CF331266 |
| C 113 | 13 | 0.3 | 13 | 1 | CF291061 | ACCESSION:CF291061 | C 186 | 13 | 0.3 | 13 | 1 | CF331273 | ACCESSION:CF331273 |
| C 114 | 13 | 0.3 | 13 | 1 | CF291167 | ACCESSION:CF291167 | C 187 | 13 | 0.3 | 13 | 1 | CF331903 | ACCESSION:CF331903 |
| C 115 | 13 | 0.3 | 13 | 1 | CF291214 | ACCESSION:CF291214 | C 188 | 13 | 0.3 | 13 | 1 | CF332079 | ACCESSION:CF332079 |
| C 116 | 13 | 0.3 | 13 | 1 | CF291427 | ACCESSION:CF291427 | C 189 | 13 | 0.3 | 13 | 1 | CF332695 | ACCESSION:CF332695 |
| C 117 | 13 | 0.3 | 13 | 1 | CF291469 | ACCESSION:CF291469 | C 190 | 13 | 0.3 | 13 | 1 | CF332696 | ACCESSION:CF332696 |
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| C 122 | 13 | 0.3 | 13 | 1 | CF291597 | ACCESSION:CF291597 | C 195 | 13 | 0.3 | 13 | 1 | CF337022 | ACCESSION:CF337022 |
| C 123 | 13 | 0.3 | 13 | 1 | CF291726 | ACCESSION:CF291726 | C 196 | 13 | 0.3 | 13 | 1 | CN546046 | ACCESSION:CN546046 |
| C 124 | 13 | 0.3 | 13 | 1 | CF291903 | ACCESSION:CF291903 | C 197 | 13 | 0.3 | 13 | 1 | CN749468 | ACCESSION:CN749468 |
| C 125 | 13 | 0.3 | 13 | 1 | CF298590 | ACCESSION:CF298590 | C 198 | 13 | 0.3 | 13 | 1 | CN752228 | ACCESSION:CN752228 |
| C 126 | 13 | 0.3 | 13 | 1 | CF298592 | ACCESSION:CF298592 | C 199 | 13 | 0.3 | 13 | 1 | CN752875 | ACCESSION:CN752875 |
| C 127 | 13 | 0.3 | 13 | 1 | CF298736 | ACCESSION:CF298736 | C 200 | 13 | 0.3 | 13 | 1 | CN753196 | ACCESSION:CN753196 |
| C 128 | 13 | 0.3 | 13 | 1 | CF298764 | ACCESSION:CF298764 | C 201 | 13 | 0.3 | 14 | 1 | BQ586422 | ACCESSION:BQ586422 |
| C 129 | 13 | 0.3 | 13 | 1 | CF298795 | ACCESSION:CF298795 | C 202 | 13 | 0.3 | 14 | 1 | BQ587890 | ACCESSION:BQ587890 |
| C 130 | 13 | 0.3 | 13 | 1 | CF298908 | ACCESSION:CF298908 | C 203 | 13 | 0.3 | 14 | 1 | BQ589191 | ACCESSION:BQ589191 |
| C 131 | 13 | 0.3 | 13 | 1 | CF299133 | ACCESSION:CF299133 | C 204 | 13 | 0.3 | 14 | 1 | BQ590242 | ACCESSION:BQ590242 |
| C 132 | 13 | 0.3 | 13 | 1 | CF299359 | ACCESSION:CF299359 | C 205 | 13 | 0.3 | 14 | 1 | BQ590261 | ACCESSION:BQ590261 |
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| C 134 | 13 | 0.3 | 13 | 1 | CF300118 | ACCESSION:CF300118 | C 207 | 13 | 0.3 | 14 | 1 | BQ591176 | ACCESSION:BQ591176 |
| C 135 | 13 | 0.3 | 13 | 1 | CF300587 | ACCESSION:CF300587 | C 208 | 13 | 0.3 | 14 | 1 | BQ591207 | ACCESSION:BQ591207 |
| C 136 | 13 | 0.3 | 13 | 1 | CF300658 | ACCESSION:CF300658 | C 209 | 13 | 0.3 | 14 | 1 | BQ591380 | ACCESSION:BQ591380 |
| C 137 | 13 | 0.3 | 13 | 1 | CF300929 | ACCESSION:CF300929 | C 210 | 13 | 0.3 | 14 | 1 | BQ591482 | ACCESSION:BQ591482 |
| C 138 | 13 | 0.3 | 13 | 1 | CF301247 | ACCESSION:CF301247 | C 211 | 13 | 0.3 | 14 | 1 | BQ591949 | ACCESSION:BQ591949 |
| C 139 | 13 | 0.3 | 13 | 1 | CF301286 | ACCESSION:CF301286 | C 212 | 13 | 0.3 | 14 | 1 | BQ593052 | ACCESSION:BQ593052 |
| C 140 | 13 | 0.3 | 13 | 1 | CF302158 | ACCESSION:CF302158 | C 213 | 13 | 0.3 | 14 | 1 | CF277935 | ACCESSION:CF277935 |
| C 141 | 13 | 0.3 | 13 | 1 | CF302830 | ACCESSION:CF302830 | C 214 | 13 | 0.3 | 14 | 1 | CF278001 | ACCESSION:CF278001 |
| C 142 | 13 | 0.3 | 13 | 1 | CF302898 | ACCESSION:CF302898 | C 215 | 13 | 0.3 | 14 | 1 | CF278452 | ACCESSION:CF278452 |
| C 143 | 13 | 0.3 | 13 | 1 | CF310516 | ACCESSION:CF310516 | C 216 | 13 | 0.3 | 14 | 1 | CF279473 | ACCESSION:CF279473 |
| C 144 | 13 | 0.3 | 13 | 1 | CF310517 | ACCESSION:CF310517 | C 217 | 13 | 0.3 | 14 | 1 | CF279992 | ACCESSION:CF279992 |
| C 145 | 13 | 0.3 | 13 | 1 | CF312721 | ACCESSION:CF312721 | C 218 | 13 | 0.3 | 14 | 1 | CF281958 | ACCESSION:CF281958 |
| C 146 | 13 | 0.3 | 13 | 1 | CF313171 | ACCESSION:CF313171 | C 219 | 13 | 0.3 | 14 | 1 | CF282350 | ACCESSION:CF282350 |
| C 147 | 13 | 0.3 | 13 | 1 | CF314239 | ACCESSION:CF314239 | C 220 | 13 | 0.3 | 14 | 1 | CF294449 | ACCESSION:CF294449 |
| C 148 | 13 | 0.3 | 13 | 1 | CF314874 | ACCESSION:CF314874 | C 221 | 13 | 0.3 | 14 | 1 | CF295570 | ACCESSION:CF295570 |
| C 149 | 13 | 0.3 | 13 | 1 | CF315395 | ACCESSION:CF315395 | C 222 | 13 | 0.3 | 14 | 1 | CF296120 | ACCESSION:CF296120 |
| C 150 | 13 | 0.3 | 13 | 1 | CF316439 | ACCESSION:CF316439 | C 223 | 13 | 0.3 | 14 | 1 | CF297969 | ACCESSION:CF297969 |
| C 151 | 13 | 0.3 | 13 | 1 | CF316440 | ACCESSION:CF316440 | C 224 | 13 | 0.3 | 14 | 1 | CF298109 | ACCESSION:CF298109 |
| C 152 | 13 | 0.3 | 13 | 1 | CF316637 | ACCESSION:CF316637 | C 225 | 13 | 0.3 | 14 | 1 | CF299368 | ACCESSION:CF299368 |
| C 153 | 13 | 0.3 | 13 | 1 | CF318290 | ACCESSION:CF318290 | C 226 | 13 | 0.3 | 14 | 1 | CF300542 | ACCESSION:CF300542 |
| C 154 | 13 | 0.3 | 13 | 1 | CF319066 | ACCESSION:CF319066 | C 227 | 13 | 0.3 | 14 | 1 | CF301020 | ACCESSION:CF301020 |
| C 155 | 13 | 0.3 | 13 | 1 | CF319531 | ACCESSION:CF319531 | C 228 | 13 | 0.3 | 14 | 1 | CF301083 | ACCESSION:CF301083 |
| C 156 | 13 | 0.3 | 13 | 1 | CF319532 | ACCESSION:CF319532 | C 229 | 13 | 0.3 | 14 | 1 | CF301380 | ACCESSION:CF301380 |
| C 157 | 13 | 0.3 | 13 | 1 | CF319919 | ACCESSION:CF319919 | C 230 | 13 | 0.3 | 14 | 1 | CF302675 | ACCESSION:CF302675 |
| C 158 | 13 | 0.3 | 13 | 1 | CF320017 | ACCESSION:CF320017 | C 231 | 13 | 0.3 | 14 | 1 | CF302846 | ACCESSION:CF302846 |
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| C 160 | 13 | 0.3 | 13 | 1 | CF320143 | ACCESSION:CF320143 | C 233 | 13 | 0.3 | 14 | 1 | CF308220 | ACCESSION:CF308220 |
| C 161 | 13 | 0.3 | 13 | 1 | CF320938 | ACCESSION:CF320938 | C 234 | 13 | 0.3 | 14 | 1 | CF308445 | ACCESSION:CF308445 |
| C 162 | 13 | 0.3 | 13 | 1 | CF326844 | ACCESSION:CF326844 | C 235 | 13 | 0.3 | 14 | 1 | CF308918 | ACCESSION:CF308918 |
| C 163 | 13 | 0.3 | 13 | 1 | CF327070 | ACCESSION:CF327070 | C 236 | 13 | 0.3 | 14 | 1 | CF310714 | ACCESSION:CF310714 |
| C 164 | 13 | 0.3 | 13 | 1 | CF327339 | ACCESSION:CF327339 | C 237 | 13 | 0.3 | 14 | 1 | CF311201 | ACCESSION:CF311201 |
| C 165 | 13 | 0.3 | 13 | 1 | CF327340 | ACCESSION:CF327340 | C 238 | 13 | 0.3 | 14 | 1 | CF311813 | ACCESSION:CF311813 |
| C 166 | 13 | 0.3 | 13 | 1 | CF327576 | ACCESSION:CF327576 | C 239 | 13 | 0.3 | 14 | 1 | CF318323 | ACCESSION:CF318323 |
| C 167 | 13 | 0.3 | 13 | 1 | CF327888 | ACCESSION:CF327888 | C 240 | 13 | 0.3 | 14 | 1 | CF318450 | ACCESSION:CF318450 |
| C 168 | 13 | 0.3 | 13 | 1 | CF327939 | ACCESSION:CF327939 | C 241 | 13 | 0.3 | 14 | 1 | CF319826 | ACCESSION:CF319826 |
| C 169 | 13 | 0.3 | 13 | 1 | CF328153 | ACCESSION:CF328153 | C 242 | 13 | 0.3 | 14 | 1 | CF321246 | ACCESSION:CF321246 |
| C 170 | 13 | 0.3 | 13 | 1 | CF328228 | ACCESSION:CF328228 | C 243 | 13 | 0.3 | 14 | 1 | CF327097 | ACCESSION:CF327097 |
| C 171 | 13 | 0.3 | 13 | 1 | CF328807 | ACCESSION:CF328807 | C 244 | 13 | 0.3 | 14 | 1 | CF327119 | ACCESSION:CF327119 |
| C 172 | 13 | 0.3 | 13 | 1 | CF329075 | ACCESSION:CF329075 | C 245 | 13 | 0.3 | 14 | 1 | CF327203 | ACCESSION:CF327203 |
| C 173 | 13 | 0.3 | 13 | 1 | CF329076 | ACCESSION:CF329076 | C 246 | 13 | 0.3 | 14 | 1 | CF327445 | ACCESSION:CF327445 |
| C 174 | 13 | 0.3 | 13 | 1 | CF329417 | ACCESSION:CF329417 | C 247 | 13 | 0.3 | 14 | 1 | CF328490 | ACCESSION:CF328490 |
| C 175 | 13 | 0.3 | 13 | 1 | CF329460 | ACCESSION:CF329460 | C 248 | 13 | 0.3 | 14 | 1 | CF328540 | ACCESSION:CF328540 |
| C 176 | 13 | 0.3 | 13 | 1 | CF329729 | ACCESSION:CF329729 | C 249 | 13 | 0.3 | 14 | 1 | CF328669 | ACCESSION:CF328669 |
| C 177 | 13 | 0.3 | 13 | 1 | CF329800 | ACCESSION:CF329800 | C 250 | 13 | 0.3 | 14 | 1 | CF328994 | ACCESSION:CF328994 |
| C 178 | 13 | 0.3 | 13 | 1 | CF329801 | ACCESSION:CF329801 | C 251 | 13 | 0.3 | 14 | 1 | CF329217 | ACCESSION:CF329217 |
| C 179 | 13 | 0.3 | 13 | 1 | CF329869 | ACCESSION:CF329869 | C 252 | 13 | 0.3 | 14 | 1 | CF329990 | ACCESSION:CF329990 |







**TITLE** Hematophagy-associated gene expression patterns in adult female  
**JOURNAL** Anopheles gambiae mosquitoes  
**COMMENT** Unpublished (2003)  
 Contact: Dana A.N.  
 Frank H. Collins Laboratory  
 University of Notre Dame  
 Center for Tropical Disease Research and Training, Dept. of Biol.  
 Sci., Notre Dame, IN 46556, USA  
 Tel: 574 - 631 - 3241  
 Fax: 574 - 631 - 3996  
 Email: adana@nd.edu

**PCR Primers**  
**FORWARD:** ctgggaagcgccattgtgttg  
**BACKWARD:** ataccgactacatggcgcaattggc  
**Seq primer:** ctgggaagcgccattgtgttg.

**FEATURES**  
**source**  
 1. .24  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="4Arr"  
 /db\_xref="taxon:7165"  
 /sex="female"  
 /tissue\_type="Abdomens"  
 /dev\_stage="Female adult 5-7 days post eclosion"  
 /lab\_host="E. coli XL1-Blue"  
 /clone\_lib="Infected Rat Blood-fed (IRB) An.gam. 30 hr  
 Abdomen library"  
 /notes="Vector: lambdaTriplex2 (Clontech); Site 1: Sfi IA;  
 Site 2: Sfi IB; Plasmidium berghei-infected rat blood-fed  
 adult female An. gambiae mosquitoes were flash frozen  
 after a 30 hour incubation of adult mosquitoes at 19  
 degrees Celsius. Total RNA extracted from abdomens  
 separated from remaining carcass. CDNA inserts >500 bp  
 cloned directionally into ltripleX2; Sfi IA site is 5'.  
 Non-normalized and Non-amplified phagemid library. Single  
 pass sequencing reactions from 5' end."

**Query Match** 0.5%; Score 19.8; DB 1; Length 24;  
**Best Local Similarity** 87.5%; Pred. No. 4.2;  
**Matches** 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 2803 AAAAAAAAAAACATCAAAACAAA 2826  
 |||||  
**Db** 24 AAAAAAAAAAAATNAAAAAAA 1

**RESULT 5**  
**AW247159/c**  
**LOCUS** AW247159 24 bp mRNA linear EST 07-JAN-2000  
**DEFINITION** 2819627.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819627 3',  
 mRNA sequence.  
**ACCESSION** AW247159.1 GI:6590152  
**VERSION** EST.  
**KEYWORDS** Homo sapiens (human)  
**SOURCE** Homo sapiens  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
**REFERENCE** 1 (bases 1 to 24)  
**AUTHORS** NIH-MGC http://imgc.nci.nih.gov/.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Other ESTs: 2819627.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb@mail.nih.gov  
 Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling  
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbr/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross\_match from University of Washington Genome Center

**PHRAP suite.** Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 24  
 contiguous PHRED high quality bases following vector sequence. Very  
 Low Quality Sequence: Trace file contained 24 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a XhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Plate: L1CM2 row: B column: 12  
 High quality sequence stop: 24.

**FEATURES**  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:2819627"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGCC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5',  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

**Query Match** 0.4%; Score 19.2; DB 1; Length 24;  
**Best Local Similarity** 87.5%; Pred. No. 7.8;  
**Matches** 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 2804 AAAAAAAAAAACATCAAAACAAA 2827  
 |||||  
**Db** 24 AAAAAAAAAAAATNAAAAAAA 1

**RESULT 6**  
**AZ458112/c**  
**LOCUS** AZ458112 24 bp DNA linear GSS 04-OCT-2000  
**DEFINITION** IM0261E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0261E24 R, genomic survey sequence.  
**ACCESSION** AZ458112  
**VERSION** AZ458112.1 GI:10616237

**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 24)  
**AUTHORS** Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0261 row: E column: 24  
 Seq primer: CACACAGGAACAGCATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.

**FEATURES**  
 Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0261E24"
/lab_hosts="Male"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAAACATCAAAACAAA 2826
    |||||
Db 24 AAAAAAAAAAATAAAAAAAAAA 1

RESULT 7
AZ621257/c      24 bp      DNA      linear      GSS 13-DEC-2000
LOCUS
DEFINITION
IM0454E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0454E23 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: E column: 23
Seq primer: CGTTGTAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
source
1. .24
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0454E23"
/lab_hosts="Male"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2804 AAAAAAAAAAACATCAAAACAAA 2827
    |||||
Db 24 AAAAAAAAAAATAAAAAAAAAA 1

RESULT 8
BZ764590/c      25 bp      DNA      linear      GSS 13-MAR-2003
LOCUS
DEFINITION
SALK_125759.44.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_125759.44.00.x, genomic
survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 25)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE
A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL
Unpublished (2001)
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At1G51830.
Class: TDNA tagged.
FEATURES
source
1. .25
Location/Qualifiers

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"

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/ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_125759.44.00.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

Query Match 0.4%; Score 19.2; DB 1; Length 25;  
 Best Local Similarity 87.5%; Pred. No. 10;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2731 AAAAAGAAACATCTTTTTTTTT 2754  
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 Db 24 AAAAAAAAAATTTTTTTTTT 1

RESULT 9  
 CF310247  
 LOCUS  
 DEFINITION  
 ABF--04-M19.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--04-M19, mRNA sequence.  
 CF310247  
 CF310247.1 GI:33682008

EST.  
 ORGANISM  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
 1 (bases 1 to 23)

AUTHORS  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

JOURNAL  
 COMMENT  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 Location/Qualifiers

1..23  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="ABF--04-M19"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /notes="vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.4%; Score 18.8; DB 1; Length 23;  
 Best Local Similarity 90.9%; Pred. No. 8.7;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTNTTTTAAAGGAAAAA 2766  
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 Db 2 TTTTNTTTTAAAGGAAAAA 23

RESULT 10  
 CF310247/c  
 LOCUS  
 DEFINITION

ABF--04-M19.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--04-M19, mRNA sequence.  
 CF310247  
 CF310247.1 GI:33682008

EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 23)

AUTHORS  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
 COMMENT  
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 Location/Qualifiers

1..23  
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 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="ABF--04-M19"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /notes="vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.4%; Score 18.8; DB 1; Length 23;  
 Best Local Similarity 90.9%; Pred. No. 8.7;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTNTTTTAAAGGAAAAA 2766  
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 Db 23 TTTTNTTTTAAAGGAAAAA 2

RESULT 11  
 CF310999  
 LOCUS  
 DEFINITION

ABF--05-P22.g1 ABF3-overexpressing transgenic rice plasmid  
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--05-P22, mRNA sequence.  
 CF310999  
 CF310999.1 GI:33682760

EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 23)

AUTHORS  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
 COMMENT  
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

## FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="ABF--05-P22"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid

cdna library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.4%; Score 18.8; DB 1; Length 23;  
Best Local Similarity 90.9%; Pred. No. 8.7;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTTCATTTTAAAGGAAAAA 2766

|||||

1 TTTTTCATTTTAAAGGAAAAA 22

## RESULT 12

CF310999/c

LOCUS

DEFINITION ABF--05-P22.g1 ABF3-overexpressing transgenic rice plasmid cdna

library (ABF) Oryza sativa (japonica cultivar-group) cdna clone

ABF--05-P22, mRNA sequence.

CF310999

CF310999.1 GI:33682760

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 23)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

## FEATURES

source

1. .23  
/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clone="ABF--05-P22"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid

cdna library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.4%; Score 18.8; DB 1; Length 23;  
Best Local Similarity 90.9%; Pred. No. 8.7;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTTCATTTTAAAGGAAAAA 2766

|||||

22 TTTTTCATTTTAAAGGAAAAA 1

## RESULT 13

AZ316719

LOCUS

DEFINITION

AZ316719 23 bp DNA linear GSS 29-SEP-2000

clone UUGC1M0035A01 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

plasmid inserts

plasmid inserts

plasmid inserts

plasmid inserts

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plasmid inserts

plasmid inserts

plasmid inserts

plasmid inserts

plasmid inserts





```

KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: O column: 08
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0129O08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2746 TTTT TTTT TTTT TTTT AAGG AAAAAA 2765
| | | | | | | | | | | | | | | |
Db 1 TTTT TTTT TTTT TTTT AAAAAA 2800

RESULT 17
AZ835133/c
LOCUS
DEFINITION
2M0129O08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0129O08 F, genomic survey sequence.
ACCESSION
AZ835133
VERSION
AZ835133.1 GI:13005041
KEYWORDS
GSS.

Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: O column: 08
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0129O08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2746 TTTT TTTT TTTT TTTT AAGG AAAAAA 2765
| | | | | | | | | | | | | | | |
Db 1 TTTT TTTT TTTT TTTT AAAAAA 2800

RESULT 18
AJ661013
LOCUS
DEFINITION
AJ661013 CSEQRAN09 Sus scrofa cDNA clone C0000935_H04, mRNA
Sequence.
ACCESSION
AJ661013
VERSION
AJ661013.1 GI:49345046
KEYWORDS
Sus scrofa (pig)

```

```

SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: O column: 08
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
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/clone="UUGC2M0129O08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2746 TTTT TTTT TTTT TTTT AAGG AAAAAA 2765
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Db 20 TTTT TTTT TTTT TTTT AAAAAA 1

RESULT 18
AJ661013
LOCUS
DEFINITION
AJ661013 CSEQRAN09 Sus scrofa cDNA clone C0000935_H04, mRNA
Sequence.
ACCESSION
AJ661013
VERSION
AJ661013.1 GI:49345046
KEYWORDS
Sus scrofa (pig)

```



```

ORGANISM      Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE     1 (bases 1 to 21)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE        Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL       Unpublished (2004)
COMMENT      Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site 1;
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES     source
1. .21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000935_H04"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/notes="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2745 TTTTCTTTTAAAGGAAAAA 2764
|||||
Db 2 TTTTCTTTTAAAGGAAAAA 21

RESULT 19
AJ661013/c      21 bp mRNA linear EST 28-JUN-2004
LOCUS          AJ661013 CSEQRAN09 Sus scrofa cDNA clone C0000935_H04, mRNA
sequence.
ACCESSION      AJ661013
VERSION        AJ661013.1 GI:49345046
KEYWORDS       EST.
SOURCE         Sus scrofa (pig)
ORGANISM       Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE     1 (bases 1 to 21)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE        Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL       Unpublished (2004)
COMMENT      Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site 1;
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES     source
1. .21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"

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/clone="C0000935_H04"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/notes="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2747 TTTTCTTTTAAAGGAAAAA 2766
|||||
Db 2 TTTTCTTTTAAAGGAAAAA 2

RESULT 20
J763587
LOCUS          CN763587 21 bp mRNA linear EST 20-MAY-2004
DEFINITION    ID0AAA7BH12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA7BH12 5',
mRNA sequence.
ACCESSION      CN763587
VERSION        CN763587.1 GI:47537510
KEYWORDS       EST.
SOURCE         Acyrthosiphon pisum (pea aphid)
ORGANISM       Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE     1 (bases 1 to 21)
AUTHORS      Hunter,W., Martinez-Torres,D., Rabbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
TITLE          An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
JOURNAL        Unpublished (2004)
COMMENT        Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAAACAGCTATGACC
Plate: 7 row: H column: 12.
FEATURES     source
1. .21
/organism="Acyrthosiphon pisum"
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/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAA7BH12"
/tissue_type="whole insect"
/lab_host="XLI-Blue"
/clone_lib="ApMS"
/notes="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;
Soil conditions: Soil ; Sowing date: 01/06/1999 ;
Harvesting date: 01/06/1999 ; Stress date: no stress ;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. ; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"
Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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|                       |   |                              |           |
|-----------------------|---|------------------------------|-----------|
| QY                    | 2747  | TTTTTTTTTAAAGGAAAAAA         | 2766      |
| Db                    | 1   | TTTTTTTTTAAAAA               | 20        |
| RESULT 21             |   |                              |           |
| LOCUS                 | CN763587/c  |                              |           |
| DEFINITION            | 21 bp mRNA linear EST 20-MAY-2004<br>ID0AA7BH12RM1 ApMs Acyrthosiphon pisum cDNA clone ID0AA7BH12 5',<br>mRNA sequence.   |                              |           |
| ACCESSION             | CN763587  |                              |           |
| VERSION               | CN763587.1  | GI:47537510                  |           |
| KEYWORDS              | EST.  |                              |           |
| SOURCE                | Acyrtosiphon pisum (pea aphid)<br>Acyrtosiphon pisum  |                              |           |
| ORGANISM              | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;<br>Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;<br>Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.  |                              |           |
| REFERENCE             | 1 (bases 1 to 21)   |                              |           |
| AUTHORS               | Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,<br>Stern, D., Tagu, D. and Wincker, P.   |                              |           |
| TITLE                 | An expressed sequence tags database for the pea aphid Acyrthosiphon<br>pisum  |                              |           |
| JOURNAL               | Unpublished (2004)  |                              |           |
| COMMENT               | Contact: D. Tagu<br>INRA Rennes<br>UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France<br>Tel: +33.2.23.48.51.65<br>Fax: +33.2.23.48.51.50<br>Risk of contamination by bacterial sequences from obligatory<br>(Buchnera) or facultative endosymbionts. These sequences were<br>obtained in the frame of the International Consortium of Aphid<br>Genomics in collaboration with Genoscope<br>PCR Primers<br>FORWARD: CAGGAACACGTATGACC<br>Plate: 7 row: H column: 12.<br>1. 21<br>Location/Qualifiers<br>/organism="Acyrtosiphon pisum"<br>/mol_type="mRNA"<br>/cultivar="developmentstage"<br>/db_xref="taxon:7029"<br>/clone="ID0AA7BH12"<br>/tissue_type="whole insect"<br>/dev_stage="nymphs and adults (parthenogenetic females)"<br>/lab_host="X11-Blue"<br>/clone_lib="ApMS"<br>/note="vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;<br>Sample name: ID0AAA ; Plant growth place: Department of<br>Ecology & Evolutionary Biology, Princeton University ;<br>Soil conditions: Soil ; Sowing date: 01/06/1999 ;<br>Harvesting date: 01/06/1999 ; Stress date: no stress ;<br>Description: Aphids inoculated on one-week old <i>Vicia faba</i><br>under non-sterile conditions. All parthenogenetic stages<br>and both winged and wingless adults were collected for<br>library construction. ; experimental condition: long<br>photoperiod (16-hr light/8-hr dark at 18 °C)" |                              |           |
| FEATURES              | source  |                              |           |
| Query Match           | 0.4%  | Score 16.8; DB 1; Length 21; |           |
| Best Local Similarity | 90.0%   | Pred. No. 36;                |           |
| Matches               | 18; Conservative  | 0; Mismatches                | 2; Indels |
| Gaps                  | 0;  |                              |           |
| QY                    | 2745  | TTTTTTTTTAAAGGAAAA           | 2764      |
| Db                    | 20  | TTTTTTTTTAAAAA               | 1         |
| RESULT 22             |   |                              |           |
| LOCUS                 | CL693164  |                              |           |
| DEFINITION            | 21 bp DNA linear GSS 10-JUL-2004<br>PR10160a.G09.2 - PR10160a.BR (21) Mixed stage fosmid library of P.<br>pacificus var. California Pristionchus pacificus genomic, genomic<br>survey sequence.   |                              |           |

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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="vector: pEpifos-5 Fosmid vector"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACHTCACAAA 2822
Db 2 AAAAAAAAAAACHTCACAAA 21

RESULT 24
LOCUS
DEFINITION
CW020436 21 bp mRNA linear GSS 28-SEP-2004
mRNA sequence.
ACCESSION
VERSION
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Cobellis,G., Nicolaus,G., Marra,E., Barbarisi,M., Sardiello,M., Di
Giorgio,F.P., Iovino,N., Zollo,M., Ballabio,A. and Cortese,R.
Tagging genes with cassette-exchange sites
Unpublished (2004)
Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/clone="A012.A8"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="vector: pLIP1"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2747 TTTTAAAAAGGAAAAAAA 2766
Db 1 TTTTAAAAAGGAAAAAAA 20

RESULT 25
LOCUS
DEFINITION
AW247159 24 bp mRNA linear EST 07-JAN-2000
mRNA sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 24)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819627.Sprime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 24
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM2 row: B column: 12
High quality sequence stop: 24.
FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819627"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match      0.4%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1152 TTTCTTTTATATATATTTT 1174
Db 1 TTTTATTTTATTTT 23

RESULT 26
LOCUS
DEFINITION
AZ621257 24 bp DNA linear GSS 13-DEC-2000
1M0454E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0454E23 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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/clone\_lib="OeHDAC1-overexpressing transgenic rice lambda  
phage cDNA library II (HDN)"  
/notes="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at  
5' end with EcoRI and 3' end with XhoI site. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 973 CCCCCCCCCCGCGCCCC 990  
          |||||          |||||  
Db 18 CCCCCCCCCCGCGCCCC 1

RESULT 29  
AZ766990  
LOCUS  
DEFINITION  
A2766990 19 bp DNA linear GSS 16-FEB-2001  
clone UUGC1M0564H19 R, genomic survey sequence.  
ACCESSION  
A2766990  
VERSION  
A2766990.1 GI:12884624  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0564 row: H column: 19  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
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1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0564H19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2576 AAAAAAAAAAATTGGA 2593  
          |||||          |||||  
Db 1 AAAAAAAAAAATTGGA 18

RESULT 30  
AZ426873/c  
LOCUS  
DEFINITION  
AZ426873 20 bp DNA linear GSS 03-OCT-2000  
clone UUGC1M0208L05 R, genomic survey sequence.  
ACCESSION  
AZ426873  
VERSION  
AZ426873.1 GI:10550886  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0208 row: L column: 05  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
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1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0208L05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2738 AAACATCTTTTTTTTTTTT 2755  
Db 20 ATACATCTTTTTTTTTTTT 3

RESULT 31  
AZ426899  
LOCUS  
DEFINITION  
1M0208A08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0208A08 R, genomic survey sequence.  
ACCESSION  
AZ426899  
VERSION  
AZ426899.1 GI:10550912  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0208 row: A column: 08  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

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1..20  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0208A08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 973 CCCCCCCCCCGCGCCCC 990  
Db 1 CCCCCCCCCCGCGCCCC 18

RESULT 32  
AZ845320/c  
LOCUS  
DEFINITION  
2M0145M02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0145M02 F, genomic survey sequence.  
ACCESSION  
AZ845320  
VERSION  
AZ845320.1 GI:13015228  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0145 row: M column: 02  
Seq primer: CCGTGTAAACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0145M02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 39;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 974 CCCCCCACCAGCCGCCCA 991  
|||||  
Db 20 CCCCCCAGCCGCCGCCA 3

RESULT 33  
CF312586/c  
LOCUS  
DEFINITION ABP--08-G13-g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) *Oryza sativa* (japonica cultivar-group) cDNA clone ABF--08-G13, mRNA sequence.

ACCESSION CF312586  
VERSION CF312586.1 GI:33684347  
KEYWORDS EST.  
SOURCE  
ORGANISM *Oryza sativa* (japonica cultivar-group)  
*Oryza sativa* (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; *Oryza*.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..16  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clones="ABP--08-G13"  
/tissue\_type="leaf"  
/dev\_stages="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_libs="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588  
|||||  
Db 16 TTTAAAAA 1

RESULT 34  
CF298591/c  
LOCUS  
DEFINITION 7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) *Oryza sativa* (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA sequence.  
ACCESSION CF298591

VERSION CF298591.1 GI:33670352  
KEYWORDS EST.  
SOURCE  
ORGANISM *Oryza sativa* (japonica cultivar-group)  
*Oryza sativa* (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; *Oryza*.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..18  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clones="7LEAF--02-A20"  
/tissue\_type="leaf"  
/dev\_stages="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_libs="Rice leaf plasmid cDNA library II (7LEAF)"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588  
|||||  
Db 18 TTTAAAAA 3

RESULT 35  
CF278272/c  
LOCUS  
DEFINITION 14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL) *Oryza sativa* (japonica cultivar-group) cDNA clone 14ETL--04-C01, mRNA sequence.

ACCESSION CF278272  
VERSION CF278272.1 GI:33655658  
KEYWORDS EST.  
SOURCE  
ORGANISM *Oryza sativa* (japonica cultivar-group)  
*Oryza sativa* (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; *Oryza*.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..19  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"



/cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="14ETL--04-C01"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 16; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTTAAAAA 2588  
 |||||  
 Db 18 TTTTAAAAA 3

RESULT 36  
 AZ458112 24 bp DNA linear GSS 04-OCT-2000  
 LOCUS  
 DEFINITION IM0261E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0261E24 R, genomic survey sequence.

ACCESSION AZ458112  
 VERSION A2458112.1 GI:10616237  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 24)  
 REFERENCE  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0261 row: E column: 24  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: Plasmid ends  
 High quality sequence stop: 24.

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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
 /clones="UUGC1M0261E24"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16; DB 1; Length 24;  
 Best Local Similarity 79.2%; Pred. No. 1.7e+02;  
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1153 TTCTTTTATATATATTTTCT 1176  
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 Db 1 TTTTITTTATTTTITTTT 24

RESULT 37  
 CF308042/c 19 bp mRNA linear EST 15-AUG-2003  
 LOCUS  
 DEFINITION ABF--01-L07 b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-L07, mRNA sequence.

ACCESSION CF308042  
 VERSION CF308042.1 GI:33679803  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
 Location/Qualifiers  
 1..19  
 /organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"  
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 /db\_xref="taxon:39947"  
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 /dev\_stage="14 days after germination"  
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 /clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 50;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2798 ATGTGAAAAA 2816  
 |||||  
 Db 19 ATGTGAAAAA 1



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RESULT 38
AZ654747/c
LOCUS
DEFINITION
  AZ654747
  19 bp      DNA      linear      GSS 14-DEC-2000
  clone UUGC1M0529F08 F, genomic survey sequence.
ACCESSION
  AZ654747
VERSION
  AZ654747.1  GI:11791893
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
REFERENCE
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
  COMMENT
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0529 row: F column: 08
    Seq primer: CGTGTAAACGACGGCCAGT
    Class: plasmid ends
    High quality sequence stop: 19.
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    /db_xref="taxon:10090"
    /clone="UUGC1M0529F08"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptored DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptored mouse DNA was annealed to
    adaptored vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
    Query Match      0.4%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 89.5%; Pred. No. 50;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  Qy 2804 AAAAAAAAAAACATCAAAA 2822
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  Db 19 AAAAAAAAAAATATAAAA 1

RESULT 39

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AZ764511/c
LOCUS
DEFINITION
  AZ764511
  19 bp      DNA      linear      GSS 16-FEB-2001
  clone UUGC1M0560B08 R, genomic survey sequence.
ACCESSION
  AZ764511
VERSION
  AZ764511.1  GI:12879549
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
REFERENCE
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
  COMMENT
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0560 row: B column: 08
    Seq primer: CACACAGGAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 19.
FEATURES
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    /db_xref="taxon:10090"
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    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptored DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptored mouse DNA was annealed to
    adaptored vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
    Query Match      0.4%; Score 15.8; DB 1; Length 19;
    Best Local Similarity 89.5%; Pred. No. 50;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  Qy 2737 AAAACATCTTTTTTTTTT 2755
      |||||
  Db 19 AAAAAATTTTTTTTTTTT 1

RESULT 40
AZ858877

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LOCUS  
 DEFINITION 2M0164D14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0164D14 F, genomic survey sequence.  
 ACCESSION AZ858877  
 VERSION AZ858877  
 KEYWORDS GSS.  
 SOURCE AZ858877.1 GI:13052498  
 ORGANISM Mus musculus (house mouse)  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0164 row: D column: 14  
 Seq primer: CTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gi|4732114|gb|AF129072.1] a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

FEATURES  
 source

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 50;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 615 GCGGCGCGCGCACGCGCG 633  
 Db 1 GCGGCGCGCGCGCGCGCG 19

RESULT 41  
 AZ858877/c  
 LOCUS AZ858877 19 bp DNA linear GSS 21-FEB-2001

DEFINITION 2M0164D14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0164D14 F, genomic survey sequence.  
 ACCESSION AZ858877  
 VERSION AZ858877.1 GI:13052498  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0164 row: D column: 14  
 Seq primer: CTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0164D14"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gi|4732114|gb|AF129072.1] a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

FEATURES  
 source

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 50;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 616 GCGGCGCGCGCACGCGCG 634  
 Db 19 GCGGCGCGCGCGCGCGCG 1

RESULT 42  
 AZ962226  
 LOCUS AZ962226 19 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

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ACCESSION   A2962226
VERSION     A2962226.1  GI:13833453
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0231 row: A column: 02
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES             source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2M0231A02"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1|, a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2584 AAAAAATTCGACAAAAAAA 2602
|||||
Db 1 AAAAAATTCGACAAAAAAA 19

RESULT 43
BG673623 BG673623 17 bp mRNA linear EST 30-APR-2001
LOCUS DRNAQC09 Rat DRG Library Rattus norvegicus cDNA clone DRNAQC09
DEFINITION 5', mRNA sequence.

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ACCESSION   BG673623
VERSION     BG673623.1  GI:13895722
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 17)
Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
22056133
MEDLINE
PUBMED
12060780
Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.
FEATURES             source
1..17
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNAQC09"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2571 TGTTTAAAAAAA 2587
|||||
Db 1 TTTTAAAAAAA 17

RESULT 44
AI471695 AI471695 19 bp mRNA linear EST 09-MAR-1999
LOCUS t199f04.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:2155231 3'
DEFINITION similar to SW:LA17 YEAST Q12446 PROLINE-RICH PROTEIN LAS17.
; contains element MSRI repetitive element ;, mRNA sequence.
AI471695
AI471695.1 GI:4333785
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Greg Lannon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

#### FEATURES

source

```

1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:215231"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col4"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: Salt; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"
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Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 74;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 974 CCCCCCACCACCGCCGCC 990
      ||||| ||||| |||||
Db 1 CCCCCCACCACCGCCGCC 17
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RESULT 45  
 AZ427731  
 LOCUS  
 DEFINITION  
 1M0209G19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0209G19 R, genomic survey sequence.

```

ACCESSION AZ427731
VERSION AZ427731
KEYWORDS GSS.
SOURCE GI:10551744
ORGANISM Mus musculus (house mouse)
```

REFERENCE  
 AUTHORS  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0209 row: G column: 19  
 Seq primer: CACACGAAACACCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
 source  
 1. .19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0209G19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 74;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 974 CCCCCCACCACCGCCGCC 990
      ||||| ||||| |||||
Db 1 CCCCCCACCACCGCCGCC 17
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#### RESULT 46

AZ650212  
 LOCUS  
 DEFINITION  
 1M0520G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0520G13 F, genomic survey sequence.

```

ACCESSION AZ650212
VERSION AZ650212
KEYWORDS GSS.
SOURCE GI:11784470
ORGANISM Mus musculus (house mouse)
```

REFERENCE  
 AUTHORS  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0520 row: G column: 13  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
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 1. .19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"

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/db_xref="taxon:10090"
/clones="UUGC1M0520G13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCCCCCCC 989  
||||||| |||||  
Db 3 CCCCCCCCCCCCCCCC 19

RESULT 47  
CD743368  
LOCUS CD743368 24 bp mRNA linear EST 25-JUN-2004  
DEFINITION IRB8\_E10\_IRB8\_072 Infected Rat Blood-fed (IRB) An.gam. 30 hr Abdomen Library Anopheles gambiae cDNA 5', mRNA sequence.  
VERSION CD743368  
KEYWORDS CD743368.1 GI:49247179  
SOURCE EST.  
ORGANISM Anopheles gambiae (African malaria mosquito)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.  
1 (bases 1 to 24)  
REFERENCE Dana, A.N., Lobo, N.F., Hillenmeyer, M.E. and Collins, F.H. Hematophagy-associated gene expression patterns in adult female Anopheles gambiae mosquitoes  
Unpublished (2003)  
CONTACT: Dana A.N.  
Frank H. Collins Laboratory  
University of Notre Dame  
Center for Tropical Disease Research and Training, Dept. of Biol. Sci., Notre Dame, IN 46556, USA  
Tel.: 574 - 631 - 3241  
Fax: 574 - 631 - 3996  
Email: adana@nd.edu  
PCR Primers  
FORWARD: ctccggagcgccattgtgtgg  
BACKWARD: ataccactataggcgaaattggc  
Seq primer: ctccggagcgccattgtgtgg.  
Location/Qualifiers  
1. .24  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="4Atr"  
/db\_xref="taxon:7165"  
/sex="female"  
/tissue\_type="Abdomens"  
/dev\_stage="Female adult 5-7 days post eclosion"

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/lab_host="E. coli XL1-Blue"  
/clone_lib="Infected Rat Blood-fed (IRB) An.gam. 30 hr Abdomen Library"  
/notes="Vector: lamdaTriplex2 (Clontech); Site 1: Sfi IA; Site 2: Sfi IB; Plasmodium berghei-infected rat blood-fed adult female An. gambiae mosquitoes were flash frozen after a 30 hour incubation of adult mosquitoes at 19 degrees Celsius. Total RNA extracted from abdomens separated from remaining carcasses. CDNA inserts >500 bp cloned directionally into lTriplex2; Sfi IA site is 5'. Non-normalized and Non-amplified phagemid library. Single pass sequencing reactions from 5' end."
```

Query Match 0.4%; Score 15.2; DB 1; Length 24;  
Best Local Similarity 81.0%; Pred. No. 2.9e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4079 TTTTCTTTAATGCTTTTTT 4099  
||||||| |||||  
Db 1 TTTTITTTAATTTTTTTTTT 21

RESULT 48  
AW246551/c  
LOCUS AW246551 15 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2822090.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822090 3', mRNA sequence.  
VERSION AW246551  
KEYWORDS AW246551.1 GI:6589544  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 15)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Other ESTs: 2822090.5prime  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-x@mail.nih.gov  
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio-llnl.gov/bbrp/image/image.html  
Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu/LowQualitySequence: 14 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LiCM8 row: I column: 3  
High quality sequence stop: 14.  
Location/Qualifiers  
1. .15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822090"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2585  
DB 15 TGTTTAAAAA 1

RESULT 49  
LOCUS CF299675  
DEFINITION 7LEAF--03-M14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-M14, mRNA sequence.  
ACCESSION CF299675  
VERSION CF299675.1 GI:33671436  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)

REFERENCE  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .17  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="7LEAF--03-M14"  
/tissue\_type="leaf"  
/dev\_stages="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

FEATURES  
source

Query Match 0.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2587  
DB 3 TTTAAAAA 17

RESULT 50  
LOCUS AJ600267  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 503E07, genomic survey sequence.  
ACCESSION AJ600267  
VERSION AJ600267.1 GI:37949895  
KEYWORDS GSS; right border; T-DNA flanking sequence.

SOURCE  
ORGANISM

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rooids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS

1  
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)  
22363535  
PUBMED 12446565

REFERENCE  
AUTHORS

2 (bases 1 to 18)  
Balzergue, S.  
Direct Submission  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (a) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source

1. .18  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Massillawskijsa"  
/db\_xref="taxon:3702"  
/clone="503E07"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
1. .18  
/note="T-DNA flanking sequence  
right border"

Query Match 0.4%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1160 TTATATATATTTT 1174

DB 3 TTATATATATTTT 17

RESULT 51  
LOCUS AZ764511

DEFINITION 1M0560B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560B08 R, genomic survey sequence.

ACCESSION AZ764511.1 GI:12879549

VERSION AZ764511

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE  
AUTHORS

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: B column: 08

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

#### FEATURES

Location/Qualifiers

source

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0560B08"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.4%; Score 15; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAATT 2590

|||||||

1 AAAAAAAAAAAAAATT 15

RESULT 52

AW248796

LOCUS

DEFINITION AW248796 18 bp mRNA linear EST 07-JAN-2000

mRNA sequence.

ACCESSION AW248796

VERSION AW248796.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2820768.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/brp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 12  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 18 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.

Plate: LHCMS row: B column: 1

High quality sequence stop: 12.

#### FEATURES

source

1..18

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGS:2820768"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_7"

/notes="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:

ECORI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 93;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2746 TTTTITTTTAAAGGAAAA 2763

|||||||

1 TTTTITTTTGGGAAAA 18

RESULT 53

CF301359/c

LOCUS

DEFINITION CF301359 18 bp mRNA linear EST 15-AUG-2003

7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa (japonica cultivar-group) cDNA clone 7LEAF-06-D05, mRNA

sequence.

ACCESSION CF301359

VERSION CF301359.1

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..18

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"



/cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF--06-D05"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 93;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 926 AGGAGAAAAAACA 943  
 |||||  
 Db 18 AGGAAAAA

RESULT 54  
 BM658913 26 bp mRNA linear EST 27-FEB-2002  
 LOCUS LQ602768282.R1 CSEQFL36 fetal brain Sus scrofa cDNA, mRNA  
 DEFINITION

ACCESSION BM658913  
 VERSION BM658913.1 GI:18959184  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Adelson,D.L. and Gill,C.A.  
 TITLE Porcine ESTs  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: David L. Adelson  
 Animal Breeding and Genetics  
 Texas A&M University  
 Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,  
 USA

Tel: 9798452616  
 Fax: 9798456970  
 Email: david.adelson@tamu.edu.  
 Location/Qualifiers  
 1..26  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /dev\_stage="fetal"

Qy 1152 TTTCTTTTATATATTTTCTT 1177  
 |||||  
 Db 1 TTTTCTTCTTTT

Query Match 0.3%; Score 14.8; DB 1; Length 26;  
 Best Local Similarity 73.1%; Pred. No. 3.5e+02;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1152 TTTCTTTTATATATTTTCTT 1177  
 |||||  
 Db 1 TTTTCTTCTTTT

RESULT 55  
 A1685758 16 bp mRNA linear EST 27-MAY-1999  
 LOCUS tu37909.x1 NCI CGAP Pr28 Homo sapiens cDNA IMAGE:253280 3'  
 DEFINITION similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL  
 SEQUENCE MOTIF PROTEIN 1 ;contains element LTR4 repetitive element

ACCESSION A1685758  
 VERSION A1685758.1 GI:4897052  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 16)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: csapbs-x@mail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/brp/image/image.html

Trace considered overall poor quality  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2253280"  
 /sex="male"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Pr28"  
 /notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)  
 with a modified polylinker; Plasmid DNA from the  
 normalized library NCI CGAP Pr22 was prepared, and ss  
 circles were made in vitro. Following RAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clonesIDs  
 985608-986759, 1101192-1101959, and 1217928-1220615).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 63;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 644 CACACATCCACGCGCA 659  
 |||||  
 Db 1 CACACATACACGCGCA 16

RESULT 56  
 AW248540/c 16 bp mRNA linear EST 07-JAN-2000  
 LOCUS 2820844.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820844 3',  
 DEFINITION mRNA sequence.

ACCESSION AW248540  
 VERSION AW248540.1 GI:6591533  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 16)  
 AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Other\_ESTs: 2820844.5prime



Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://www-bio.llnl.gov/bbrp/image/image.html> Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross\_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LUCM5 row: E column: 5  
High quality sequence stop: 15.  
Location/Qualifiers

## FEATURES

source

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1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820844"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 63;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2570 GTGTTTAAAAAAA 2585

Db 16 GTTTTAAAAAAA 1

RESULT 57  
AW248958  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW248958 16 bp mRNA linear EST 07-JAN-2000  
2819454.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819454 3', mRNA sequence.

AW248958  
EST.  
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819454.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross\_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LUCM1 row: K column: 7  
High quality sequence stop: 15.  
Location/Qualifiers

## FEATURES

source

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1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819454"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 63;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2746 TTTTATTTTAAAGGAA 2761

Db 1 TTTTATTTTAAAGGAA 16

RESULT 58  
CF317778/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF317778 16 bp mRNA linear EST 15-AUG-2003  
HD--07-J13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--07-J13, mRNA sequence.

CF317778  
EST.  
Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .16  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"



Best Local Similarity 93.8%; Pred. No. 95;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2570 GTGTTTAAAAA 2585  
Db 16 GTTTTAAAAA 1

RESULT 61  
CF299997/c  
LOCUS  
DEFINITION  
17 bp mRNA linear EST 15-AUG-2003  
7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-D19, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source  
1..17  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clones="7LEAF--04-D19"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 95;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 62  
CF300456/c  
LOCUS  
DEFINITION  
18 bp mRNA linear EST 15-AUG-2003  
7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N23, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source  
1..18  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clones="7LEAF--04-N23"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 929 AGAAAAAACA 944  
Db 18 AGAAAAAACA 3

RESULT 63  
CF329285/c  
LOCUS  
DEFINITION  
18 bp mRNA linear EST 18-AUG-2003  
NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa (japonica cultivar-group) cDNA clone NACL--04-I22, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source  
1..18  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clones="NACL--04-I22"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match      0.3%;   Score 14.4;   DB 1;   Length 18;
Best Local Similarity 99.8%;   Pred.No. 1.3e+00;
Matches 15;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      929  AGRAAAAAAAAAACAAA  944
          | | | | | | | | | |
Db      17  AGRAAAAAAAAAAAAAA  2

```

|            |            |  |   |           |   |                           |
|------------|------------|--|---|-----------|---|---------------------------|
| RESULT_64  | AW249689/c | AW249689   | 15 bp   | mrna      | linear                                    | EST 07-JAN-2000           |
| LOCUS      |            | 2819706.3  | prime   | NIH_MGC_7 | Homo sapiens cDNA clone IMAGE:2819706 3', |                           |
| DEFINITION |            |  | sequence.   |           |   |                           |
| ACCESSION  |            | AW249689   |   |           |   |                           |
| VERSION    |            | AW249689.1   | GI:6592682  |           |   |                           |
| KEYWORDS   |            | EST.   |   |           |   |                           |
| SOURCE     |            | Homo sapiens   | (human)   |           |   |                           |
| ORGANISM   |            | Homo sapiens   |   |           |   |                           |
|            |            | Eukaryota;   | Metazoa;  | Chordata; | Cranialia;                                | Vertebrata; Euteleostomi; |
|            |            | Mammalia;  | Eutheria;   | Primates; | Catarrhini;                               | Hominidae; Homo.          |
| REFERENCE  |            | 1 (bases 1 to 15)  |   |           |   |                           |
| AUTHORS    |            | NIH-MGC  | <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> . |           |   |                           |
| TITLE      |            | National Institutes of Health, Mammalian Gene Collection (MGC) |   |           |   |                           |
| JOURNAL    |            | Unpublished (1999)   |   |           |   |                           |
| COMMENT    |            | Other ESTs: 2819706.5  | prime   |           |   |                           |
|            |            | Contact: Robert Strausberg, Ph.D.                              |   |           |   |                           |

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (iLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/iLNL at: [www.bio.linn.gov/bbrp/image/image.html](http://www.bio.linn.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center. PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 13 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a xhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

```

FEATURES
source
1. 115
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819706"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)".

```

Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;

|            |   |               |      |        |
|------------|---|---------------|------|--------|
| Qy         | 2799  | TGTGAAAAAAAAA | 2812 |        |
| Ds         | 14  | TGTGAAAAAAAAA | 1    |        |
| RESULT 65  |   |               |      |        |
| LOCUS      | CF295100  | 15 bp         | mRNA | linear |
| DEFINITION | 30DGS-04-O02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS-04-O02, mRNA sequence.   |               |      |        |
| ACCESSION  | CF295100  |               |      |        |
| VERSION    | CF295100.1  | GI:33664133   |      |        |
| KEYWORDS   | EST.  |               |      |        |
| SOURCE     | Oryza sativa (japonica cultivar-group)  |               |      |        |
| ORGANISM   | Oryza sativa (japonica cultivar-group)  |               |      |        |
|            | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  |               |      |        |
| REFERENCE  | 1 (bases 1 to 15)   |               |      |        |
| AUTHORS    | Kim, J.-S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.-K., Kim, Y.-K. and Nahm, B.H.  |               |      |        |
| TITLE      | Large-scale Sequencing Analysis of Rice ESTs  |               |      |        |
| JOURNAL    | Unpublished (2003)  |               |      |        |
| COMMENT    | Contact: Nahm B.H.<br>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University<br>Yongin, Kyeonggi, Korea<br>Tel: 82 31 330 6193<br>Fax: 82 31 321 6355<br>Email: bhnahm@qsbio.com, bhnahm@bio.myongji.ac.kr. |               |      |        |

**FEATURES**

```

source
1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--04-002"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

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Query Match          0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;
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Qy 2575 TAAAAAAAAAAAAA 2588  
Db 15 TAAAAAAAAAAAAA 2

RESULT 66  
CF301470/c  
LOCUS  
CF301470 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-F15, mRNA  
sequence.

|           |            |             |
|-----------|------------|-------------|
| ACCESSION | CF301470   | sequence.   |
| VERSION   | CF301470.1 | GI:33673231 |
| KEYWORDS  | EST.       |             |

|           |  |
|-----------|--|
| SOURCE    | <i>Oryza sativa</i> (japonica cultivar-group)                      |
| ORGANISM  | <i>Oryza sativa</i> (japonica cultivar-group)                      |
|           | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
|           | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;         |
|           | Ehrhartoideae; Oryzeae; <i>Oryza</i> .                             |
| REFERENCE | 1 (bases 1 to 15)  |

| REFERENCE         | AUTHORS  | TITLE  |
|-------------------|--|--|
| 1 (bases 1 to 15) | Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. | Large-scale Sequencing Analysis of Rice ESTs |

JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1. .15  
 Location/Qualifiers  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF-06-F15"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2803 AAAAAAAAAAACA 2816  
 Db 14 AAAAAAAAAAACA 1

RESULT 67  
 CR789161  
 LOCUS 15 bp mRNA linear EST 01-OCT-2004  
 DEFINITION DKFP468J1632\_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone  
 DKFP468J1632 5', mRNA sequence.

ACCESSION CR789161  
 VERSION CR789161.1 GI:53708043  
 KEYWORDS EST.  
 SOURCE Pongo pygmaeus (orangutan)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,  
 Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
 Wiemann,S.  
 TITLE Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regiert,T., et al.)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: MIPS

MIPS  
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,  
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
 Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact  
 RZPD for ordering:  
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFP468J1632  
 Further information about the clone and the sequencing project is  
 available at http://mips.gsf.de/projects/cdna/.

FEATURES  
 source  
 1. .15  
 Location/Qualifiers  
 /organism="Pongo pygmaeus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9600"  
 /clone="DKFP468J1632"  
 /tissue\_type="heart"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="468 (synonym: phrt1)"  
 /notes="vector: pSPori\_Sfi; Site\_1: SfiIA; Site\_2: SfiIB"

Query Match 0.3%; Score 14; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2803 AAAAAAAAAAACA 2816  
 Db 2 AAAAAAAAAAACA 15

RESULT 68  
 BQ590507/c  
 LOCUS 16 bp mRNA linear EST 06-DEC-2002  
 DEFINITION E012844-024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
 cDNA clone 024-019-M04 3-PRIME, mRNA sequence.

ACCESSION BQ590507  
 VERSION BQ590507.1 GI:26120090  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Anaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
 Insert length: 16 Std Error: 0.00  
 Plate: 19 row: M column: 04  
 Seq primer: T7; GTAATACGACTCTACTATAGGC.

FEATURES  
 source  
 1. .16  
 Location/Qualifiers  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:189608"  
 /db\_xref="taxon:161934"  
 /clone="024-019-M04"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-storage root"  
 /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinzelleneber Saatucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 14; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2575 TAAAAAAAAAAAAA 2588  
 Db 16 TAAAAAAAAAAAAA 3

RESULT 69  
 BQ595369/c

```

LOCUS      BQ595369              16 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION S01317-024-022-P02-T7 MPZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION  BQ595369
VERSION    BQ595369.1      GI:26124952
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
JOURNAL   fingerprinting allows access to 25 000 potential sugar beet genes
MEDLINE   Plant J. 32 (5), 845-857 (2002)
PUBMED    22362189
COMMENT   Contact: Weisshaar B
            ADIS DNA core facility at MPZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
            Insert Length: 16 Std Error: 0.00
            Plate: 22 row: P column: 02
            Seq primer: T7; GTAATACGACTCATTATAGGC.
            Location/Qualifiers
FEATURES   source
            1..16
                /organism="Beta vulgaris"
                /mol_type="mRNA"
                /cultivar="KWS2320 (double haploid, monogerm breeding
                line)"
                /db_xref="taxon:161934"
                /clone="024-022-P02"
                /tissue_type="developing root"
                /lab_host="EMDH10B"
                /clone_lib="MPZ-ADIS-024-developing root"
                /note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database: http://gabi.rzpd.de"
            Query Match      0.3%; Score 14; DB 1; Length 16;
            Best Local Similarity 100.0%; Pred. No. 94;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2575 TAAAAAATAAAAA 2588
Db      16 TAAAAAATAAAAA 3

RESULT 70
LOCUS    CF296130/c              16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HP-02-G01-g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--02-G01, mRNA sequence.
ACCESSION CF296130
VERSION    CF296130.1      GI:33685774
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoidae; Oryzaceae; Oryza.
            1 (bases 1 to 16)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
FEATURES   source
            1..16
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD-02-G01"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"

Qy      2575 TAAAAAATAAAAA 2588
Db      16 TAAAAAATAAAAA 3

RESULT 70
LOCUS    CF296130/c              16 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA
            sequence.
ACCESSION CF296130
VERSION    CF296130.1      GI:33665163
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
FEATURES   source
            1..16
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="30DGS--06-F22"
                /tissue_type="leaf"
                /dev_stage="30 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
            Query Match      0.3%; Score 14; DB 1; Length 16;
            Best Local Similarity 100.0%; Pred. No. 94;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2575 TAAAAAATAAAAA 2588
Db      16 TAAAAAATAAAAA 3

RESULT 71
LOCUS    CF314013/c              16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HP-02-G01-g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--02-G01, mRNA sequence.
ACCESSION CF314013
VERSION    CF314013.1      GI:33685774
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoidae; Oryzaceae; Oryza.
            1 (bases 1 to 16)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
FEATURES   source
            1..16
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD-02-G01"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"

```

```

/lab_host="E.coli DH10B"
/clone_lib="OeHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Query Match      0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2575 TAAAAAATAAAAAA 2588
      |||||
Db 16 TAAAAAATAAAAAA 3

```

```

RESULT 72
CF329320/c
LOCUS
DEFINITION NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
sequence.

```

```

ACCESSION CF329320
VERSION CF329320.1 GI:33806877
KEYWORDS EST.
SOURCE

```

## ORGANISM

```

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

```

```
REFERENCE 1 (bases 1 to 16)

```

```
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

```

```
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

## FEATURES

```
source
1..16
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

```

```
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-J17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

Query Match      0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy 2575 TAAAAAATAAAAAA 2588
      |||||
Db 16 TAAAAAATAAAAAA 3

```

## RESULT 73

```
AW245664/c
LOCUS
```

```
DEFINITION 2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
mRNA sequence.

```

```

ACCESSION AW245664
VERSION AW245664.1 GI:6588657
KEYWORDS EST.
SOURCE Homo sapiens (human)

```

## ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```
REFERENCE 1 (bases 1 to 17)

```

```
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2822994.5prime

```

```
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov

```

```
Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project
Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 17 contiguous distinct peaks
following vector sequence.

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Plate: L1CM10 row: N column: 19.

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Location/Qualifiers
1..17
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/mol_type="mRNA"

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/clone="IMAGE:2822994"
/tissue_type="small cell carcinoma"

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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"

```

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/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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## FEATURES

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source
1..17
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="IMAGE:2822994"

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/tissue_type="small cell carcinoma"

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/cell_line="MGC3"

```

```
/lab_host="DH10B (phage-resistant)"

```

```
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

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Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2803 AAAAAAAAAAACA 2816
      |||||

```

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Db 17 AAAAAAAAAAACA 4

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## RESULT 74

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BQ590128/c
LOCUS
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DEFINITION E012843-024-019-E19-T7 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-E19 3-PRIME, mRNA sequence.

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ACCESSION BQ590128

```

```
VERSION BQ590128.1 GI:26119711

```

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KEYWORDS EST.

```

```
SOURCE Beta vulgaris

```

## ORGANISM

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Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

```

```
REFERENCE 1 (bases 1 to 17)

```

```
AUTHORS

```

```
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
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TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weissshaar B  
ADIS DNA core facility at MPZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 19 row: E column: 19  
Seq primer: T7: GTAATACGACTCACTATAGGCG.

Location/Qualifiers  
1. .17  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:189986"  
/db\_xref="taxon:161934"  
/clone="024-019-E19"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## FEATURES

source

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2575 TAAAAA AAAAAAAAAA 2588  
|||||  
Db 17 TAAAAA AAAAAAAAAA 4  
RESULT 75  
BQ591181/c  
LOCUS  
DEFINITION E012715-024-017-H16-T7 MPZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-H16 3-PRIME, mRNA sequence.  
ACCESSION BQ591181  
VERSION BQ591181.1 GI:26120764  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weissshaar B  
ADIS DNA core facility at MPZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA AAAAAAAAAA 2588

Db 17 TAAAAA AAAAAAAAAA 4

RESULT 75  
BQ591181/c  
LOCUS  
DEFINITION E012715-024-017-H16-T7 MPZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-H16 3-PRIME, mRNA sequence.  
ACCESSION BQ591181  
VERSION BQ591181.1 GI:26120764  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weissshaar B  
ADIS DNA core facility at MPZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weissshaar B  
ADIS DNA core facility at MPZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851  
Email: weissshaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 17 row: H column: 16  
Seq primer: T7: GTAATACGACTCACTATAGGCG.

## FEATURES

source

Location/Qualifiers  
1. .17  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:189932"  
/db\_xref="taxon:161934"  
/clone="024-017-H16"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA AAAAAAAAAA 2588

Db 16 TAAAAA AAAAAAAAAA 3

## RESULT 76

BQ591588/c

LOCUS

DEFINITION E012616-024-017-C15-SP6 MPZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-C15 5-PRIME, mRNA sequence.

ACCESSION BQ591588

VERSION BQ591588.1 GI:26121171

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

## REFERENCE

AUTHORS

## TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

## JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weissshaar B

ADIS DNA core facility at MPZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaar@mpiz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 17 row: C column: 15

Seq primer: SP6: CATACGATTAGTGACACTATAG.

## FEATURES

source

1. .17

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding



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line)"
/db_xref="GABI:188532"
/db_xref="taxon:161934"
/clone="024-017-C15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-storage root"
/notes=vector: pcwvSPORT6; Site 1: Sali; Site 2: Noti;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulze@kws.de; cloning sites Sali-Noti, primer sites and
orientation:
SP6-Sali-CCACCGTCGC-5prime-cDNA-polyA-CC-Noti-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match          0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAT 2589
Db 16 AAAAAAAAAAAT 3

RESULT 77
CF291802/c
LOCUS
DEFINITION
14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G05, mRNA
sequence.
CF291802
CF291802.1 GI:33660835
EST.
ORYZA sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--04-E17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAAAAA 2588
Db 17 TAAAAAAAAA 4

RESULT 79
CF295988/c
LOCUS
DEFINITION
30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
CF295988
CF295988.1 GI:33665021
EST.
ORYZA sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Query Match          0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACA 2816

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14 AAAAAAAAAAACA 1

RESULT 78
CF294668/c
LOCUS
DEFINITION
30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--04-E17, mRNA
sequence.
CF294668
CF294668.1 GI:33663701
EST.
ORYZA sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="30DGS--04-E17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAAAAA 2588
Db 17 TAAAAAAAAA 4

RESULT 79
CF295988/c
LOCUS
DEFINITION
30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
CF295988
CF295988.1 GI:33665021
EST.
ORYZA sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

```

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source  
1. 17  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="30DGS-06-C17"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAAAAAAAAA 2588

Db 17 TAAAAAAAAAAAAA 4

RESULT 80  
CF311499/c  
LOCUS  
DEFINITION ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
ABF--06-L20, mRNA sequence.

ACCESSION CF311499.1 GI:33683260

KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
JOURNAL of Bioscience and Bioinformatics, Myongji University  
COMMENT Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source  
1. 17  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/clone="ABF-06-L20"  
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/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression

line."

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAAAAAAAAA 2588

Db 16 TAAAAAAAAAAAAA 3

RESULT 81  
CF319075/c  
LOCUS  
DEFINITION CF319075 17 bp mRNA linear EST 15-AUG-2003  
HD--09-H06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--09-H06, mRNA sequence.

ACCESSION CF319075

VERSION CF319075.1 GI:33690836

KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
JOURNAL of Bioscience and Bioinformatics, Myongji University  
COMMENT Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source  
1. 17  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/clone="HD--09-H06"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OsHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2575 TAAAAAAAAAAAAA 2588

Db 16 TAAAAAAAAAAAAA 3

RESULT 82  
CF336950/c  
LOCUS  
DEFINITION JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
JMT--07-D04, mRNA sequence.

ACCESSION CF336950

VERSION CF336950.1 GI:33822280

KEYWORDS EST.

|                       |  |
|-----------------------|--|
| SOURCE                | Oryza sativa (japonica cultivar-group)   |
| ORGANISM              | Oryza sativa (japonica cultivar-group)   |
| REFERENCE             | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriarthoideae; Oryzeae; Oryza.   |
| AUTHORS               | 1 (bases 1 to 17)  |
| TITLE                 | Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.   |
| JOURNAL               | Large-scale Sequencing Analysis of Rice ESTs   |
| COMMENT               | Unpublished (2003)<br>Contact: Nahm B.H.<br>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University<br>Yongin, Gyeonggi, Korea<br>Tel: 82 31 330 6193<br>Fax: 82 31 321 6355<br>Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.   |
| FEATURES              | Location/Qualifiers  |
| source                | 1..17  |
|                       | /organism="Oryza sativa (japonica cultivar-group)"   |
|                       | /mol_type="mRNA"   |
|                       | /cultivar="Nackdong"   |
|                       | /db_xref="taxon:39947"   |
|                       | /clone="JMT--07-D04"   |
|                       | /tissue_type="leaf"  |
|                       | /dev_stage="14 days after germination"   |
|                       | /lab_host="E.coli DH10B"   |
|                       | /clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"   |
|                       | /notes="vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."   |
| Query Match           | 0.3%; Score 14; DB 1; Length 17;   |
| Best Local Similarity | 100.0%; Pred. No. 1.4e+02;   |
| Matches               | 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |
| Qy                    | 2575 TAAAAAAAAAAAAA 2588   |
| Db                    |  |
|                       | 17 TAAAAAAAAAAAAA 4  |
| RESULT 83             |  |
| AW247976/c            |  |
| LOCUS                 | 2820717.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820717 3',   |
| DEFINITION            | 17 bp mRNA linear EST 07-JAN-2000  |
| ACCESSION             | mRNA sequence.   |
| VERSION               | AW247976   |
| KEYWORDS              | EST.   |
| SOURCE                | AW247976.1 GI:6591064  |
| ORGANISM              | Homo sapiens (human)   |
| REFERENCE             | Homo sapiens   |
| AUTHORS               | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  |
| TITLE                 | 1 (bases 1 to 17)  |
| JOURNAL               | NIH-MGC http://mgc.nci.nih.gov/.   |
| COMMENT               | National Institutes of Health, Mammalian Gene Collection (MGC)<br>Unpublished (1999)<br>Other ESTs: 2820717.5prime<br>Contact: Robert Strausberg, Ph.D.<br>Email: cgaaps-t@mail.nih.gov<br>Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling<br>Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL). DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Trimming: cross_match from University of Washington Genome Center. Vector PHRAP suite. Poly-T identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous |

## RT-PCR..

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.6e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 928 GAGAAAAAACAACA 944  
 |||||  
 Db 17 GAAAAAACAACA 1

RESULT 85  
 CF298591  
 LOCUS  
 DEFINITION  
 ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone  
 ABF--08-P19, mRNA sequence.

ACCESSION  
 VERSION  
 CF298591.1 GI:33670352

KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 17)

AUTHORS  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE  
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
 Unpublished (2003)

COMMENT  
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source

1..17

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="ABF--08-P19"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Qy 928 GAGAAAAAACAACA 944

|||

Db 17 GAAAAAACAACA 1

RESULT 86  
 CF298591  
 LOCUS  
 DEFINITION  
 7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA  
 sequence.

ACCESSION  
 VERSION  
 CF298591.1 GI:33670352

KEYWORDS

SOURCE  
ORGANISM

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source

1..18

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--02-A20"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Qy 3264 TTTTTCCTTTTAA 3280

|||||

Db 1 TTTTTCCTTTTAA 17

## RESULT 87

## LOCUS

## DEFINITION

## ORGANISM

## KEYWORDS

## SOURCE

## ACCESSION

## VERSION

## ORGANISM

## KEYWORDS

## SOURCE

## ACCESSION

## VERSION

## ORGANISM

## KEYWORDS

## SOURCE

## ACCESSION

## VERSION

## ORGANISM

## KEYWORDS

## SOURCE

## ACCESSION

## VERSION

## ORGANISM

## KEYWORDS

## SOURCE

## ACCESSION

## VERSION

## ORGANISM

## KEYWORDS

## SOURCE

```

/clones="14FTL--04-C01"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="Rice etiolated leaf plasmid cDNA library
(14FTL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match 0.3%; Score 13.8; DB 1; Length 19;  
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTCTTAA 3280  
 Db 1 TTTTTCCTCTTAA 17

RESULT 88  
 AW245585  
 LOCUS  
 DEFINITION 15 bp mRNA linear EST 07-JAN-2000  
 2822740.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822740 3',  
 mRNA sequence.  
 ACCESSION AW245585  
 VERSION AW245585.1 GI:6598578  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 JOURNAL 1 (bases 1 to 15)  
 COMMENT NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Other ESTs: 2822740.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling  
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 6  
 PHRED high quality bases following vector sequence. Very Low  
 Quality Sequence: Trace file contained 15 contiguous distinct peaks  
 following vector sequence. Polyadenylation: Based upon the presence  
 of a XhoI site followed by a run of 14 or more T residues at the  
 beginning of the sequence, this cDNA insert was polyadenylated.  
 Plate: LLCM10 row: D column: 5  
 High quality sequence stop: 6.  
 Location/Qualifiers

FEATURES  
 source  
 1..15  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clones="IMAGE:2822740"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."  
 Query Match 0.3%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3598 TTTTTCCTCTTAA 3612  
 Db 1 TTTTTCCTCTTAA 15

RESULT 89  
 AW250976/c  
 LOCUS  
 DEFINITION 15 bp mRNA linear EST 07-JAN-2000  
 2822229.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822229 3',  
 mRNA sequence.  
 ACCESSION AW250976  
 VERSION AW250976.1 GI:6594065  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 JOURNAL 1 (bases 1 to 15)  
 COMMENT NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Other ESTs: 2822229.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling  
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 11  
 PHRED high quality bases following vector sequence. Very  
 Low Quality Sequence: Trace file contained 15 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a XhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Plate: LLCM8 row: N column: 22  
 High quality sequence stop: 11.  
 Location/Qualifiers

FEATURES  
 source  
 1..15  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clones="IMAGE:2822229"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2798 ATGTGAAAAA 2812



Plate: 30 row: D column: 05

# FEATURES

source  
Location/Qualifiers  
1. .15  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:936579"  
/db\_xref="taxon:161934"  
/clones="024-030-D05"  
/tissue\_type="leaf"  
/lab\_host="EMDH108"  
/clone\_lib="MPDZ-ADIS-024-leaf"  
/note="vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAA 2814

Db 1 GTCAAAAAAAAAAAAA 15

# RESULT 93

LOCUS  
DEFINITION  
ABF--08-G13.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-G13, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 16)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

# FEATURES

source  
Location/Qualifiers  
1. .16  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF--08-G13"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH108"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2743 TCCTTTTTTTTTTAA 2757

Db 1 TTTTTTTTTTTTAA 15

# RESULT 94

LOCUS  
DEFINITION  
14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G05, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 16)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

# FEATURES

source  
Location/Qualifiers  
1. .16  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="14ROOT--02-G05"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH108"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 930 GAAAAAAAAAACAAA 944

Db 2 GAAAAAAAAAAAAAAAA 16

# RESULT 95

LOCUS  
DEFINITION  
CF295672  
30DGS--05-L12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--05-L12, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
CF295672.1 GI:33664705  
EST.



```

SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongui University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS-05-L12"
/tissue_type="leaf"
/dev_stages="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2743 TCTTTTTCATTTTAA 2757
      |||||
Db 1 TTTTTCATTTTTCATTTTAA 15

RESULT 96
A2766990/c
LOCUS
DEFINITION  A2766990 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0564H19 R, genomic survey sequence.
ACCESSION  A2766990
VERSION    A2766990.1 GI:12884624
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Stokes,R., Tingley,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0564 row: H column: 19
            Seq primer: CACACGGAACAGCTATGACC
            Class: plasmid ends

SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongui University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS-05-L12"
/tissue_type="leaf"
/dev_stages="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2741 CATCTTTTTCATTTT 2755
      |||||
Db 16 CATTTTTCATTTTTCATTTT 2

RESULT 97
A2962226/c
LOCUS
DEFINITION  A2962226 Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0231A02 F, genomic survey sequence.
ACCESSION  A2962226
VERSION    A2962226.1 GI:13833453
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Stokes,R., Tingley,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0231 row: A column: 02
            Seq primer: CGTTGTAAAACGACGCCACT
            Class: plasmid ends

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529F08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. NO. 4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1157 TTTTATATATATATATATTTT 1174
      ||||| | | |||||
Db 1 TTTTATATATATATATATTTT 18

RESULT 100
AA918967/c
LOCUS
DEFINITION
  o182905.g1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1536152 3'
  similar to TR:Q69566 Q69566 ;contains element PTR7 repetitive
  element ;, mRNA sequence.
ACCESSION
  AA918967
VERSION
  AA918967.1 GI:3058857
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 13)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1058 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
  1..13
/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1536152"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kids"
/notes="Organ: kidney; Vector: pRT3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AACTGAAGAATTCCGGCGCGCAATATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. NO. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 ACACGGCGCACACA 649
      ||||| | | |||||
Db 13 ACACGGCGCACACA 1

RESULT 101
BQ583549
LOCUS
DEFINITION
  BQ583549 13 bp mRNA linear EST 06-DEC-2002
  cDNA clone 024-005-C14 S-PRIME, mRNA sequence.
ACCESSION
  BQ583549
VERSION
  BQ583549.1 GI:26113126
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 13)
AUTHORS
  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
TITLE
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  22362189
MEDLINE
  12472698
PUBMED
  12472698
COMMENT
  Contact: Weisshaar B
  ADIS DNA core facility at MPiZ
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
  Insert Length: 13 Std Error: 0.00
  Plate: 5 row: C column: 14
  Seq primer: SP6; CATACGATTAGTGACACTATAG.
  Location/Qualifiers
    1..13
    /organism="Beta vulgaris"
    /mol_type="mRNA"
    /cultivar="KWS2320 (double haploid, monogerm breeding
    line)"
    /db_xref="GABI:183152"
    /db_xref="taxon:161934"
    /clone="024-005-C14"
    /tissue_type="inflorescence"
    /lab_host="EMDH10B"
    /clone_lib="MPiZ-ADIS-024-inflorescence"
    /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
    cDNA library from sugar beet, library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
    orientation:

```

SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

#### RESULT 102

BO589180/c

LOCUS

DEFINITION S014009-024-015-122-T7 MP1Z-ADIS-024-storage root Beta vulgaris EST 06-DEC-2002

VERSION BO589180

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: [weisshaar@mpiz-koeln.mpg.de](mailto:weisshaar@mpiz-koeln.mpg.de)

Insert Length: 13 Std Error: 0.00

Plate: 15 row: 1 column: 22

Seq primer: T7; GTAATACGACTCACTATAGGC.

Location/Qualifiers

1..13

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:187886"

/db\_xref="taxon:161934"

/clones="024-015-122"

/tissue\_type="storage root"

/lab\_host="EMDH108"

/clone\_lib="MP1Z-ADIS-024-storage root"

/note="Vector: PCWSP0RT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:

SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

#### RESULT 104

CF278426/c

LOCUS

DEFINITION

14ETL--04-F09.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F09,

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

#### RESULT 103

BO590337

LOCUS

DEFINITION

BO590337

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: [weisshaar@mpiz-koeln.mpg.de](mailto:weisshaar@mpiz-koeln.mpg.de)

Insert Length: 13 Std Error: 0.00

Plate: 19 row: G column: 12

Seq primer: SP6; CATACGATTAGTGACACTATAG.

Location/Qualifiers

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/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:189780"

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/lab\_host="EMDH108"

/clone\_lib="MP1Z-ADIS-024-storage root"

/note="Vector: PCWSP0RT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:

SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13



### Query Match

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 110
CF290971 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-D13, mRNA
sequence.
ACCESSION CF290971
VERSION CF290971.1 GI:33660004
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-E10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 111
CF291011/c 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E10, mRNA
sequence.
ACCESSION CF291011
VERSION CF291011.1 GI:33660044
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)

```

```

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-E10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 112
CF291060/c 13 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F11, mRNA
sequence.
ACCESSION CF291060
VERSION CF291060.1 GI:33660093
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-F11"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

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|           |   |
|-----------|---|
| ACCESSION | CF291167                                      |
| VERSION   | CF291167.1                                    |
| KEYWORDS  | GI:33650200                                   |
| SOURCE    | EST.  |
| ORGANISM  | <i>Oryza sativa</i> (japonica cultivar-group) |
|           | <i>Oryza sativa</i> (japonica cultivar-group) |

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1. 13
source
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Naxdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-122"
/tissue_type="root"
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-O17"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 119
CF291514/c
LOCUS
DEFINITION 14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--01-P13, mRNA
sequence.
ACCESSION CF291514.1 GI:33660547
VERSION CF291514
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-P13"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

RESULT 121
CF291596/c
LOCUS
DEFINITION 14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B12, mRNA
sequence.
ACCESSION CF291596
VERSION CF291596.1 GI:33660629
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-P13"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 120
CF291515
LOCUS
DEFINITION 14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--01-P13, mRNA
sequence.
ACCESSION CF291515
VERSION CF291515.1 GI:33660548
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-P13"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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FEATURES
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  1..13
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  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="14ROOT--02-B12"
  /tissue_type="root"
  /dev_stage="14 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice root plasmid cDNA library (14ROOT)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."

  Query Match      0.3%; Score 13; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 63;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 122
LOCUS CF291597
DEFINITION 14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B12, mRNA
sequence.
ACCESSION CF291597
VERSION 1.13
KEYWORDS /
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-B12"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

  Query Match      0.3%; Score 13; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 63;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

FEATURES
source
  Location/Qualifiers
  1..13
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="14ROOT--02-B12"
  /tissue_type="root"
  /dev_stage="14 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice root plasmid cDNA library (14ROOT)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."

  Query Match      0.3%; Score 13; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 63;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

FEATURES
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  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="14ROOT--02-B12"
  /tissue_type="root"
  /dev_stage="14 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice root plasmid cDNA library (14ROOT)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."

  Query Match      0.3%; Score 13; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 63;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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RESULT 123
LOCUS CF291726/c
DEFINITION 14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E10, mRNA
sequence.
ACCESSION CF291726
VERSION 1.13
KEYWORDS /
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-E10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

  Query Match      0.3%; Score 13; DB 1; Length 13;
  Best Local Similarity 100.0%; Pred. No. 63;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 124
LOCUS CF291903
DEFINITION 14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-I10, mRNA
sequence.
ACCESSION CF291903
VERSION 1.13
KEYWORDS /
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

```

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source 1. .13

/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

# RESULT 125

CF298590/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A19, mRNA sequence.

ACCESSION CF298590

VERSION CF298590.1 GI:33670351

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

# FEATURES

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1. .13

/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

# RESULT 126

CF298592/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A21, mRNA sequence.

ACCESSION CF298592

VERSION CF298592.1 GI:33670353

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

# FEATURES

source

1. .13

/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

# RESULT 127

CF298736/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-E22, mRNA sequence.

ACCESSION CF298736

VERSION CF298736.1 GI:33670497

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

**JOURNAL  
COMMENT**

Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@qbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES
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            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 13 AAAAAAAAAAAAAA 1

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|            |  |       |      |        |                 |
|------------|--|-------|------|--------|-----------------|
| RESULT 128 | CF298764/c   | 13 bp | mRNA | linear | EST 15-AUG-2003 |
| LOCUS      | CF298764/c   |       |      |        |                 |
| DEFINITION | 7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-F20, mRNA sequence. |       |      |        |                 |

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CP298764.  
CP298764.1 GI:33670525  
Esr.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,  
Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongui University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@qbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF-02-E20"
/tissue_type="leaf"
/dev_stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR-TOPO; Site: 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|  |    |      |               |      |
|--|----|------|---------------|------|
|  | Qy | 2576 | AAAAAAAAAAAAA | 2588 |
|  |    |      |               |      |
|  | Dp | 13   | AAAAAAAAAAAAA | 1    |

|            |            |  |             |      |        |                 |
|------------|------------|--|-------------|------|--------|-----------------|
| RESULT 129 | CF298795/c | CF298795   | 13 bp       | mRNA | linear | EST 15-AUG-2003 |
| LOCUS      | CF298795/c |  |             |      |        |                 |
| DEFINITION |            | 7LEAF-02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF-02-G14, mRNA sequence. |             |      |        |                 |
| ACCESSION  |            | CF298795   |             |      |        |                 |
| VERSION    |            | CF298795.1   | GI:33670556 |      |        |                 |
| KEYWORDS   |            | EST.   |             |      |        |                 |

| SOURCE | ORGANISM   | EST. |
|--------|--|------|
|        | <i>Oryza sativa</i> (japonica cultivar-group)                      |      |
|        | <i>Oryza sativa</i> (japonica cultivar-group)                      |      |
|        | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |      |
|        | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;         |      |
|        | Ehrhartoideae; Oryzaceae; <i>Oryza</i> .                           |      |

**REFERENCE**  
**AUTHORS**  
 Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,  
 Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.  
**TITLE**  
 Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL**  
 Unpublished (2003)  
**COMMENT**  
 Contact: Nahm B. H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: [bnahm@bio.myongji.ac.kr](mailto:bnahm@bio.myongji.ac.kr).

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FEATURES
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Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF-02-G14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was
with oligoribonucleotides and then used as template
RT-PCR."

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Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|    |      |               |      |
|----|------|---------------|------|
| Qy | 2576 | AAAAAAAAAAAAA | 2588 |
|    |      |               |      |
| Dp | 13   | AAAAAAAAAAAAA | 1    |

RESULT 130  
CF298908/c  
LOCUS  
DEFINITION  
CF298908 13 bp mRNA linear EST 15-AUG-2003  
7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--02-K03, mRNA  
sequence.

| ACCESSION | VERSION    | KEYWORDS    | SOURCE | ORGANISM   |
|-----------|------------|-------------|--------|--|
| CF298908  | CF298908.1 | GI:33670669 | EST    |  |
|           |            |             |        | <i>Oryza sativa</i> (japonica cultivar-group)  |
|           |            |             |        | <i>Oryza sativa</i> (japonica cultivar-group)  |
|           |            |             |        | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; <i>Oryza</i> . |

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REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            /clone="7LEAF--03-K03"
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            /dev_stages="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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Qy 2576 AAAAAAAAAAAAAA 2588
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Db 13 AAAAAAAAAAAAAA 1

RESULT 131
LOCUS     CF299133
DEFINITION CF299133 13 bp mRNA linear EST 15-AUG-2003
           7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
           sativa (japonica cultivar-group) cDNA clone 7LEAF--03-A06, mRNA
           sequence.
ACCESSION CF299133
VERSION   CF299133.1 GI:33670894
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
      |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 131
LOCUS     CF299133
DEFINITION CF299133 13 bp mRNA linear EST 15-AUG-2003
           7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
           sativa (japonica cultivar-group) cDNA clone 7LEAF--03-A06, mRNA
           sequence.
ACCESSION CF299133
VERSION   CF299133.1 GI:33670894
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred.No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
      |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 132
LOCUS     CF299359/c
DEFINITION CF299359 13 bp mRNA linear EST 15-AUG-2003
           7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
           sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F15, mRNA
           sequence.
ACCESSION CF299359
VERSION   CF299359.1 GI:33671120
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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            with oligoribonucleotides and then used as templates for
            RT-PCR."

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Best Local Similarity 100.0%; Pred.No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 133
LOCUS     CF299937/c
DEFINITION CF299937 13 bp mRNA linear EST 15-AUG-2003
           7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
           sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C12, mRNA
           sequence.
ACCESSION CF299937
VERSION   CF299937.1 GI:33671698
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)

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LOCUS               CF3021286               13 bp   mRNA       linear       EST 15-AUG-2003
DEFINITION          7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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                    sequence.
ACCESSION            CF301286
VERSION              CF301286.1   GI:33673047
KEYWORDS             EST.
SOURCE               Oryza sativa (japonica cultivar-group)
                    Oryza sativa (japonica cultivar-group)
ORGANISM             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 330 6193
                    Fax: 82 31 321 6355
                    Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 140
CF302158/c
LOCUS               CF302158               13 bp   mRNA       linear       EST 15-AUG-2003
DEFINITION          7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                    sativa (japonica cultivar-group) cDNA clone 7LEAF--07-G20, mRNA
                    sequence.
ACCESSION            CF302158
VERSION              CF302158.1   GI:33673919
KEYWORDS             EST.
SOURCE               Oryza sativa (japonica cultivar-group)
                    Oryza sativa (japonica cultivar-group)
ORGANISM             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 330 6193
                    Fax: 82 31 321 6355
                    Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                        with oligoribonucleotides and then used as templates for
                        RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 140
CF302158/c
LOCUS               CF302158               13 bp   mRNA       linear       EST 15-AUG-2003
DEFINITION          7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                    sativa (japonica cultivar-group) cDNA clone 7LEAF--07-G20, mRNA
                    sequence.
ACCESSION            CF302158
VERSION              CF302158.1   GI:33673919
KEYWORDS             EST.
SOURCE               Oryza sativa (japonica cultivar-group)
                    Oryza sativa (japonica cultivar-group)
ORGANISM             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 330 6193
                    Fax: 82 31 321 6355
                    Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 141
CF302830/c
LOCUS               CF302830               13 bp   mRNA       linear       EST 15-AUG-2003
DEFINITION          7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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                    sequence.
ACCESSION            CF302830
VERSION              CF302830.1   GI:33674591
KEYWORDS             EST.
SOURCE               Oryza sativa (japonica cultivar-group)
                    Oryza sativa (japonica cultivar-group)
ORGANISM             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 330 6193
                    Fax: 82 31 321 6355
                    Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 141
CF302830/c
LOCUS               CF302830               13 bp   mRNA       linear       EST 15-AUG-2003
DEFINITION          7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
                    sativa (japonica cultivar-group) cDNA clone 7LEAF--08-L16, mRNA
                    sequence.
ACCESSION            CF302830
VERSION              CF302830.1   GI:33674591
KEYWORDS             EST.
SOURCE               Oryza sativa (japonica cultivar-group)
                    Oryza sativa (japonica cultivar-group)
ORGANISM             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE            1 (bases 1 to 13)
AUTHORS              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE               Large-scale Sequencing Analysis of Rice ESTs
JOURNAL              Unpublished (2003)
COMMENT             Contact: Nahm B.H.
                    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                    of Bioscience and Bioinformatics, Myongji University
                    Yongin, Kyeonggi, Korea
                    Tel: 82 31 330 6193
                    Fax: 82 31 321 6355
                    Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                        /note="Vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped
                        with oligoribonucleotides and then used as templates for
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Query Match          0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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RESULT 142
CF302898/c
LOCUS
DEFINITION
13 bp mRNA linear EST 15-AUG-2003
7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-N08, mRNA
sequence.
CF302898
CF302898.1 GI:33674659
EST.
ORIGIN
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
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with oligoribonucleotides and then used as templates for
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Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1
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with oligoribonucleotides and then used as templates for
RT-PCR."

RESULT 143
CF310516/c
LOCUS
DEFINITION
13 bp mRNA linear EST 15-AUG-2003
ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-D09, mRNA sequence.
CF310516
CF310516.1 GI:33682277
EST.
ORIGIN
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
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1..13
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
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cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
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line."
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Db 13 AAAAAAAAAAAAAA 1
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/tissue_type="leaf"
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cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

RESULT 144
CF310517
LOCUS
DEFINITION
13 bp mRNA linear EST 15-AUG-2003
ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-D09, mRNA sequence.
CF310517
CF310517.1 GI:33682278
EST.
ORIGIN
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
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cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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|---|-------------|---------------|-------|------------|----|--------|----|------|----|
| element binding transcription factor 3 overexpression line."  |             |               |       |            |    |        |    |      |    |
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| Best Local Similarity   | 100.0%;     | Pred. No. 63; |       |            |    |        |    |      |    |
| Matches   | 13;         | Conservative  | 0;    | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| Qy  | 2576        | AAAAAAAAAAAAA | 2588  |            |    |        |    |      |    |
| Db  | 1           | AAAAAAAAAAAAA | 13    |            |    |        |    |      |    |
| RESULT 145  |             |               |       |            |    |        |    |      |    |
| CF312721/c  |             |               |       |            |    |        |    |      |    |
| LOCUS   |             |               |       |            |    |        |    |      |    |
| DEFINITION  |             |               |       |            |    |        |    |      |    |
| ABF--08-J13-g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone   |             |               |       |            |    |        |    |      |    |
| ABF--08-J13, mRNA sequence.   |             |               |       |            |    |        |    |      |    |
| CF312721  |             |               |       |            |    |        |    |      |    |
| CF312721.1  | GI:33684482 |               |       |            |    |        |    |      |    |
| EST.  |             |               |       |            |    |        |    |      |    |
| Oryza sativa (japonica cultivar-group)  |             |               |       |            |    |        |    |      |    |
| Oryza sativa (japonica cultivar-group)  |             |               |       |            |    |        |    |      |    |
| Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  |             |               |       |            |    |        |    |      |    |
| 1 (bases 1 to 13)   |             |               |       |            |    |        |    |      |    |
| Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  |             |               |       |            |    |        |    |      |    |
| Large-scale Sequencing Analysis of Rice ESTs  |             |               |       |            |    |        |    |      |    |
| Unpublished (2003)  |             |               |       |            |    |        |    |      |    |
| Contact: Nahm B.H.  |             |               |       |            |    |        |    |      |    |
| Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  |             |               |       |            |    |        |    |      |    |
| Yongin, Kyeonggi, Korea   |             |               |       |            |    |        |    |      |    |
| Tel: 82 31 330 6193   |             |               |       |            |    |        |    |      |    |
| Fax: 82 31 321 6355   |             |               |       |            |    |        |    |      |    |
| Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.   |             |               |       |            |    |        |    |      |    |
| Location/Qualifiers   |             |               |       |            |    |        |    |      |    |
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| /db_xref="taxon:39947"  |             |               |       |            |    |        |    |      |    |
| /clone="ABF--08-J13"  |             |               |       |            |    |        |    |      |    |
| /tissue_type="leaf"   |             |               |       |            |    |        |    |      |    |
| /dev_stage="14 days after germination"  |             |               |       |            |    |        |    |      |    |
| /lab_host="E coli DH10B"  |             |               |       |            |    |        |    |      |    |
| /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"   |             |               |       |            |    |        |    |      |    |
| /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line." |             |               |       |            |    |        |    |      |    |
| Query Match   | 0.3%;       | Score 13;     | DB 1; | Length 13; |    |        |    |      |    |
| Best Local Similarity   | 100.0%;     | Pred. No. 63; |       |            |    |        |    |      |    |
| Matches   | 13;         | Conservative  | 0;    | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| Qy  | 2576        | AAAAAAAAAAAAA | 2588  |            |    |        |    |      |    |
| Db  | 13          | AAAAAAAAAAAAA | 1     |            |    |        |    |      |    |
| RESULT 146  |             |               |       |            |    |        |    |      |    |
| CF313171/c  |             |               |       |            |    |        |    |      |    |
| LOCUS   |             |               |       |            |    |        |    |      |    |
| DEFINITION  |             |               |       |            |    |        |    |      |    |
| HD--01-D10.b1 OSHDACL-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  |             |               |       |            |    |        |    |      |    |
| HD--01-D10, mRNA sequence.  |             |               |       |            |    |        |    |      |    |
| CF313171  |             |               |       |            |    |        |    |      |    |
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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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line."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 149
CF314874/c
LOCUS
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library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--03-J07, mRNA sequence.
ACCESSION CF314874
VERSION CF314874.1 GI:33686635
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhna@gbio.com, bhna@bio.myongji.ac.kr.
FEATURES
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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 150
CF316439/c
LOCUS
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library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-L17, mRNA sequence.
ACCESSION CF316439
VERSION CF316439.1 GI:33688200
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)

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Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 149
CF315395/c
LOCUS
DEFINITION HD--04-E20.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-E20, mRNA sequence.
ACCESSION CF315395
VERSION CF315395.1 GI:33687156
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhna@gbio.com, bhna@bio.myongji.ac.kr.
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line."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

RESULT 150
CF316439/c
LOCUS
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library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-L17, mRNA sequence.
ACCESSION CF316439
VERSION CF316439.1 GI:33688200
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)

```

```

AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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                derived from rice Histone Deacetylase overexpression
                line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      13 AAAAAAAAAAAAAA 1

RESULT 151
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            HD--05-L17, mRNA sequence.
ACCESSION  CF316440
VERSION     CF316440.1 GI:33688201
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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                /lab_host="E.coli DH10B"
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                cDNA library (HD)"
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                derived from rice Histone Deacetylase overexpression
                line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      13 AAAAAAAAAAAAAA 1

RESULT 151
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DEFINITION HD--05-L17.gi OshDAC1-overexpressing transgenic rice plasmid cDNA
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            HD--05-L17, mRNA sequence.
ACCESSION  CF316440
VERSION     CF316440.1 GI:33688201
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      13 AAAAAAAAAAAAAA 1

RESULT 152
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            HD--06-A04, mRNA sequence.
ACCESSION  CF316637
VERSION     CF316637.1 GI:33688398
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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                cDNA library (HD)"
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                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      13 AAAAAAAAAAAAAA 1

RESULT 153
LOCUS      CF318290
DEFINITION HD--06-A04.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--06-A04, mRNA sequence.
ACCESSION  CF318290
VERSION     CF318290.1 GI:33688398
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES     source
              1..13
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                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      13 AAAAAAAAAAAAAA 1

RESULT 153
LOCUS      CF318290
DEFINITION HD--06-A04.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--06-A04, mRNA sequence.
ACCESSION  CF318290
VERSION     CF318290.1 GI:33688398
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 13)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES     source
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                /lab_host="E.coli DH10B"
                /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
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                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

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LOCUS CF318290 13 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD--08-F19.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--08-F19, mRNA sequence.  
 ACCESSION CF318290  
 VERSION CF318290.1 GI:33690051  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 13)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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 /clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

RESULT 154  
 CF319066/c  
 LOCUS CF319066 13 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD--09-H02.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--09-H02, mRNA sequence.

ACCESSION CF319066  
 VERSION CF319066.1 GI:33690827  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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 /clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 63;  
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Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

RESULT 155  
 CF319531/c  
 LOCUS CF319531 13 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD--10-B03.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD--10-B03, mRNA sequence.

ACCESSION CF319531  
 VERSION CF319531.1 GI:33691292  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

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 /clone="HD--10-B03"  
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line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1  
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RESULT 156

CF319532

LOCUS

DEFINITION HD--10-B03.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 321 6355  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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 line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13  
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RESULT 157

CF319919

LOCUS

DEFINITION HD--10-J17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

VERSION

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 13)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 321 6355  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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 derived from rice Histone Deacetylase overexpression  
 line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
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QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13  
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RESULT 158

CF320017/c

LOCUS

DEFINITION HD--10-L20.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 13)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 321 6355  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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derived from rice Histone Deacetylase overexpression
line."

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Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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RESULT 159
CF320018
LOCUS
DEFINITION
HD--10-L20.g1 OSHADCl-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--10-L20, mRNA sequence.

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```

ACCESSION
CF320018
VERSION
CF320018.1 GI:33691779

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EST.

SOURCE

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ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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1 (bases 1 to 13)

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REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

```

JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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line."

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Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1

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RESULT 161
CF320938/c
LOCUS
DEFINITION
HD--12-A06.b1 OSHADCl-overexpressing transgenic rice plasmid
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--12-A06, mRNA sequence.

```

```

ACCESSION
CF320938
VERSION
CF320938.1 GI:33692699

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EST.

SOURCE

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ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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1 (bases 1 to 13)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

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Db 1 AAAAAAAAAAAAAA 13

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RESULT 160

CF320143/c

LOCUS

DEFINITION

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HD--10-O13.b1 OSHADCl-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--10-O13, mRNA sequence.

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CF320143

ACCESSION

CF320143

VERSION

CF320143.1 GI:33691904

KEYWORDS

SOURCE

EST.

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

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cDNA library (HD)"

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derived from rice Histone Deacetylase overexpression

line."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

RESULT 161

CF320938/c

LOCUS

DEFINITION

HD--12-A06.b1 OSHADCl-overexpressing transgenic rice plasmid

library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD--12-A06, mRNA sequence.

CF320938

ACCESSION

CF320938

VERSION

CF320938.1 GI:33692699

KEYWORDS

SOURCE

EST.

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,



Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
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 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

# FEATURES

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 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
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 Db 13 AAAAAAAAAAAAAA 1

RESULT 162  
 CF326844/C  
 LOCUS  
 DEFINITION  
 NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa (japonica cultivar-group) cDNA clone NACL--01-B12, mRNA  
 sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 AUTHORS  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongui University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

# FEATURES

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 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /db\_xref="taxon:39947"  
 /clone="NACL--01-B12"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
 |||||  
 Db 13 AAAAAAAAAAAAAA 1

RESULT 163  
 CF327070/C  
 LOCUS  
 DEFINITION  
 NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza-  
 sativa (japonica cultivar-group) cDNA clone NACL--01-G09, mRNA  
 sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 AUTHORS  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongui University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

# FEATURES

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 /clone="NACL--01-G09"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
 |||||  
 Db 13 AAAAAAAAAAAAAA 1

RESULT 164  
 CF327339/C  
 LOCUS  
 DEFINITION  
 NACL--01-M15.b1 Rice callus plasmid cDNA library (NACL) Oryza-  
 sativa (japonica cultivar-group) cDNA clone NACL--01-M15, mRNA  
 sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 CF327339  
 CF327339.1 GI:33802936  
 EST.



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SOURCE
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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         /lab_host="E.coli DH10B"
         /note="lib=Rice callus plasmid cDNA library (NACL)"
         /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
         with oligoribonucleotides and then used as templates for
         RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2576 AAAAAAAAAAAAAA 2588
Db   13 AAAAAAAAAAAAAA 1

RESULT 165
CF327340
LOCUS     CF327340
DEFINITION NACL--01-M15.g1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa (japonica cultivar-group) cDNA clone NACL--01-M15, mRNA
           sequence.
ACCESSION CF327340
VERSION   CF327340.1 GI:33802938
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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         /db_xref="taxon:39947"
         /clone="NACL--01-M15"
         /tissue_type="callus"
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         /lab_host="E.coli DH10B"
         /note="lib=Rice callus plasmid cDNA library (NACL)"
         /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
         with oligoribonucleotides and then used as templates for
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2576 AAAAAAAAAAAAAA 2588
Db   13 AAAAAAAAAAAAAA 1

RESULT 165
CF327340
LOCUS     CF327340
DEFINITION NACL--01-M15.g1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa (japonica cultivar-group) cDNA clone NACL--01-M15, mRNA
           sequence.
ACCESSION CF327340
VERSION   CF327340.1 GI:33802938
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone="NACL--01-M15"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2576 AAAAAAAAAAAAAA 2588
Db   13 AAAAAAAAAAAAAA 13

RESULT 166
CF327576/c
LOCUS     CF327576/c
DEFINITION NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa (japonica cultivar-group) cDNA clone NACL--02-B22, mRNA
           sequence.
ACCESSION CF327576
VERSION   CF327576.1 GI:33803404
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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         /lab_host="E.coli DH10B"
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         with oligoribonucleotides and then used as templates for
         RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2576 AAAAAAAAAAAAAA 2588
Db   13 AAAAAAAAAAAAAA 1

RESULT 167
CF327888/c
LOCUS     CF327888
DEFINITION NACL--02-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa (japonica cultivar-group) cDNA clone NACL--02-I22, mRNA

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sequence.
ACCESSION CF327888
VERSION CF327888.1 GI:33804024
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/lab_host="E.coli DH10B"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1
RESULT 168
CF327939/c
LOCUS CF327939.1 GI:33804127
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-K02, mRNA
sequence.
ACCESSION CF327939
VERSION CF327939.1 GI:33804127
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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location/Qualifiers
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/lab_host="E.coli DH10B"
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with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1
RESULT 169
CF328153/c
LOCUS CF328153.1 GI:33804556
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-O19, mRNA
sequence.
ACCESSION CF328153
VERSION CF328153.1 GI:33804556
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1
RESULT 170
CF328153/c
LOCUS CF328153.1 GI:33804556
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-O19, mRNA
sequence.
ACCESSION CF328153
VERSION CF328153.1 GI:33804556
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
location/Qualifiers
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/cultivar="Nackdong"
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/clone="NACL--02-O19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 13 AAAAAAAAAAAAAA 1
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CF328228/c
LOCUS       CF328228                13 bp    mRNA    linear    EST 18-AUG-2003
DEFINITION   NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza
             sativa (japonica cultivar-group) cDNA clone NACL--03-A13, mRNA
             sequence.
ACCESSION    CF328228
VERSION      CF328228.1  GI:33804702
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
             Oryza sativa (japonica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
      |||||
Db   13 AAAAAAAAAAAAAA 1

RESULT 171
CF328807/c
LOCUS       CF328807                13 bp    mRNA    linear    EST 18-AUG-2003
DEFINITION   NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
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             sequence.
ACCESSION    CF328807
VERSION      CF328807.1  GI:33806393
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
             Oryza sativa (japonica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..13
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--03-A13"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
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Db   13 AAAAAAAAAAAAAA 1

RESULT 171
CF328807/c
LOCUS       CF328807                13 bp    mRNA    linear    EST 18-AUG-2003
DEFINITION   NACL--03-O07.b1 Rice callus plasmid cDNA library (NACL) Oryza
             sativa (japonica cultivar-group) cDNA clone NACL--03-O07, mRNA
             sequence.
ACCESSION    CF328807
VERSION      CF328807.1  GI:33805856
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
             Oryza sativa (japonica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193

```

```

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
  1..13
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
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  /clone="NACL--03-O07"
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  /lab_host="E.coli DH10B"
  /clone_lib="Rice callus plasmid cDNA library (NACL)"
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  with oligoribonucleotides and then used as templates for
  RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
      |||||
Db   13 AAAAAAAAAAAAAA 1

RESULT 172
CF329075/c
LOCUS       CF329075                13 bp    mRNA    linear    EST 18-AUG-2003
DEFINITION   NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
             sativa (japonica cultivar-group) cDNA clone NACL--04-E07, mRNA
             sequence.
ACCESSION    CF329075
VERSION      CF329075.1  GI:33806393
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
             Oryza sativa (japonica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2576 AAAAAAAAAAAAAA 2588
      |||||
Db   13 AAAAAAAAAAAAAA 1

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
|||||

Db 13 AAAAAAAAAAAAAA 1

## RESULT 176

CF329729

LOCUS

DEFINITION  
NACL--05-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-C14, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 13)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"  
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Query Match

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2576 AAAAAAAAAAAAAA 2588

Db

1 AAAAAAAAAAAAAA 13

## RESULT 177

CF329800/c

LOCUS

DEFINITION  
NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-E04, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 13)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

TITLE

JOURNAL

COMMENT

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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Query Match

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2576 AAAAAAAAAAAAAA 2588

Db

13 AAAAAAAAAAAAAA 1

RESULT 178

CF329801

LOCUS

DEFINITION

NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-E04, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 13)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

JOURNAL

COMMENT

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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## RT-PCR."

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 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
 |||||

Db 1 AAAAAAAAAAAAAA 13

## RESULT 179

CF329869/c

LOCUS NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-F18, mRNA  
 sequence.

ACCESSION CF329869.1 GI:33807959

VERSION CF329869

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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 /lab\_host="E.coli DH10B"  
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 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 63;  
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QY 2576 AAAAAAAAAAAAAA 2588  
 |||||

Db 13 AAAAAAAAAAAAAA 1

## RESULT 180

CF329946/c

LOCUS NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-H12, mRNA  
 sequence.

ACCESSION CF329946.1 GI:33808114

VERSION CF329946

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 1 (bases 1 to 13)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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 /clone="NACL--05-H12"  
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 /clone\_lib="Rice callus plasmid cDNA library (NACL)"  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

## Query Match

Best Local Similarity

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
 |||||

Db 13 AAAAAAAAAAAAAA 1

## RESULT 181

CF329988/c

LOCUS NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza

DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-I10, mRNA

sequence.

ACCESSION CF329988.1 GI:33808198

VERSION CF329988

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

SONG,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..13

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

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/clone="NACL--05-I10"

/tissue\_type="callus"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

RESULT 182  
CF330023/c

LOCUS 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--05-J05.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-J05, mRNA sequence.

ACCESSION CF330023  
VERSION CF330023.1 GI:33808268

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
source

1..13  
/organism="Oryza sativa (japonica cultivar-group)"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 13 AAAAAAAAAAAAAA 1

RESULT 183  
CF330725

LOCUS 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-J01, mRNA sequence.

ACCESSION CF330725  
VERSION CF330725.1 GI:33809672

KEYWORDS

SOURCE

ORGANISM

EST.

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES  
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1..13  
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/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 184

CF331041/c

LOCUS

DEFINITION

NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-A04, mRNA sequence.

ACCESSION CF331041

VERSION CF331041.1 GI:33810299

KEYWORDS EST.

SOURCE

ORGANISM

13 bp mRNA linear EST 18-AUG-2003  
NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-A04, mRNA sequence.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1..13

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 185
CF331266/c 13 bp mRNA linear EST 18-AUG-2003
NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--07-F06, mRNA
sequence.
CF331266 GI:33810744
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="NACL--07-F06"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 187
CF331903/c 13 bp mRNA linear EST 18-AUG-2003
NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-D07, mRNA
sequence.
CF331903 GI:33812027
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..13
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 186
CF331273/c 13 bp mRNA linear EST 18-AUG-2003
NACL--07-F09.q1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
sequence.
CF331273 GI:33810757
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 186
CF331273/c 13 bp mRNA linear EST 18-AUG-2003
NACL--07-F09.q1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
sequence.
CF331273 GI:33810757
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 186
CF331273/c 13 bp mRNA linear EST 18-AUG-2003
NACL--07-F09.q1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
sequence.
CF331273 GI:33810757
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="NACL--07-F06"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 13 AAAAAAAAAAAAAA 1

RESULT 186
CF331273/c 13 bp mRNA linear EST 18-AUG-2003
NACL--07-F09.q1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA
sequence.
CF331273 GI:33810757
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
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/tissue_type="callus"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 1
```





of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

1. .13  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

## RESULT 191

CF333486/c

LOCUS

DEFINITION

13 bp mRNA linear EST 18-AUG-2003  
JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
JMT--02-G11, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"  
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cDNA library (JMT)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

## Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

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Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

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/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

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was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||

1 AAAAAAAAAAAAAA 13

#### RESULT 194

CF334347/c

LOCUS

JMT--03-J19.bl AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--03-J19, mRNA sequence.

CF334347

CF334347.1 GI:33817022

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

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1..13  
Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clone="JMT--03-J19"  
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/lab\_host="E.coli DH10B"  
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prepared from Arabidopsis Jasmonate Carboxyl  
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Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||

13 AAAAAAAAAAAAAA 1

#### RESULT 195

CF337022/c

LOCUS

JMT--07-E22.bl AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--07-E22, mRNA sequence.

CF337022

CF337022.1 GI:33822426

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

source

1..13  
Location/Qualifiers  
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/mol\_type="mRNA"

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/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

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prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||

13 AAAAAAAAAAAAAA 1

#### RESULT 196

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CN546046/c
LOCUS      CN546046      13 bp      mRNA      linear      EST 30-APR-2004
DEFINITION clone B3CS00RL007H03 3', mRNA sequence.
ACCESSION  CN546046
VERSION     CN546046.1  GI:46910671
SOURCE      EST.
ORGANISM    Vitis vinifera
            Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 13)
AUTHORS     Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Ronieu,C. and Terrier,N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33- (0) 5-57-12-25-50
            Fax: 00-33- (0) 5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: 17:
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            /organism="Vitis vinifera"
            /mol_type="mRNA"
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            /dev_stage="ripening stage"
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            /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
DB  13 AAAAAAAAAAAAAA 1

RESULT 197
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DEFINITION ApAL3SD-XII-B12 ApAL3SD Acyrthosiphon pisum cDNA clone
            ApAL3SDXIIIB12 5', mRNA sequence.
ACCESSION  CN749468
VERSION     CN749468.1  GI:47514465
KEYWORDS    EST.
SOURCE      Acyrthosiphon pisum (pea aphid)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
            1 (bases 1 to 13)
REFERENCE   1  (bases 1 to 13)
AUTHORS     Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
TITLE       An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
JOURNAL     Unpublished (2004)
COMMENT     Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            Risk of contamination by bacterial sequences from obligatory
            (Buchnera) or facultative endosymbionts.
            PCR Primers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: XXVIII row: A column: 5.
            Location/Qualifiers
            1..13
            /organism="Acyrthosiphon pisum"
            /mol_type="mRNA"
            /cultivar="yr2"
            /db_xref="taxon:7029"
            /clone="ApAL3SDXIIIB12"
            /tissue_type="head"
            /dev_stage="third instar nymph (L3)"

CN546046
LOCUS      CN546046      13 bp      mRNA      linear      EST 30-APR-2004
DEFINITION clone B3CS00RL007H03 3', mRNA sequence.
ACCESSION  CN546046
VERSION     CN546046.1  GI:46910671
SOURCE      EST.
ORGANISM    Vitis vinifera
            Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 13)
AUTHORS     Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Ronieu,C. and Terrier,N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33- (0) 5-57-12-25-50
            Fax: 00-33- (0) 5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: 17:
            Location/Qualifiers
            1..13
            /organism="Vitis vinifera"
            /mol_type="mRNA"
            /cultivar="Cabernet Sauvignon"
            /db_xref="taxon:29760"
            /clone="B3CS00RL007H03"
            /dev_stage="ripening stage"
            /clone_lib="Ripe Grape Skin Triplex2 Library"
            /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
            SfiIA; Site_2: SfiIB; Oriented library"

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
DB  13 AAAAAAAAAAAAAA 1

RESULT 197
LOCUS      CN749468      13 bp      mRNA      linear      EST 19-MAY-2004
DEFINITION ApAL3SD-XII-B12 ApAL3SD Acyrthosiphon pisum cDNA clone
            ApAL3SDXIIIB12 5', mRNA sequence.
ACCESSION  CN749468
VERSION     CN749468.1  GI:47514465
KEYWORDS    EST.
SOURCE      Acyrthosiphon pisum (pea aphid)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
            1 (bases 1 to 13)
REFERENCE   1  (bases 1 to 13)
AUTHORS     Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
TITLE       An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
JOURNAL     Unpublished (2004)
COMMENT     Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            Risk of contamination by bacterial sequences from obligatory
            (Buchnera) or facultative endosymbionts.
            PCR Primers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: XXVIII row: A column: 5.
            Location/Qualifiers
            1..13
            /organism="Acyrthosiphon pisum"
            /mol_type="mRNA"
            /cultivar="yr2"
            /db_xref="taxon:7029"
            /clone="ApAL3SDXIIIB12"
            /tissue_type="head"
            /dev_stage="third instar nymph (L3)"

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```

Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts.
PCR Primers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: XII row: B column: 12.
Location/Qualifiers
1..13
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="ApAL3SDXIIIB12"
/tissue_type="antennae"
/dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="ApAL3SD"
/note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
Sample name: ApAL3SD ; Plant growth place: INRA-Rennes,
UMR BiO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil
conditions: peat ; Sowing date: 25/03/2003 ; Harvesting
date: 10/04/2003 ; Stress date: no stress ; Description:
aphids inoculated on one-week old Vicia faba germinations
under non sterile conditions. ; experimental condition:
short photoperiod (12-hr light/12-hr dark at 18 c)"

Query Match      0.3%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2802 GAAAAAAAAAAAAA 2814
DB  1 GAAAAAAAAAAAAA 13

RESULT 198
LOCUS      CN752228      13 bp      mRNA      linear      EST 19-MAY-2004
DEFINITION ApHL3SD-XXVIII-A5 ApHL3SD Acyrthosiphon pisum cDNA clone
            ApHL3SDXXVIIIAS 5', mRNA sequence.
ACCESSION  CN752228
VERSION     CN752228.1  GI:47517225
KEYWORDS    EST.
SOURCE      Acyrthosiphon pisum (pea aphid)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
            1 (bases 1 to 13)
REFERENCE   1  (bases 1 to 13)
AUTHORS     Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
            Stern,D., Tagu,D. and Wincker,P.
TITLE       An expressed sequence tags database for the pea aphid Acyrthosiphon
            pisum
JOURNAL     Unpublished (2004)
COMMENT     Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            Risk of contamination by bacterial sequences from obligatory
            (Buchnera) or facultative endosymbionts.
            PCR Primers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: XXVIII row: A column: 5.
            Location/Qualifiers
            1..13
            /organism="Acyrthosiphon pisum"
            /mol_type="mRNA"
            /cultivar="yr2"
            /db_xref="taxon:7029"
            /clone="ApHL3SDXXVIIIAS"
            /tissue_type="head"
            /dev_stage="third instar nymph (L3)"

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/lab\_host="TOP10"  
/clone\_lib="AphL3SD"  
/note="Vector: pDNR-LIB; Site 1: SfIIA; Site 2: SfiIB;  
Sample name: AphL3SD ; Plant growth place: INRA-Rennes,  
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil  
conditions: peat ; Sowing date: 20/03/2003 ; Harvesting  
date: 10/04/2003 ; Stress date: no stress ; Description:  
aphids inoculated on one-week old Vicia faba germinations  
under non sterile conditions. ; experimental condition:  
short photoperiod (12-hr light/12-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
Db 1 AAAAAAAAAAAAAA 13

RESULT 199  
CN752875  
LOCUS  
DEFINITION  
13 bp mRNA linear EST 19-MAY-2004  
AphL3LD-VII-H10 AphL3LD Acyrthosiphon pisum cDNA clone  
AphL3LDVIIH10 5', mRNA sequence.

ACCESSION  
CN752875  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Acyrthosiphon pisum (pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.  
1 (bases 1 to 13)

REFERENCE  
AUTHORS  
Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,  
Stern,D., Tagu,D. and Wincker,P.

TITLE  
An expressed sequence tags database for the pea aphid Acyrthosiphon  
pisum

JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: D. Tagu  
INRA Rennes

UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France  
Tel: +33.2.23.48.51.65  
Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory  
(Buchnera) or facultative endosymbionts.

PCR Primers  
FORWARD: GCCGCATAACTTCGTATAGCA  
Plate: VII row: H column: 10.

FEATURES  
source  
Location/Qualifiers  
1..13

/organism="Acyrthosiphon pisum"  
/mol\_type="mRNA"  
/cultivar="yr2"  
/db\_xref="taxon:7029"  
/clone="AphL3LDVIIH10"  
/tissue\_type="head"  
/dev\_stages="third instar nymph (L3)"  
/lab\_host="TOP10"  
/clone\_lib="AphL3LD"

/note="Vector: pDNR-LIB; Site 1: SfIIA; Site 2: SfiIB;  
Sample name: AphL3SD ; Plant growth place: INRA-Rennes,  
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil  
conditions: peat ; Sowing date: 18/01/2003 ; Harvesting  
date: 03/02/2003 ; Stress date: no stress ; Description:  
aphids inoculated on one-week old Vicia faba germinations  
under non sterile conditions. ; experimental condition:  
long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
Db 1 AAAAAAAAAAAAAA 13

RESULT 200  
CN753196

LOCUS  
DEFINITION  
13 bp mRNA linear EST 19-MAY-2004  
AphL3LDXVIA12 5', mRNA sequence.

ACCESSION  
CN753196  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Acyrthosiphon pisum (pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.  
1 (bases 1 to 13)

REFERENCE  
AUTHORS  
Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,  
Stern,D., Tagu,D. and Wincker,P.

TITLE  
An expressed sequence tags database for the pea aphid Acyrthosiphon  
pisum

JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: D. Tagu  
INRA Rennes

UMR Bio3P, BP 35327, F-35653 Le Rheu Cedex France  
Tel: +33.2.23.48.51.65  
Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory  
(Buchnera) or facultative endosymbionts.

PCR Primers  
FORWARD: GCCGCATAACTTCGTATAGCA  
Plate: XVI row: A column: 12.

FEATURES  
source  
Location/Qualifiers  
1..13

/organism="Acyrthosiphon pisum"  
/mol\_type="mRNA"  
/cultivar="yr2"  
/db\_xref="taxon:7029"  
/clone="AphL3LDXVIA12"  
/tissue\_type="head"  
/dev\_stages="third instar nymph (L3)"  
/lab\_host="TOP10"  
/clone\_lib="AphL3LD"

/note="Vector: pDNR-LIB; Site 1: SfIIA; Site 2: SfiIB;  
Sample name: AphL3LD ; Plant growth place: INRA-Rennes,  
UMR Bio3P, BP 35327, 35653 Le Rheu cedex, France ; Soil  
conditions: peat ; Sowing date: 18/01/2003 ; Harvesting  
date: 03/02/2003 ; Stress date: no stress ; Description:  
aphids inoculated on one-week old Vicia faba germinations  
under non sterile conditions. ; experimental condition:  
long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.3%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
Db 1 AAAAAAAAAAAAAA 13

RESULT 201  
BQ586422/c

LOCUS  
DEFINITION  
14 bp mRNA linear EST 06-DEC-2002  
S013307-024-013-002-T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-013-002 3-PRIME, mRNA sequence.

ACCESSION  
BQ586422  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

## TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 13 row: O column: 02  
Seq primer: T7; GTAATACGACTCACTATAGGCG.  
Location/Qualifiers  
1. 14

## FEATURES

source

/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:186441"  
/db\_xref="taxon:161934"  
/clone="024-013-002"  
/tissue\_type="leaf"  
/lab\_host="EMDH108"  
/clone\_lib="MPIZ-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzelleneber Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

## RESULT 202

## BQ587890/c

## LOCUS

DEFINITION S013302-024-009-B02-T7 MP12-ADIS-024-leaf Beta vulgaris cDNA clone 024-009-B02 3-PRIME, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

BQ587890 14 bp mRNA linear EST 06-DEC-2002  
024-009-B02 3-PRIME, mRNA sequence.  
BQ587890.1 GI:26117472  
EST.  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

## AUTHORS

1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

## TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 9 row: B column: 02  
Seq primer: T7; GTAATACGACTCACTATAGGCG.  
Location/Qualifiers  
1. 14

## FEATURES

source

/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:184980"  
/db\_xref="taxon:161934"  
/clone="024-009-B02"  
/tissue\_type="leaf"  
/lab\_host="EMDH108"  
/clone\_lib="MPIZ-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzelleneber Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

## RESULT 203

## BQ589191/c

## LOCUS

DEFINITION S014009-024-015-I20-T7 MP12-ADIS-024-storage root Beta vulgaris cDNA clone 024-015-I20 3-PRIME, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

BQ589191 14 bp mRNA linear EST 06-DEC-2002  
024-015-I20 3-PRIME, mRNA sequence.  
BQ589191.1 GI:26118774  
EST.  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

## AUTHORS

1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

## TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 15 row: I column: 20

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Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1..14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:187878"
/db_xref="taxon:161934"
/clone="024-015-120"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 205
BQ590261/c
LOCUS
DEFINITION E012840-024-019-E16-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ590261
VERSION BQ590261.1 GI:26119825
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 19 row: E column: 16
Seq primer: SP6; CATACGATTGAGTACACTATAG.
Location/Qualifiers
1..14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189878"
/db_xref="taxon:161934"
/clone="024-019-E16"

Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1..14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:187878"
/db_xref="taxon:161934"
/clone="024-015-120"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
    |||||
Db 14 AAAAAAAAAAAAAA 2

RESULT 205
BQ590261/c
LOCUS
DEFINITION E012840-024-019-E16-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ590261
VERSION BQ590261.1 GI:26119844
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 19 row: K column: 14
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1..14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189851"
/db_xref="taxon:161934"
/clone="024-019-K14"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet

```

project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

DB 14 AAAAAAAAAAAAAA 2

RESULT 206  
BQ591168/c  
LOCUS  
DEFINITION  
E012715-024-017-H18-T7 MP12-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-H18 3-PRIME, mRNA sequence.

ACCESSION  
BQ591168  
VERSION  
BQ591168.1 GI:26120751

KEYWORDS  
EST.  
SOURCE  
Beta vulgaris

ORGANISM

REFERENCE  
AUTHORS  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS  
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL  
MEDLINE  
PUBMED  
22362189

COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851

Email: [weissaha@mpiz-koeln.mpg.de](mailto:weissaha@mpiz-koeln.mpg.de)

Insert Length: 14 Std Error: 0.00

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Seq primer: T7: GTAATACGACTCACTATAGGCG.

FEATURES

source

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/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"

/db\_xref="GABI:188939"

/db\_xref="taxon:161934"

/clone="024-017-H18"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MP12-ADIS-024-storage root"

/note="Vector: PCMVSPORT6; site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||

DB 14 AAAAAAAAAAAAAA 2

RESULT 207

BQ591176/c

LOCUS

DEFINITION

E012715-024-017-N20-T7 MP12-ADIS-024-storage root Beta vulgaris

CDNA clone 024-017-N20 3-PRIME, mRNA sequence.

ACCESSION

BQ591176

VERSION

BQ591176.1 GI:26120759

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 14)

TITLE

JOURNAL

MEDLINE

PUBMED

22362189

COMMENT

Contact: Weishaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: [weissaha@mpiz-koeln.mpg.de](mailto:weissaha@mpiz-koeln.mpg.de)

Insert Length: 14 Std Error: 0.00

Plate: 17 row: N column: 20

Seq primer: T7: GTAATACGACTCACTATAGGCG.

FEATURES

source

1..14

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"

/db\_xref="GABI:188947"

/db\_xref="taxon:161934"

/clone="024-017-N20"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MP12-ADIS-024-storage root"

/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||

DB 14 AAAAAAAAAAAAAA 2

RESULT 208

BQ591207/c

LOCUS

DEFINITION

E012715-024-017-B04-T7 MP12-ADIS-024-storage root Beta vulgaris

CDNA clone 024-017-B04 3-PRIME, mRNA sequence.

ACCESSION

BQ591207

VERSION

BQ591207.1 GI:26120790

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||

DB 14 AAAAAAAAAAAAAA 2

RESULT 208

BQ591207/c

LOCUS

DEFINITION





```

Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: M column: 04
Seq primer: T7: GTATACGACTCACTATAGGCG.

FEATURES
    source
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        Location/Qualifiers
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            /mol_type="mRNA"
            /cultivar="KWS2320 (double haploid, monogerm breeding
            line)"
            /db_xref="GABI:188633"
            /db_xref="taxon:161934"
            /clone="024-016-M04"
            /tissue_type="storage root"
            /lab_host="EMDH10B"
            /clone_lib="MP1Z-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            Project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 211
BQ591949/c
LOCUS
DEFINITION E012580-024-016-CL5-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ591949
VERSION BQ591949.1 GI:26121532
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 16 row: C column: 15
Seq primer: SP6: CATACGATTAGTGACACTATAG.

FEATURES
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    1..14
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            line)"
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            /db_xref="taxon:161934"
            /clone="024-028-C03"
            /tissue_type="developing root"
            /lab_host="EMDH10B"
            /clone_lib="MP1Z-ADIS-024-developing root"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            Project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2577 AAAAAAAAAAAAAA 2589
Db 13 AAAAAAAAAAAAAA 1

RESULT 212
BQ593052/c
LOCUS
DEFINITION E012375-024-028-C03-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
ACCESSION BQ593052
VERSION BQ593052.1 GI:26122635
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 28 row: C column: 03
Seq primer: SP6: CATACGATTAGTGACACTATAG.

FEATURES
    source
    1..14
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            /mol_type="mRNA"
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            line)"
            /db_xref="GABI:193808"
            /db_xref="taxon:161934"
            /clone="024-028-C03"
            /tissue_type="developing root"
            /lab_host="EMDH10B"
            /clone_lib="MP1Z-ADIS-024-developing root"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            Project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"

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orientation:
SP6-Sali-CCACGGCTCG-SPRIME-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 213
CF277935/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-K11,
mRNA sequence.
ACCESSION
CF277935
VERSION
CF277935.1 GI:33655321
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1. (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="14ETL--03-K11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 215
CF278452/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-F22,
mRNA sequence.
ACCESSION
CF278452
VERSION
CF278452.1 GI:33655838
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1. (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="14ETL--03-K11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 214
CF278001/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-L21,
mRNA sequence.
orientation:
SP6-Sali-CCACGGCTCG-SPRIME-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 214
CF278001/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--03-L21,
mRNA sequence.
orientation:
SP6-Sali-CCACGGCTCG-SPRIME-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL-04-F22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match 0.3%; Score 13; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

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RESULT 216
CF279473/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL-05-M14,
mRNA sequence.
CF279473
14 bp mRNA linear EST 14-AUG-2003

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```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

```

FEATURES

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1..14
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="14ETL-05-M14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match 0.3%; Score 13; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

```

RESULT 217
CF279992/c
LOCUS
DEFINITION

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14ETL-06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL-06-I01,
mRNA sequence.
CF279992
14 bp mRNA linear EST 14-AUG-2003

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```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

```

```

REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

```

FEATURES

```

source
1..14
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL-06-I01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match 0.3%; Score 13; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

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RESULT 218
CF281958/c
LOCUS
DEFINITION

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14ETL-09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL-09-D24,
mRNA sequence.
CF281958
14 bp mRNA linear EST 14-AUG-2003

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```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

```

```

REFERENCE
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

#### FEATURES

source  
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/organism="Oryza sativa (japonica cultivar-group)"  
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/clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

#### RESULT 219

CF282350/c  
LOCUS  
DEFINITION  
14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N05,  
mRNA sequence.

ACCESSION CF282350.1 GI:33659737

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Contact: Nahm B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

#### FEATURES

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Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

#### RESULT 220

CF294449/c  
LOCUS  
DEFINITION  
30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--03-P15, mRNA  
sequence.

ACCESSION CF294449

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

#### FEATURES

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/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

#### RESULT 221

CF295570/c  
LOCUS  
DEFINITION  
30DGS--05-J06.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--05-J06, mRNA  
sequence.

ACCESSION CF295570

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
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 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

## FEATURES

Location/Qualifiers  
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 /organism="Oryza sativa (japonica cultivar-group)"  
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 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
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 Qy 2576 AAAAAAAAAAAAAA 2588  
 Db 14 AAAAAAAAAAAAAA 2

RESULT 222  
 CF296120/c  
 LOCUS  
 DEFINITION 30DGS--06-F17 b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 sativa (japonica cultivar-group) cDNA clone 30DGS--06-F17, mRNA  
 sequence.

ACCESSION CF296120  
 VERSION CF296120.1 GI:33665153  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.  
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## FEATURES

Location/Qualifiers  
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 /organism="Oryza sativa (japonica cultivar-group)"  
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with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;  
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 Matches 13; Conservative 0; Mismatches 0;  
 Qy 2576 AAAAAAAAAAAAAA 2588  
 Db 14 AAAAAAAAAAAAAA 2

## RESULT 223

CF297969/c  
 LOCUS  
 DEFINITION 7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-C16, mRNA  
 sequence.

ACCESSION CF297969  
 VERSION CF297969.1 GI:33669730  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1. 14  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
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 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
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 RT-PCR."

## FEATURES

Location/Qualifiers  
 1. 14  
 /organism="Oryza sativa (japonica cultivar-group)"  
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 /db\_xref="taxon:39947"  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
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Query Match 0.3%; Score 13; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0;  
 Qy 2576 AAAAAAAAAAAAAA 2588  
 Db 14 AAAAAAAAAAAAAA 2

## RESULT 224

CF298109/c  
 LOCUS  
 DEFINITION 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-F19, mRNA  
 sequence.

ACCESSION CF298109  
 VERSION CF298109.1 GI:33669870  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Yongin, Kyeonggi, Korea

Tel.: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

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1. 14  
/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/tissue\_type="leaf"

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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

#### Query Match

Best Local Similarity 0.3%; Score 13; DB 1; Length 14;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

#### RESULT 225

CF299368/c

LOCUS

DEFINITION 7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F21, mRNA sequence.

ACCESSION CF299368

VERSION CF299368.1

KEYWORDS GI:33671129

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel.: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

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1. 14

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--03-F21"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

#### Query Match

Best Local Similarity 0.3%; Score 13; DB 1; Length 14;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

#### RESULT 226

CF300542/c

LOCUS

DEFINITION 7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-B01, mRNA sequence.

ACCESSION CF300542

VERSION CF300542.1

KEYWORDS GI:33672303

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel.: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

source

1. 14

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

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/dev\_stage="7 days after germination"

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

#### Query Match

Best Local Similarity 0.3%; Score 13; DB 1; Length 14;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

#### RESULT 227

CF301020/c

LOCUS

DEFINITION 7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-L10, mRNA sequence.

ACCESSION CF301020

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CF301020.1 GI:33672781
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
/lab_host="E.coli DH10B"
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/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1. .14
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/mol_type="mRNA"
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with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 229
CF301380/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
CF301380
CF301380.1 GI:33673141
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 228
CF301083/c
LOCUS
DEFINITION
7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M19, mRNA
sequence.
CF301083
CF301083.1 GI:33672844
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1. .14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--05-M19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
CF302675
CF302675.1 GI:33673141
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
CF302675
CF302675.1 GI:33673141
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
CF302675
CF302675.1 GI:33673141
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
CF302675
CF302675.1 GI:33673141
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEFINITION
7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D16, mRNA
sequence.
CF302675
CF302675.1 GI:33673141
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 13; Conservative 0; Mismatches 0;
Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 230
CF302675/c
LOCUS
DEF
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DEFINITION 7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-G18, mRNA sequence.

ACCESSION CF302675

VERSION CF302675.1 GI:33674436

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Oryza sativa (japonica cultivar-group)

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..14

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--08-G18"

/tissue\_type="leaf"

/dev\_stages="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 231

CF302846/c

LOCUS 7LEAF--08-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-M05, mRNA sequence.

DEFINITION CF302846

14 bp mRNA linear EST 15-AUG-2003

ACCESSION CF302846.1 GI:33674607

VERSION CF302846

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..14

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clones="ABF--01-K10"

/tissue\_type="leaf"

/dev\_stages="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

FEATURES

source

1..14

/organism="Oryza sativa (japonica cultivar-group)"

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/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--08-M05"

/tissue\_type="leaf"

/dev\_stages="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

RESULT 232

CF308006/c

LOCUS ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

DEFINITION ABF--01-K10, mRNA sequence.

ACCESSION CF308006

VERSION CF308006.1 GI:33679767

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..14

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clones="ABF--01-K10"

/tissue\_type="leaf"

/dev\_stages="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

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Db      14 AAAAAAAAAAAAAA 2
|||||
CF308220      14 bp mRNA linear EST 15-AUG-2003
ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--01-P06, mRNA sequence.
CF308220
ACCESSION      CF308220.1 GI:33679981
VERSION        CF308220
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
REFERENCE      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 321 6355
                Fax: 82 31 321 6355
                Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
                Location/Qualifiers
                1..14
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="ABF--01-P06"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="ABF3-overexpressing transgenic rice plasmid
                cDNA library (ABF)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive
                element binding transcription factor 3 overexpression
                line."
                Query Match      0.3%; Score 13; DB 1; Length 14;
                Best Local Similarity 100.0%; Pred. No. 1e+02;
                Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES      source
Qy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2
|||||
RESULT 233
CF308220/c
LOCUS
DEFINITION    ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--02-E10, mRNA sequence.
ACCESSION      CF308220
VERSION        CF308220
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
REFERENCE      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 321 6355
                Fax: 82 31 321 6355
                Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
                Location/Qualifiers
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                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="ABF--01-P06"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="ABF3-overexpressing transgenic rice plasmid
                cDNA library (ABF)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive
                element binding transcription factor 3 overexpression
                line."
                Query Match      0.3%; Score 13; DB 1; Length 14;
                Best Local Similarity 100.0%; Pred. No. 1e+02;
                Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2
|||||
RESULT 234
CF308445/c
LOCUS
DEFINITION    ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--02-E10, mRNA sequence.
ACCESSION      CF308445
VERSION        CF308445.1 GI:33680206
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
REFERENCE      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 321 6355
                Fax: 82 31 321 6355
                Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
                Location/Qualifiers
                1..14
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
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                /clone="ABF--02-E10"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="ABF3-overexpressing transgenic rice plasmid
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                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive
                element binding transcription factor 3 overexpression
                line."
                Query Match      0.3%; Score 13; DB 1; Length 14;
                Best Local Similarity 100.0%; Pred. No. 1e+02;
                Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2
|||||
RESULT 235
CF308918/c
LOCUS
DEFINITION    ABF--02-016.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--02-016, mRNA sequence.
ACCESSION      CF308918
VERSION        CF308918.1 GI:33680679
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
REFERENCE      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 321 6355
                Fax: 82 31 321 6355
                Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
                Location/Qualifiers
                1..14
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="ABF--02-016"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="ABF3-overexpressing transgenic rice plasmid
                cDNA library (ABF)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive
                element binding transcription factor 3 overexpression
                line."
                Query Match      0.3%; Score 13; DB 1; Length 14;
                Best Local Similarity 100.0%; Pred. No. 1e+02;
                Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2
|||||
RESULT 236
CF308918/c
LOCUS
DEFINITION    ABF--02-016.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--02-016, mRNA sequence.
ACCESSION      CF308918
VERSION        CF308918.1 GI:33680679
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
REFERENCE      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS        Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 321 6355
                Fax: 82 31 321 6355
                Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
                Location/Qualifiers
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                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
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                /clone="ABF--02-E10"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="ABF3-overexpressing transgenic rice plasmid
                cDNA library (ABF)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive
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                line."
                Query Match      0.3%; Score 13; DB 1; Length 14;
                Best Local Similarity 100.0%; Pred. No. 1e+02;
                Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

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/lab\_host="E.coli DH10B"  
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cDNA library (ABF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

## RESULT 239

CF318323/c

LOCUS

DEFINITION HD--08-G13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-G13, mRNA sequence.

ACCESSION CF318323

VERSION CF318323.1

KEYWORDS GI:33690084

SOURCE EST.

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

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cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2576 AAAAAAAAAAAAAA 2588

Db

14 AAAAAAAAAAAAAA 2

## RESULT 240

CF318450/c

LOCUS

DEFINITION HD--08-J08.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-J08, mRNA sequence.

ACCESSION CF318450

VERSION CF318450.1

KEYWORDS GI:33690211

SOURCE EST.

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

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cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2576 AAAAAAAAAAAAAA 2588

Db

14 AAAAAAAAAAAAAA 2

## RESULT 241

CF319826/c

LOCUS

DEFINITION HD--10-H16.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-H16, mRNA sequence.

ACCESSION CF319826

VERSION CF319826.1

KEYWORDS GI:33691587

SOURCE EST.

Oryza sativa (japonica cultivar-group)

```

ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
              1 (bases 1 to 14)
              Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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                /lab_host="E.coli DH10B"
                /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
                /note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2

RESULT 242
CF321246/c
LOCUS
DEFINITION     HD--12-G24.g1 OshDAC1-overexpressing transgenic rice plasmid
                library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
                cDNA library (HD)
ACCESSION     CF321246
VERSION       CF321246.1 GI:33693007
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     1 (bases 1 to 14)
              Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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                /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
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                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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                derived from rice Histone Deacetylase overexpression
                line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2

RESULT 242
CF321246/c
LOCUS
DEFINITION     HD--12-G24.g1 OshDAC1-overexpressing transgenic rice plasmid
                library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
                cDNA library (HD) Oryza sativa (japonica cultivar-group)
                cDNA clone NACL--01-H01, mRNA
                sequence.
ACCESSION     CF327097
VERSION       CF327097.1 GI:33802449
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     1 (bases 1 to 14)
              Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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                RT-PCR."

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/cultivar="Nackdong"
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/clones="HD-12-G24"
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cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2

RESULT 243
CF327097/c
LOCUS
DEFINITION     NACL--01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza
                sativa (japonica cultivar-group) cDNA clone NACL--01-H01, mRNA
                sequence.
ACCESSION     CF327097
VERSION       CF327097.1 GI:33802449
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     1 (bases 1 to 14)
              Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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                with oligoribonucleotides and then used as templates for
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Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      14 AAAAAAAAAAAAAA 2

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RESULT 244
CF327119/c
LOCUS       NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION  sativa (japonica cultivar-group) cDNA clone NACL--01-H14, mRNA
sequence.
ACCESSION   CF327119.1  GI:33802493
VERSION     CF327119.1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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RT-PCR."
Query Match      0.3%; Score 13; DB 1; Length 14;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2576 AAAAAAAAAAAAAA 2588
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Db  14 AAAAAAAAAAAAAA 2

RESULT 245
CF327203/c
LOCUS       NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION  sativa (japonica cultivar-group) cDNA clone NACL--01-J16, mRNA
sequence.
ACCESSION   CF327203.1  GI:33802665
VERSION     CF327203.1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

```

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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match      0.3%; Score 13; DB 1; Length 14;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2576 AAAAAAAAAAAAAA 2588
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Db  13 AAAAAAAAAAAAAA 1

RESULT 246
CF327445/c
LOCUS       NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION  sativa (japonica cultivar-group) cDNA clone NACL--01-O24, mRNA
sequence.
ACCESSION   CF327445.1  GI:33803149
VERSION     CF327445.1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2576 AAAAAAAAAAAAAA 2588
      |||||
Db  13 AAAAAAAAAAAAAA 1

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Db      14 AAAAAAAAAAAAAA 2
|||||
RESULT 247
CF328490/c      14 bp      mRNA      linear      EST 18-AUG-2003
LOCUS      NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone NACL--03-G21, mRNA
sequence.
ACCESSION      CF328490
VERSION      CF328490.1 GI:33805226
KEYWORDS      EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
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/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
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Location/Qualifiers
1. 14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-G21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
|||||
Db      14 AAAAAAAAAAAAAA 2
|||||

RESULT 249
CF328669/c      14 bp      mRNA      linear      EST 18-AUG-2003
LOCUS      NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone NACL--03-K23, mRNA
sequence.
ACCESSION      CF328669
VERSION      CF328669.1 GI:33805587
KEYWORDS      EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. 14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-K23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
|||||
Db      14 AAAAAAAAAAAAAA 2
|||||

RESULT 248
CF328540/c      14 bp      mRNA      linear      EST 18-AUG-2003
LOCUS      NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone NACL--03-H24, mRNA
sequence.
ACCESSION      CF328540
VERSION      CF328540.1 GI:33805324
KEYWORDS      EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 250
CF328994/C
LOCUS
DEFINITION
NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-C11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 252
CF329990
LOCUS
DEFINITION
NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--05-I11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 251
CF329217/C
LOCUS
DEFINITION
NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-H10, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--05-I11"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--04-H10"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 252
CF329990
LOCUS
DEFINITION
NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--05-I11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-I11"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

#### RESULT 253

CF330198/c  
LOCUS  
DEFINITION NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-N04, mRNA sequence.

ACCESSION CF330198

VERSION CF330198.1 GI:33808624

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

#### FEATURES

source

1..14

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clones="NACL--05-N04"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2803 AAAAAAAAAAAAC 2815

Db 14 AAAAAAAAAAAAC 2

#### RESULT 254

CF330784/c  
LOCUS  
DEFINITION NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-K10, mRNA sequence.

ACCESSION CF330784

VERSION CF330784.1 GI:33809790

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

#### FEATURES

source

1..14

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clones="NACL--06-K10"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588

Db 14 AAAAAAAAAAAAAA 2

#### RESULT 255

CF331272/c

LOCUS

DEFINITION NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--07-F09, mRNA sequence.

ACCESSION CF331272

VERSION CF331272.1 GI:33810755

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

#### FEATURES

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1..14

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clones="NACL--07-F09"

/tissue\_type="callus"

|            |  |                                      |        |                 |
|------------|--|--------------------------------------|--------|-----------------|
| RESULT_257 | CF333214   | 14 bp                                | linear | EST 18-AUG-2003 |
| LOCUS      | JMT--02-A10.b1                                       | AtJMT-overexpressing transgenic rice |        |                 |
| DEFINITION | library (JMT) Oryza sativa (japonica cultivar-group) |                                      |        |                 |
|            | JMT--02-A10.   | mRNA sequence.                       |        |                 |
| ACCESSION  | CF333214   |                                      |        |                 |

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="JMT--02-A10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOP0; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

RESULT 259
CF333399/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

ACCESSION
VERSION CF333399.1 GI:33815074
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="JMT--02-E12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOP0; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

RESULT 259
CF333399/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
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/notes="Vector: pCR4-TOP0; Site 1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.3%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

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Db 14 AAAAAAAAAAAAAA 2

RESULT 260
CF334202/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid
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prepared from Arabidopsis Jasmonate Carboxyl
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 261
CF334281/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

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methyltransferase overexpression line."

Query Match      0.3%; Score 13; DB 1; Length 14;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

RESULT 261
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

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/notes="Vector: pCR4-TOP0; Site 1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 14 AAAAAAAAAAAAAA 2

```

JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 14 AAAAAAAAAAAAAA 2

RESULT 262  
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LOCUS  
DEFINITION Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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prepared from Arabidopsis Jasmonate Carboxyl  
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Query Match 0.3%; Score 13; DB 1; Length 14;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 14 AAAAAAAAAAAAAA 2

RESULT 262  
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LOCUS  
DEFINITION Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 14 AAAAAAAAAAAAAA 2

RESULT 263  
CF335781/c  
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DEFINITION Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 14 AAAAAAAAAAAAAA 2

RESULT 264  
CF336094/c  
LOCUS  
DEFINITION Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."



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RESULT 267
CF336906/c
LOCUS
DEFINITION
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    library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
    JMT--07-C05, mRNA sequence.
ACCESSION
    CF336906
VERSION
    CF336906.1 GI:33822182
KEYWORDS
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SOURCE
    Oryza sativa (japonica cultivar-group)
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    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 14)
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Qy 2576 AAAAAAAAAAAAAA 2588
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Db 14 AAAAAAAAAAAAAA 2

RESULT 268
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LOCUS
DEFINITION
    AJ690565 KN261 Bos taurus cDNA clone KN261-054_B13, mRNA sequence.
ACCESSION
    AJ690565
VERSION
    AJ690565.1 GI:49423173
KEYWORDS
    EST.
SOURCE
    Bos taurus (cow)
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
    Bovinae; Bos.
REFERENCE
    1 (bases 1 to 15)
    Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
    Development of cDNA and EST resources for studying reproduction and
    embryo development in pigs and cattle
    Unpublished (2004)
    Contact: Anderson SI
    Genomics and Bioinformatics

    Query Match 0.3%; Score 13; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 1e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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Db 14 AAAAAAAAAAAAAA 2

RESULT 269
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LOCUS
DEFINITION
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ACCESSION
    BE230585
VERSION
    BE230585.1 GI:8956782
KEYWORDS
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SOURCE
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    Oryza sativa (indica cultivar-group)
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REFERENCE
    1 (bases 1 to 15)
    Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
    Nahm,B.H.
    Large-scale Sequencing Analysis of ESTs from Rice Seedling
    Unpublished (1999)
    Contact: Eun M.Y.
    Department of Cytogenetics
    National Inst. of Agri. Sci. and Tech, RDA
    Suwon, Kyunggido, Korea
    Tel: 82 331 290 0301
    Fax: 82 331 290 0307
    Email: myeun@sun20.asti.re.kr.
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    Best Local Similarity 100.0%; Pred. No. 1.6e+02;
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Db 15 AAAAAAAAAAAAAA 3

RESULT 269
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DEFINITION
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    (indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION
    BE230585
VERSION
    BE230585.1 GI:8956782
KEYWORDS
    EST.
SOURCE
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    Oryza sativa (indica cultivar-group)
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    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 15)
    Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
    Nahm,B.H.
    Large-scale Sequencing Analysis of ESTs from Rice Seedling
    Unpublished (1999)
    Contact: Eun M.Y.
    Department of Cytogenetics
    National Inst. of Agri. Sci. and Tech, RDA
    Suwon, Kyunggido, Korea
    Tel: 82 331 290 0301
    Fax: 82 331 290 0307
    Email: myeun@sun20.asti.re.kr.
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    Best Local Similarity 100.0%; Pred. No. 1.6e+02;
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Db 15 AAAAAAAAAAAAAA 3

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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI
R. Site2: SmaI 3' Seq Primer M13f Normalised library constructed
from bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
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    constructed from bovine ovary."
    Query Match 0.3%; Score 13; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 1.6e+02;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
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Db 15 AAAAAAAAAAAAAA 3

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Db 1 AAAAAAAAAAAAAA 13

RESULT 270
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          CDNA clone 024-007-B02 3-PRIME, mRNA sequence.
ACCESSION BQ582543
VERSION   BQ582543
KEYWORDS  EST.
SOURCE    BQ582543.1 GI:26112120
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          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
          Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
          and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
MEDLINE   22362189
PUBMED    12472698
COMMENT   Contact: Weisshaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaar@mplz-koeln.mpg.de
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          Plate: 7 row: B column: 02
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     /lab_host="EMDH10B"
     /clone_lib="MP1Z-ADIS-024-inflorescence"
     /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
     CDNA library from sugar beet, library provided by KWS
     Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
     orientation:
     SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
     Sequencing granted in the context of the GABI-Beet
     project, local PI: Dr. Katharina Schneider, coordinator:
     Prof. Christian Jung; Sequence submission managed by
     RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3

RESULT 271
BQ585820/c
LOCUS
DEFINITION BQ585820
          15 bp mRNA linear EST 06-DEC-2002
          CDNA clone 024-014-H17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris
          CDNA clone 024-014-H17 5-PRIME, mRNA sequence.
ACCESSION BQ585820
VERSION   BQ585820
KEYWORDS  EST.
SOURCE    BQ585820.1 GI:26115402
          Beta vulgaris
          ORGANISM Beta vulgaris
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
          Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
          and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
MEDLINE   22362189
PUBMED    12472698
COMMENT   Contact: Weisshaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaar@mplz-koeln.mpg.de
          Insert Length: 15 Std Error: 0.00
          Plate: 14 row: H column: 17
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          Location/Qualifiers
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     /tissue_type="leaf"
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     /clone_lib="MP1Z-ADIS-024-leaf"
     /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
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     Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
     orientation:
     SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
     Sequencing granted in the context of the GABI-Beet
     project, local PI: Dr. Katharina Schneider, coordinator:
     Prof. Christian Jung; Sequence submission managed by
     RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION BQ585820
VERSION   BQ585820.1 GI:26115402
KEYWORDS  EST.
SOURCE    Beta vulgaris
          ORGANISM Beta vulgaris
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
          Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
          and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
MEDLINE   22362189
PUBMED    12472698
COMMENT   Contact: Weisshaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaar@mplz-koeln.mpg.de
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          Location/Qualifiers
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     /clone="024-014-H17"
     /tissue_type="leaf"
     /lab_host="EMDH10B"
     /clone_lib="MP1Z-ADIS-024-leaf"
     /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
     CDNA library from sugar beet, library provided by KWS
     Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
     orientation:
     SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
     Sequencing granted in the context of the GABI-Beet
     project, local PI: Dr. Katharina Schneider, coordinator:
     Prof. Christian Jung; Sequence submission managed by
     RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3

RESULT 272
BQ590410/c
LOCUS
DEFINITION E012844-024-019-M08-T7 MP1Z-ADIS-024-storage root Beta vulgaris
          CDNA clone 024-019-M08 3-PRIME, mRNA sequence.
ACCESSION BQ590410
VERSION   BQ590410
KEYWORDS  EST.
SOURCE    BQ590410.1 GI:26119993
          Beta vulgaris
          ORGANISM Beta vulgaris
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

```



Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

**TITLE** Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

**JOURNAL** Plant J. 32 (5), 845-857 (2002)

**MEDLINE** 22362189

**PUBMED** 12472698

**COMMENT**

Contact: Weisshaar B

ADIS DNA core facility at MPiZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaa@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 19 row: M column: 08

Seq primer: T7; GTAATACGACTCATTATAGGC.

**FEATURES**

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/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site.1: Sali; Site.2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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**Query Match** 0.3%; Score 13; DB 1; Length 15;

**Best Local Similarity** 100.0%; Pred. No. 1.6e+02;

**Matches** 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 2576 AAAAAAAAAAAAAA 2588

**Db** 15 AAAAAAAAAAAAAA 3

**RESULT** 273

**BQ590656/c**

**LOCUS**

**DEFINITION** BQ590656 15 bp mRNA linear EST 06-DEC-2002

**CNA clone** 024-018-L13-SP6 MPiZ-ADIS-024-storage root Beta vulgaris

**Accession** BQ590656.1 GI:26120239

**Version** EST.

**Keywords** Beta vulgaris

**Source** Beta vulgaris

**Organism** Beta vulgaris

**REFERENCE** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

**1** (bases 1 to 15)

**Authors** Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

**Title** Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

**Journal** Plant J. 32 (5), 845-857 (2002)

**Medline** 22362189

**Pubmed** 12472698

**Comment**

Contact: Weisshaar B

ADIS DNA core facility at MPiZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaa@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 18 row: L column: 13

Seq primer: SP6; CATACGATTAGTCACACTATAG.

**FEATURES**

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/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site.1: Sali; Site.2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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**Query Match** 0.3%; Score 13; DB 1; Length 15;

**Best Local Similarity** 100.0%; Pred. No. 1.6e+02;

**Matches** 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 2576 AAAAAAAAAAAAAA 2588

**Db** 15 AAAAAAAAAAAAAA 3

**RESULT** 274

**BQ591170/c**

**LOCUS**

**DEFINITION** BQ591170 15 bp mRNA linear EST 06-DEC-2002

**CNA clone** 024-017-N18-T7 MPiZ-ADIS-024-storage root Beta vulgaris

**Accession** BQ591170.1 GI:26120753

**Version** EST.

**Keywords** Beta vulgaris

**Source** Beta vulgaris

**Organism** Beta vulgaris

**REFERENCE** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

**1** (bases 1 to 15)

**Authors** Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

**Title** Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

**Journal** Plant J. 32 (5), 845-857 (2002)

**Medline** 22362189

**Pubmed** 12472698

**Comment**

Contact: Weisshaar B

ADIS DNA core facility at MPiZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaa@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 17 row: N column: 18

Seq primer: T7; GTAATACGACTCATTATAGGC.

**FEATURES**

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/mol_type="mRNA"
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Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
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 Db 15 AAAAAAAAAAAAAA 3

RESULT 277  
 BQ594689/c  
 LOCUS  
 DEFINITION E012404-024-024-M05-T7 MP1Z-ADIS-024-developing root Beta vulgaris  
 CDNA clone 024-024-M05 3-PRIME, mRNA sequence.  
 ACCESSION BQ594689  
 VERSION BQ594689  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 23362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 15 Std Error: 0.00  
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 Seq primer: T7; GTAATAGCACTCACTATAGGCG.

FEATURES  
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 SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
 |||||  
 Db 15 AAAAAAAAAAAAAA 3

RESULT 278  
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LOCUS  
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 14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-M23, mRNA sequence.  
 ACCESSION CF277319  
 VERSION CF277319.1 GI:33654705  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gsbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 Location/Qualifiers  
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Query Match 0.3%; Score 13; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
 |||||  
 Db 15 AAAAAAAAAAAAAA 3

RESULT 279  
 CF281923/c

LOCUS  
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 14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-D04, mRNA sequence.  
 ACCESSION CF281923  
 VERSION CF281923.1 GI:33659310  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193

Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

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/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 280  
CF290920/c  
LOCUS  
DEFINITION  
14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-C09, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.  
REFERENCE  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

1. .15  
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/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source

1. .15  
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/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/clone="14ROOT--01-C09"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 281  
CF291029/c  
LOCUS  
DEFINITION  
14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-E19, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

1. .15  
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/tissue\_type="root"  
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/lab\_host="E.coli DH10B"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 282  
CF291103/c  
LOCUS  
DEFINITION  
14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 282  
CF291103/c  
LOCUS  
DEFINITION  
14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

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Location/Qualifiers  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||  
15 AAAAAAAAAAAAAA 3

## RESULT 283

CF291717/c

LOCUS

DEFINITION 14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-E04, mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||  
15 AAAAAAAAAAAAAA 3

## RESULT 284

CF291798/c

LOCUS

DEFINITION 14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G02, mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

|||||  
15 AAAAAAAAAAAAAA 3

## RESULT 285

CF292458/c

LOCUS

DEFINITION 30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--01-E17, mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

RESULT 286  
CF292461/c  
LOCUS  
DEFINITION  
30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--01-E19, mRNA  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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with oligoribonucleotides and then used as templates for  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
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Db 15 AAAAAAAAAAAAAA 3

RESULT 286  
CF292461/c  
LOCUS  
DEFINITION  
30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--01-E19, mRNA  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

RESULT 287  
CF296652/c  
LOCUS  
DEFINITION  
30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--07-C02, mRNA  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
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RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588  
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Db 14 AAAAAAAAAAAAAA 2

RESULT 288  
CF298148/c  
LOCUS  
DEFINITION  
7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G17, mRNA  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

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1. .15  
Location/Qualifiers  
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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

#### RESULT 289

CF298630/c

LOCUS CF298630 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-B23, mRNA sequence.

ACCESSION CF298630.1 GI:33670391  
VERSION CF298630.1  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

source

1. .15  
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/clone="7LEAF--02-B23"  
/tissue\_type="leaf"

/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

#### RESULT 290

CF298733/c

LOCUS CF298733 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-E20, mRNA sequence.

ACCESSION CF298733  
VERSION CF298733.1 GI:33670494  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

source

1. .15  
Location/Qualifiers  
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/clone="7LEAF--02-E20"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

#### RESULT 291

CF298805/c

LOCUS CF298805 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-G20, mRNA sequence.

ACCESSION CF298805

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VERSION      CF298805.1  GI:33670566
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
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                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
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                /issue_type="leaf"
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                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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              with oligoribonucleotides and then used as templates for
              RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
     |||||
Db   15 AAAAAAAAAAAAAA 3

RESULT 293
LOCUS   CF299602/c
DEFINITION  Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L01, mRNA
sequence.
ACCESSION  CF299602
VERSION    CF299602.1  GI:33671363
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
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                /issue_type="leaf"
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                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
              with oligoribonucleotides and then used as templates for
              RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2576 AAAAAAAAAAAAAA 2588
     |||||
Db   15 AAAAAAAAAAAAAA 3

RESULT 294
LOCUS   CF299608/c
DEFINITION  Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-J09, mRNA
sequence.
ACCESSION  CF298889
VERSION    CF298889.1  GI:33670650
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1..15
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                /mol_type="mRNA"

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DEFINITION 7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L04, mRNA sequence.

ACCESSION CF299608

VERSION CF299608.1 GI:33671369

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1. (bases 1 to 15)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
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Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
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1. .15

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Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

RESULT 295  
CF300121/c  
LOCUS

DEFINITION CF300121 15 bp mRNA linear EST 15-AUG-2003  
7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G12, mRNA sequence.

ACCESSION CF300121

VERSION CF300121.1 GI:33671882

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1. (bases 1 to 15)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
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Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers  
1. .15

/organism="Oryza sativa (japonica cultivar-group)"  
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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

RESULT 296  
CF300361/c  
LOCUS

DEFINITION CF300361 15 bp mRNA linear EST 15-AUG-2003  
7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L16, mRNA sequence.

ACCESSION CF300361

VERSION CF300361.1 GI:33672122

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1. (bases 1 to 15)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
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Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers  
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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
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Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3



RESULT 297  
CF300992/c  
LOCUS  
DEFINITION  
15 bp mRNA linear EST 15-AUG-2003  
7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-K19, mRNA  
sequence.  
CF300992  
CF300992.1 GI:33672753  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS  
1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
TITLE  
JOURNAL  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongui University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
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/mol\_type="mRNA"  
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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."  
Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

RESULT 298  
CF302034/c  
LOCUS  
DEFINITION  
15 bp mRNA linear EST 15-AUG-2003  
7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C24, mRNA  
sequence.  
CF302034  
CF302034.1 GI:33673795  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS  
1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
TITLE  
JOURNAL  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongui University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.  
FEATURES  
source  
1..15  
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RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2576 AAAAAAAAAAAAAA 2588  
|||||  
Db 15 AAAAAAAAAAAAAA 3

RESULT 299  
CF302124/c  
LOCUS  
DEFINITION  
15 bp mRNA linear EST 15-AUG-2003  
7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-F16, mRNA  
sequence.  
CF302124  
CF302124.1 GI:33673885  
EST.  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS  
1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
TITLE  
JOURNAL  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongui University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source  
1..15  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2576 AAAAAAAAAAAAAA 2588
Db      15 AAAAAAAAAAAAAA 3

RESULT 300
CF302182/c
LOCUS   7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-H20, mRNA
sequence.
ACCESSION CF302182      15 bp mRNA linear EST 15-AUG-2003
VERSION   CF302182.1 GI:33673943
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 15;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      15 AAAAAAAAAAAAAA 3

RESULT 301
CF307923/c
LOCUS   ABF--01-I15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--01-I15, mRNA sequence.
ACCESSION CF307923      15 bp mRNA linear EST 15-AUG-2003
VERSION   CF307923.1 GI:33679684
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs

```

```

JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2576 AAAAAAAAAAAAAA 2588
Db      15 AAAAAAAAAAAAAA 3

RESULT 302
CF311159/c
LOCUS   ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-E11, mRNA sequence.
ACCESSION CF311159      15 bp mRNA linear EST 15-AUG-2003
VERSION   CF311159.1 GI:33682920
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
| | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 3

RESULT 303
CF311907/c
LOCUS
DEFINITION
ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-G04, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="ABF-07-G04"
/tissue_type="leaf"
/dev_stages="14 days after germination"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
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line."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
| | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 3

RESULT 304
CF311319/c
LOCUS
DEFINITION
HD--01-G13.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-G13, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/tissue_type="leaf"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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HD--01-G13, mRNA sequence.
CF313319
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..15
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/mol_type="mRNA"
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/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2576 AAAAAAAAAAAAAA 2588
| | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 3

RESULT 305
CF313320
LOCUS
DEFINITION
HD--01-G13.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-G13, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

```

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

# FEATURES

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Location/Qualifiers  
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/organism="Oryza sativa (japonica cultivar-group)"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

## RESULT 306

CF316251  
LOCUS  
DEFINITION  
HD--05-H15, b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--05-H15, mRNA sequence.

ACCESSION  
CF316251

VERSION  
CF316251.1 GI:33688012

KEYWORDS  
EST.

## SOURCE

ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

AUTHORS  
1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

## TITLE

JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source  
Location/Qualifiers  
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/organism="Oryza sativa (japonica cultivar-group)"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

## RESULT 307

CF318035/c  
LOCUS  
DEFINITION  
HD--07-P06, b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--07-P06, mRNA sequence.

ACCESSION  
CF318035

VERSION  
CF318035.1 GI:33689796

## KEYWORDS

## SOURCE

ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

AUTHORS  
1 (bases 1 to 15)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## TITLE

## JOURNAL

## COMMENT

## FEATURES

source  
Location/Qualifiers  
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/organism="Oryza sativa (japonica cultivar-group)"  
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/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

## RESULT 308

CF327434/c  
LOCUS  
DEFINITION  
NACL--01-018, b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-018, mRNA sequence.

ACCESSION  
CF327434

VERSION  
CF327434.1 GI:33803127

## KEYWORDS

## SOURCE

ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



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KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..15
/organism="Oryza sativa (japonica cultivar-group)"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3

RESULT 313
CF336202/c
LOCUS
DEFINITION
JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--06-C20, mRNA sequence.
ACCESSION
CF336202
VERSION
1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
Db 15 AAAAAAAAAAAAAA 3

RESULT 313
CF547282
LOCUS
DEFINITION
CR547282 15 bp mRNA linear EST 12-JUL-2004
DKFP4681112_r1_468 (synonym: phrt1) Pongo pygmaeus cDNA clone
ACCESSION
CR547282
VERSION
CR547282.1 GI:50240938
KEYWORDS
SOURCE
ORGANISM
Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Bloeker,H., Boesher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
Osanger,A., Fobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Bloeker,H., Boesher,M., Brandt,P., et al.)
Unpublished (2004)
CONTACT: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany)
within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFP4681112) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/projects/cdna/.

FEATURES
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Query Match
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
Db 1 AAAAAAAAAAAAAA 13

RESULT 314

```





PUBMED 12472698  
COMMENT Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaa@mpiz-koeln.mpg.de  
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Seq primer: SP6r; ATTAGGTGACACTATAGAAGA.

FEATURES  
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/clone="024-028-F08"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: PCMVSPORF6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 317

BQ592965/c  
LOCUS 16 bp mRNA linear EST 06-DEC-2002  
DEFINITION S013324-024-028-A01-T7 MP1Z-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-028-A01 3-PRIME, mRNA sequence.

ACCESSION BQ592965  
VERSION BQ592965.1 GI:26122548  
KEYWORDS EST.  
SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaa@mpiz-koeln.mpg.de  
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Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES  
source

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/note="Vector: PCMVSPORF6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 13; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0;

Qy 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

RESULT 318

BQ595717

LOCUS 16 bp mRNA linear EST 06-DEC-2002

DEFINITION E012692-024-022-H07-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-022-H07 5-PRIME, mRNA sequence.

ACCESSION BQ595717

VERSION BQ595717.1 GI:26125300

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT Contact: Weishaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaa@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 22 row: H column: 07

Seq primer: SP6; CATACGATTGACACTATAG.

FEATURES

source

Location/Qualifiers  
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/db\_xref="GABI:191134"

/db\_xref="taxon:161934"

/clone="024-022-H07"

/tissue\_type="developing root"



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/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Binbeck, Germany, contact:
b.schulz@kwa.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 1 AAAAAAAAAAAAAA 13

RESULT 319
CF279325/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
mRNA sequence.
ACCESSION
CF279325
VERSION
CF279325.1 GI:33656711
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="14ETL--05-J09"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/cdna_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 1 AAAAAAAAAAAAAA 13

RESULT 319
CF279325/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
mRNA sequence.
ACCESSION
CF279325
VERSION
CF279325.1 GI:33656711
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="14ETL--05-J09"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/cdna_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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RESULT 320
CF311057/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
mRNA sequence.
ACCESSION
CF311057
VERSION
CF311057.1 GI:33682818
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..16
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/db_xref="taxon:39947"
/clone="ABF--06-C03"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/cdna_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 16 AAAAAAAAAAAAAA 4

RESULT 321
CF314377/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
mRNA sequence.
ACCESSION
CF314377
VERSION
CF314377.1 GI:33686138
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588
DB 16 AAAAAAAAAAAAAA 4

RESULT 321
CF314377/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
mRNA sequence.
ACCESSION
CF314377
VERSION
CF314377.1 GI:33686138
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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1. .16  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
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/clone="HD--02-001"  
/tissue\_type="callus"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.3%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

## RESULT 322

CF315789/c

## LOCUS

DEFINITION HD--04-N10.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--04-N10, mRNA sequence.

## ACCESSION

CF315789

## VERSION

CF315789.1 GI:33687550

## KEYWORDS

EST.

## SOURCE

Oryza sativa (japonica cultivar-group)

## ORGANISM

Oryza sativa (japonica cultivar-group)

## Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 (bases 1 to 16)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .16

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clone="HD--04-N10"

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/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was  
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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.3%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

## RESULT 323

CF316056/c

## LOCUS

DEFINITION HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--05-D07, mRNA sequence.

## ACCESSION

CF316056

## VERSION

CF316056.1 GI:33687817

## KEYWORDS

EST.

## SOURCE

Oryza sativa (japonica cultivar-group)

## ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 (bases 1 to 16)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa (japonica cultivar-group)"

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/cultivar="Nackdong"

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/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
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Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 16 AAAAAAAAAAAAAA 4

## RESULT 324

CF317718/c

## LOCUS

DEFINITION HD--07-I05.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--07-I05, mRNA sequence.

## ACCESSION

CF317718

## LOCUS

CF317718

## DEFINITION

HD--07-I05.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
HD--07-I05, mRNA sequence.

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VERSTON      CF317718.1  GI:33689479
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Eshrtaoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      16 AAAAAAAAAAAAAA 4
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RESULT 325
CF318894/c
LOCUS
DEFINITION    HD--09-D06.g1 OSHDA1-overexpressing transgenic rice plasmid
               library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
               HD--09-D06, mRNA sequence.
ACCESSION     CF318894
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Eshrtaoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      16 AAAAAAAAAAAAAA 4
|||||
RESULT 325
CF318894/c
LOCUS
DEFINITION    HD--09-D06.g1 OSHDA1-overexpressing transgenic rice plasmid
               library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
               HD--09-D06, mRNA sequence.
ACCESSION     CF318894
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Eshrtaoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      15 AAAAAAAAAAAAAA 3
|||||
RESULT 326
CF319827/c
LOCUS
DEFINITION    HD--10-H16.g1 OSHDA1-overexpressing transgenic rice plasmid
               library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
               HD--10-H16, mRNA sequence.
ACCESSION     CF319827
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Eshrtaoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
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               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      15 AAAAAAAAAAAAAA 3
|||||
RESULT 326
CF319827/c
LOCUS
DEFINITION    HD--10-H16.g1 OSHDA1-overexpressing transgenic rice plasmid
               library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
               HD--10-H16, mRNA sequence.
ACCESSION     CF319827
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Eshrtaoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--10-H16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-D06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      15 AAAAAAAAAAAAAA 3
|||||
RESULT 326
CF319827/c
LOCUS
DEFINITION    HD--10-H16.g1 OSHDA1-overexpressing transgenic rice plasmid
               library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
               HD--10-H16, mRNA sequence.
ACCESSION     CF319827
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Eshrtaoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--10-H16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      3598 TTTTITTTTAAAT 3610
Db      15 TTTTITTTTAAAT 3

RESULT 327
CF320356/c
LOCUS   HD--11-D14_b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
DEFINITION HD--11-D14_b1 OshDACL1-overexpressing transgenic rice plasmid cDNA clone
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--11-D14, mRNA sequence.
ACCESSION CF320356
VERSION   1
KEYWORDS  CF320356.1 GI:33692117
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..16
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:39947"
     /clone="NACL--02-F06"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 30 days"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"
     /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      16 AAAAAAAAAAAAAA 4

RESULT 329
CF327923/c
LOCUS   NACL--02-J18_g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--02-J18, mRNA
            sequence.
ACCESSION CF327923
VERSION   1
KEYWORDS  CF327923.1 GI:33804096
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 16)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..16
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:39947"
     /clone="HD--11-D14"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
     /lab_host="E.coli DH10B"
     /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
           cDNA library (HD)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
           treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
           reverse transcribed and then used for PCR. mRNA was
           derived from rice Histone Deacetylase overexpression
           line."

Query Match      0.3%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2576 AAAAAAAAAAAAAA 2588
Db      16 AAAAAAAAAAAAAA 4

RESULT 328
CF327722/c
LOCUS   NACL--02-F06_b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA
            sequence.
ACCESSION CF327722
VERSION   1
KEYWORDS  CF327722.1 GI:33803695
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.

```

/note="Vector: PCR4-TOPO; Site.1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 330

CF328223/c

LOCUS

DEFINITION

NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-A10, mRNA sequence.

ACCESSION

CF328223

VERSION

CF328223.1

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..16

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="NACL--03-A10"

/tissue\_type="callus"

/dev\_host="E.coli DH10B"

/lab\_host="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO; Site.1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

RESULT 331

CF333386

LOCUS

DEFINITION

JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--02-E05, mRNA sequence.

CF333386

VERSION

CF333386.1

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)

1..16

/organism="Pongo pygmaeus"

/mol\_type="mRNA"

Query Match 0.3%; Score 13; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 15 AAAAAAAAAAAAAA 3

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..16

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="JMT--02-E05"

/tissue\_type="leaf"

/dev\_host="E.coli DH10B"

/lab\_host="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"

/note="Vector: PCR4-TOPO; Site.1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 13; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAAA 2588

Db 1 AAAAAAAAAAAAAA 13

RESULT 332

CR786609

LOCUS

DEFINITION

DKFZp468C2031.r1.468 (synonym: phrt1) Pongo pygmaeus cDNA clone

DKFZp468C2031.5, mRNA sequence.

ACCESSION

CR786609.1

VERSION

CR786609.1

KEYWORDS

EST.

SOURCE

Pongo pygmaeus (orangutan)

Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.

1 (bases 1 to 16)

Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

Pongo pygmaeus mRNA (Koehler,K., Beyer,A., Mewes,H.W., et al.)

Unpublished (2004)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,

Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email s.wiemann@dkfz-heidelberg.de; mforachung GmbH in Berlin,

Germany. Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp468C2031

Further information about the clone and the sequencing project is

available at http://mips.gsf.de/projects/cdna/.

Location/Qualifiers

1..16

/organism="Pongo pygmaeus"

/mol\_type="mRNA"



Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

1..17  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="7LEAF--03-M14"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2745 TTTTCTTTTAA 2757

Db 16 TTTTCTTTTAA 4

RESULT 336  
CL693164/c

LOCUS  
DEFINITION  
PRI0160a\_G09\_2 - PRI0160a.BR (21) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL693164.1 GI:50215072

VERSION GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (bases 1 to 21)

REFERENCE  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.  
AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

source

1..21

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.3%; Score 13; DB 1; Length 21;  
Best Local Similarity 76.2%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAAATGGTTTTT 4098

||||| || ||| |||||

Db

RESULT 337

CL693165/c

LOCUS

DEFINITION

PRI0160a\_G10\_2 - PRI0160a.BR (21) Note: Recurring String Mixed

stage fosmid library of P. pacificus var. California Pristionchus

pacificus genomic, genomic survey sequence.

ACCESSION CL693165

VERSION GSS.

KEYWORDS

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (bases 1 to 21)

REFERENCE

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

AppADB: an AcedB database for the nematode satellite organism

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

source

1..21

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.3%; Score 13; DB 1; Length 21;  
Best Local Similarity 76.2%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1157 TTTTATATATATTTTCTT 1177

Db 21 TTTTCTTTTCTTTTCTT 1

RESULT 338

CW020436/c

LOCUS

DEFINITION

CW0698 TIGEM gene trap library Mus musculus cDNA clone A012.A8,

mRNA sequence.

ACCESSION CW020436

VERSION CW020436.1 GI:52789696

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 21)

REFERENCE

Cobellis,G., Nicolaus,G., Marra,E., Barbarisi,M., Sardiello,M., Di

Giorgio,F., Iovino,N., Zollo,M., Ballabio,A. and Cortese,R.

Tagging genes with cassette-exchange sites

Unpublished (2004)

Contact: TIGEM

107

TIGEM

Via P. Castellino, 111, 80131 NAPOLI, ITALY

Tel: +390816132205

21 TTTTGTGTATTTTTTTTT 1

CL693165 21 bp DNA linear GSS 10-JUL-2004  
PRI0160a\_G10\_2 - PRI0160a.BR (21) Note: Recurring String Mixed  
stage fosmid library of P. pacificus var. California Pristionchus  
pacificus genomic, genomic survey sequence.

ACCESSION CL693165

VERSION GSS.

KEYWORDS

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (bases 1 to 21)

REFERENCE

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

AppADB: an AcedB database for the nematode satellite organism

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

source

1..21

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.3%; Score 13; DB 1; Length 21;  
Best Local Similarity 76.2%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1157 TTTTATATATATTTTCTT 1177

Db 21 TTTTCTTTTCTTTTCTT 1

CW020436 21 bp mRNA linear GSS 28-SEP-2004  
CW0698 TIGEM gene trap library Mus musculus cDNA clone A012.A8,  
mRNA sequence.

ACCESSION CW020436

VERSION CW020436.1 GI:52789696

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 21)

REFERENCE

Cobellis,G., Nicolaus,G., Marra,E., Barbarisi,M., Sardiello,M., Di

Giorgio,F., Iovino,N., Zollo,M., Ballabio,A. and Cortese,R.

Tagging genes with cassette-exchange sites

Unpublished (2004)

Contact: TIGEM

107

TIGEM

Via P. Castellino, 111, 80131 NAPOLI, ITALY

Tel: +390816132205

Fax: +390815790919  
Email: cobelli@tigem.it  
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM  
Class: Gene Trap.  
Location/Qualifiers

## FEATURES

source

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1. .21
/organism="Mus musculus"
/mol_type="mRNA"
/strain="I29 ola"
/db_xref="taxon:10090"
/clone="A012.A8"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"
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Query Match 0.3%; Score 13; DB 1; Length 21;  
Best Local Similarity 76.2%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2748 TTTTTCCTTAAGGAAAAATA 2768

|||||  
1 1 TTTTTCCTTAAGGAAAAATA 1

## RESULT 339

BQ590507

LOCUS

DEFINITION E012844-024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris 16 bp mRNA linear EST 06-DEC-2002

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 16)  
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PubMed 12472698

## COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 19 row: M column: 04  
Seq primer: T7; GTAATACGACTCCTACTATAGGCG.

## FEATURES

source

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1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189608"
/db_xref="taxon:161934"
/clone="024-019-M04"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
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cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTCTTTTA 3279

|||||  
1 1 TTTTTCCTTCTTTTA 16

## RESULT 340

BQ595369

LOCUS

DEFINITION S013317-024-022-P02-T7 MP1Z-ADIS-024-developing root Beta vulgaris 16 bp mRNA linear EST 06-DEC-2002

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 16)  
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PubMed 12472698

## COMMENT

Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 22 row: P column: 02  
Seq primer: T7; GTAATACGACTCCTACTATAGGCG.

## FEATURES

source

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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:191489"
/db_xref="taxon:161934"
/clone="024-022-P02"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de
```



```

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTTCCTTTT 3279
Db 1 TTTTTCCTTTTTCCTTTT 16

RESULT 341
CF296130 16 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA
sequence.
ACCESSION CF296130.1 GI:33665163
VERSION CF296130
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--02-G01"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTTCCTTTT 3279
Db 1 TTTTTCCTTTTTCCTTTT 16

RESULT 343
CF296130 16 bp mRNA linear EST 18-AUG-2003
LOCUS 30DGS--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
sequence.
ACCESSION CF296130.1 GI:33806877
VERSION CF296130
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--02-G01"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTTCCTTTT 3279
Db 1 TTTTTCCTTTTTCCTTTT 16

RESULT 342
CF314013 16 bp mRNA linear EST 15-AUG-2003
LOCUS HD--02-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--02-G01, mRNA sequence.
ACCESSION CF314013
VERSION CF314013.1 GI:33685774
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

```

/dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTT 3279  
 Db 1 TTTTTCCTTTT 16

RESULT 344  
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 LOCUS 2821557.3prime NIH\_MGC\_7 16 bp mRNA linear EST 07-JAN-2000  
 DEFINITION 2821557.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821557 3',  
 mRNA sequence.  
 ACCESSION AW246487  
 VERSION AW246487.1 GI:6589480  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 16)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Other ESTs: 2821557.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: DCTD/FTP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 11  
 contiguous PHRED high quality bases following vector sequence. Very  
 Low Quality Sequence: Trace file contained 16 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a XhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Plate: L1CM7 row: B column: 22  
 High quality sequence stop: 11.  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2821557"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.9kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

#### FEATURES

source  
 Location/Qualifiers  
 1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2821557"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.9kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTTCCTTTT 2761  
 Db 1 TTTTTCCTTTT 16

RESULT 345  
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 LOCUS 2821557.3prime NIH\_MGC\_7 16 bp mRNA linear EST 07-JAN-2000  
 DEFINITION 2821557.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821557 3',  
 mRNA sequence.

ACCESSION AW246487  
 VERSION AW246487.1 GI:6589480  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Other ESTs: 2821557.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: DCTD/FTP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 11  
 contiguous PHRED high quality bases following vector sequence. Very  
 Low Quality Sequence: Trace file contained 16 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a XhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Plate: L1CM7 row: B column: 22  
 High quality sequence stop: 11.  
 Location/Qualifiers  
 1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2821557"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12.8; DB 1; Length 16;  
 Best Local Similarity 87.5%; Pred. No. 2.7e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2796 TTATCTGAAAAA 2811  
 Db 16 TTCTGTAATAAAAA 1

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RESULT 346
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LOCUS
DEFINITION
      16 bp      mRNA      linear      EST 07-JAN-2000
      2821591.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821591 3',
      mRNA sequence.
ACCESSION
AW246490
VERSION
AW246490.1 GI:6569483
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Other ESTs: 2821591.5prime
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTP/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCW7 row: D column: 8
High quality sequence stop: 12.
FEATURES
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             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2821591"
             /tissue_type="small cell carcinoma"
             /cell_line="MGC3"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH_MGC_7"
             /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally
             cloned into EcoRI/XhoI sites using the following 5',
             adaptor: GGACGAG(G). Size-selected >500bp for average
             insert size 1.8kb. Library constructed by Ling Hong in
             the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
             (Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2572 GTTTAAAAA 2587
      |||||
      16 GTTTGCAAAAAA 1
Db

RESULT 347
AW251049/c
LOCUS
DEFINITION
      16 bp      mRNA      linear      EST 07-JAN-2000
      2821507.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821507 3',
      mRNA sequence.
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ACCESSION
AW251049
VERSION
AW251049.1 GI:6593995
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Other ESTs: 2821507.5prime
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCW6 row: P column: 20
High quality sequence stop: 10.
FEATURES
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             /organism="Homo sapiens"
             /mol_type="mRNA"
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             /clone="IMAGE:2821507"
             /tissue_type="small cell carcinoma"
             /cell_line="MGC3"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH_MGC_7"
             /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally
             cloned into EcoRI/XhoI sites using the following 5',
             adaptor: GGACGAG(G). Size-selected >500bp for average
             insert size 1.8kb. Library constructed by Ling Hong in
             the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
             (Stratagene) and Superscript II RT (Life Technologies)."
```

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Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3221 CCTGTTAAACAGAAA 3236
      |||||
      16 CCTGTTAAAAA 1
Db

RESULT 348
BQ590688
LOCUS
DEFINITION
      16 bp      mRNA      linear      EST 06-DEC-2002
      S013717-024-018-023-T7 MPI2-ADIS-024-storage root Beta vulgaris
      cDNA clone 024-018-023 3-PRIME, mRNA sequence.
ACCESSION
BQ590688
VERSION
BQ590688.1 GI:26120271
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
```

```

REFERENCE
AUTHORS      Caryophyllales; Amaranthaceae; Beta.
              1 (bases 1 to 16)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.

TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698

COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPiZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 16 Std Error: 0.00
              Plate: 18 row: O column: 23
              Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
source      Location/Qualifiers
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              /organism="Beta vulgaris"
              /mol_type="mRNA"
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              line)"
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              /db_xref="taxon:161934"
              /clone="024-018-023"
              /tissue_type="storage root"
              /lab_host="EMDH10B"
              /clone_lib="MPiZ-ADIS-024-storage root"
              /notes="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
              orientation:
              SP6-Sall-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      973 CCCCCCCCACCCCGCC 988
Db      1 CCCCCCCCCCCCCCCC 16

RESULT 349
BQ590128
LOCUS      E012843-024-019-E19-T7 MPiZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
ACCESSION  BQ590128
VERSION     BQ590128.1 GI:26119711
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllales; Amaranthaceae; Beta.
              1 (bases 1 to 17)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.

REFERENCE    Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
              Plant J. 32 (5), 845-857 (2002)
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698

```

```

COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPiZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 17 Std Error: 0.00
              Plate: 19 row: E column: 19
              Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
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              /tissue_type="storage root"
              /lab_host="EMDH10B"
              /clone_lib="MPiZ-ADIS-024-storage root"
              /notes="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
              orientation:
              SP6-Sall-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3264 TTTTTCCTCTTTA 3279
Db      2 TTTTTCCTCTTTA 17

RESULT 350
BQ591181
LOCUS      E012715-024-017-H16-T7 MPiZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-H16 3-PRIME, mRNA sequence.
ACCESSION  BQ591181
VERSION     BQ591181.1 GI:26120764
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllales; Amaranthaceae; Beta.
              1 (bases 1 to 17)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.

REFERENCE    Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
              Plant J. 32 (5), 845-857 (2002)
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPiZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 17 Std Error: 0.00
              Plate: 17 row: H column: 16
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FEATURES
              Location/Qualifiers

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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-BEET
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
Best Local Similarity 0.3%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
Db 1 TTTTTCCTTTT 16

RESULT 351
CF294668 17 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--04-E17, mRNA
sequence.
CF294668.1 GI:33663701
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
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/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279
Db 2 TTTTTCCTTTT 17

RESULT 353
CF311499 17 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.
CF311499.1 GI:33683260
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 17)

```

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/notes="Vector: pCRA-TOPO; Site\_1: EcoRI; Leaf was dried  
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line."

Query Match 0.3%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279  
Db 1 TTTTTCCTTTT 16

RESULT 354  
CF319075  
LOCUS HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
DEFINITION HD--09-H06, mRNA sequence.  
ACCESSION CF319075  
VERSION CF319075.1 GI:33690836  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarthoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Qy 3264 TTTTTCCTTTT 3279  
Db 1 TTTTTCCTTTT 16

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LOCUS HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
DEFINITION HD--09-H06, mRNA sequence.  
ACCESSION CF319075  
VERSION CF319075.1 GI:33690836  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarthoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279  
Db 1 TTTTTCCTTTT 16

RESULT 354  
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LOCUS HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
DEFINITION HD--09-H06, mRNA sequence.  
ACCESSION CF319075  
VERSION CF319075.1 GI:33690836  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarthoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279  
Db 1 TTTTTCCTTTT 16

RESULT 354  
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LOCUS HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
DEFINITION HD--09-H06, mRNA sequence.  
ACCESSION CF319075  
VERSION CF319075.1 GI:33690836  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarthoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/clone="HD--09-H06"  
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Query Match 0.3%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279  
Db 1 TTTTTCCTTTT 16

RESULT 354  
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LOCUS HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
DEFINITION HD--09-H06, mRNA sequence.  
ACCESSION CF319075  
VERSION CF319075.1 GI:33690836  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarthoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/clone="HD--09-H06"  
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/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

Query Match 0.3%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTT 3279  
Db 1 TTTTTCCTTTT 16

RESULT 354  
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LOCUS HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
DEFINITION HD--09-H06, mRNA sequence.  
ACCESSION CF319075  
VERSION CF319075.1 GI:33690836  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriarthoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim

DEFINITION 2820717.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820717 3', mRNA sequence.

ACCESSION AW247976

VERSION AW247976.1 GI:6591064

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 17)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2820717.5prime

Contact: Robert Strausberg, Ph.D.

Email: [cga@bbs-research.nih.gov](mailto:cga@bbs-research.nih.gov)

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing Project

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM4 row: 0 column: 22.

#### FEATURES

source

1..17

Location/Qualifiers

/organism="Homo sapiens"

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/clone="IMAGE:2820717"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/note="lib="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 3.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTTCCTTAAATGAT 3613

Db 1 TTTTTCCTTAAACAT 16

#### RESULT 357

CF308042

LOCUS ABF--01-L07.b1 ABF3-overexpressing transgenic rice plasmid cDNA 19 bp mRNA linear EST 15-AUG-2003

DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

ABF--01-L07, mRNA sequence.

ACCESSION CF308042

VERSION CF308042.1 GI:33679803

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: [bhnaahm@bio.com](mailto:bhnaahm@bio.com), [bhnaahm@bio.myongji.ac.kr](mailto:bhnaahm@bio.myongji.ac.kr).

#### FEATURES

source

1..19

Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="ABF--01-L07"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 12.8; DB 1; Length 19;

Best Local Similarity 87.5%; Pred. No. 4.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTCTTTTA 3279

Db 1 TTTTTCCTTCTTTTA 16

#### RESULT 358

CF295100

LOCUS 30DGS--04-002.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--04-002, mRNA sequence.

DEFINITION CF295100.1 GI:33664133

ACCESSION CF295100

VERSION CF295100.1

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: [bhnaahm@bio.com](mailto:bhnaahm@bio.com), [bhnaahm@bio.myongji.ac.kr](mailto:bhnaahm@bio.myongji.ac.kr).

#### FEATURES

source

1..15

Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"



```

/clone="30DGS--04-002"
/tissue_type="leaf"
/dev_host="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 0.3%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2743 TCTTTTCTTTTCTTA 2756
| | | | | | | | | | | | | | |
Db 2 TTTTCTTTTCTTTTCTTA 15

RESULT 359
LOCUS BQ591588 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012616-024-017-C15-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-C15 5-PRIME, mRNA sequence.
ACCESSION BQ591588
VERSION BQ591588.1 GI:26121171
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig,R.; Schulz,B.; Weishaar,B.; Hennig,S.; Steinfath,M.;
Drungowski,M.; Stahl,D.; Wruck,W.; Menze,A.; O'Brien,J.; Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: C column: 15
Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
Source
1..17
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188532"
/db_xref="taxon:161934"
/clone="024-017-C15"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulze@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
0.3%; Score 12.4; DB 1; Length 17;

Best Local Similarity
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match
Best Local Similarity 92.9%; Pred. No. 4.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTTTTTTTT 2755
| | | | | | | | | | | | | | |
Db 3 ATTTTTTTTTTTTTT 16

RESULT 360
LOCUS AW246528 17 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821879.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821879 3',
mRNA sequence.
ACCESSION AW246528
VERSION AW246528.1 GI:6589521
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2821879.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
scores: PHRED from University of Washington Genome Center
Trimming: cross match from University of Washington Genome Center
PRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 13
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 17 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM7 row: P column: 8
High quality sequence stop: 13.
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821879"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```



```
RESULT 361
AW246551
LOCUS
DEFINITION      15 bp  mRNA  linear  EST 07-JAN-2000
                2822090.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822090 3',
                mRNA sequence.
ACCESSION      AW246551
VERSION        AW246551
KEYWORDS       AW246551.1  GI:6589544
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822090.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 14
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 15 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: L10C8 row: I column: 3
High quality sequence stop: 14.
Location/Qualifiers
1..15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822090"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
Query Match      0.3%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2746 TTTTITTTTTTAA 2757
      |||||
Db 1 TTTTITTTTTTAA 12

RESULT 362
AW245585/c
LOCUS
DEFINITION      15 bp  mRNA  linear  EST 07-JAN-2000
                2822740.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822740 3',
                mRNA sequence.
ACCESSION      AW245585
```

```
VERSION        AW245585.1  GI:6588578
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822740.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 6 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 15 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: L10C10 row: D column: 5
High quality sequence stop: 6.
Location/Qualifiers
1..15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822740"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
Query Match      0.3%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2585
      |||||
Db 12 TTAATAAAAAAAAAA 1

RESULT 363
AW248540
LOCUS
DEFINITION      16 bp  mRNA  linear  EST 07-JAN-2000
                2820844.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820844 3',
                mRNA sequence.
ACCESSION      AW248540
VERSION        AW248540.1  GI:6591533
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NIH-MGC http://mgc.nci.nih.gov/.
```

**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Other ESTs: 2820844.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DNP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbtp/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross\_match from University of Washington Genome Center.  
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 15  
 contiguous PHRED high quality bases following vector sequence. Very  
 Low Quality Sequence: Trace file contained 16 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a xhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Plate: LNCM5 row: E column: 5  
 High quality sequence stop: 15.  
**FEATURES** source  
 1..16  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2820844"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="WGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"  
 /note="Organ: lung; Vector: pOTF7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

**Query Match** 0.3%; Score 12; DB 1; Length 16;  
**Best Local Similarity** 100.0%; Pred. No. 4.4e+02;  
**Matches** 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 2746 TTTTITTTTAA 2757  
 |||||  
**Db** 1 TTTTITTTTAA 12

**RESULT 364**  
**CF319827**  
**LOCUS** CF319827 16 bp mRNA linear EST 15-AUG-2003  
**DEFINITION** HD-10-H16.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone  
 HD-10-H16, mRNA sequence.  
**ACCESSION** CF319827  
**VERSION** CF319827.1 GI:33691588  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa (japonica cultivar-group)  
**ORGANISM** Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 16)  
**AUTHORS** Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.  
**FEATURES** source  
 1..16  
 Location/Qualifiers  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="HD-10-H16"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."  
**Query Match** 0.3%; Score 12; DB 1; Length 16;  
**Best Local Similarity** 100.0%; Pred. No. 4.4e+02;  
**Matches** 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 2574 TTTAAAAA 2585  
 |||||  
**Db** 4 TTTAAAAA 15

**RESULT 365**  
**AW251049**  
**LOCUS** AW251049 16 bp mRNA linear EST 07-JAN-2000  
**DEFINITION** 2821507.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821507',  
 mRNA sequence.  
**ACCESSION** AW251049  
**VERSION** AW251049.1 GI:6593995  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 16)  
**AUTHORS** NIH-MGC http://mgi.nci.nih.gov/.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Other ESTs: 2821507.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/PTP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbtp/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 10  
 contiguous PHRED high quality bases following vector sequence. Very  
 Low Quality Sequence: Trace file contained 16 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a xhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Plate: LNCM6 row: P column: 20  
 High quality sequence stop: 10.  
**FEATURES** source  
 1..16  
 Location/Qualifiers  
 /organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821507"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2746 TTTTTCCTTAA 2757

Db 1 TTTTTCCTTAA 12

#### RESULT 366

CF301359

LOCUS

DEFINITION

7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-D05, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CF301359.1 GI:33673120

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..18

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--06-D05"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

#### Query Match

Best Local Similarity 0.3%; Score 12; DB 1; Length 18;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTCT 3275

Db 7 TTTTTCCTTCT 18



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KEYWORDS      .
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 14)
AUTHORS
TITLE         ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL       EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES      LOCATION/Qualifiers
source        1..14
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACCTACTGTGTG 1232
Db 14 TGCACCTACTGTGTG 1

RESULT 479
A40526/c
LOCUS         A40526
DEFINITION   Sequence 63 from Patent WO9425578.
ACCESSION    A40526
VERSION      A40526.1 GI:2296561
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES    LOCATION/Qualifiers
source      1..14
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACCTACTGTGTG 1232
Db 14 TGCACCTACTGTGTG 1

RESULT 479
A40526/c
LOCUS         A40526
DEFINITION   Sequence 63 from Patent WO9425578.
ACCESSION    A40526
VERSION      A40526.1 GI:2296561
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES    LOCATION/Qualifiers
source      1..14
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAA 1357
Db 14 CAGATCCTGAGCAA 1

RESULT 480
A40534/c
LOCUS         A40534
DEFINITION   Sequence 71 from Patent WO9425578.
ACCESSION    A40534
VERSION      A40534.1 GI:2296569
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES    LOCATION/Qualifiers
source      1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAA 1357
Db 14 CAGATCCTGAGCAA 1

RESULT 480
A40534/c
LOCUS         A40534
DEFINITION   Sequence 71 from Patent WO9425578.
ACCESSION    A40534
VERSION      A40534.1 GI:2296569
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES    LOCATION/Qualifiers
source      1..14
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Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AAAATGCCATCCCG 1574
Db 14 AAAATGCCATCCCG 1

RESULT 482
A40538/c
LOCUS         A40538
DEFINITION   Sequence 75 from Patent WO9425578.
ACCESSION    A40538
VERSION      A40538.1 GI:2296573
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES    LOCATION/Qualifiers
source      1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AAAATGCCATCCCG 1574
Db 14 AAAATGCCATCCCG 1

RESULT 482
A40538/c
LOCUS         A40538
DEFINITION   Sequence 75 from Patent WO9425578.
ACCESSION    A40538
VERSION      A40538.1 GI:2296573
KEYWORDS     .
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
FEATURES    LOCATION/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match   0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCCACTTCTACAG 1588
Db 14 CCCACTTCTACAG 1588
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DEFINITION LUNX gene and method for detecting micrometastasis of cancer.  
ACCESSION E53842  
VERSION E53842.1 GI:18633612  
KEYWORDS JP 2001078772-A/3.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Kadota,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.  
TITLE LUNX gene and method for detecting micrometastasis of cancer  
JOURNAL Patent: JP 2001078772-A 3 27-MAR-2001;  
OFSUKA PHARMACEUT CO LTD  
COMMENT OS Unidentified  
PN JP 2001078772-A/3  
PD 27-MAR-2001  
PF 07-SEP-1999 JP 1999253186  
PR MORITO KADOTA,YOSHIYUKI FUJIWARA,RYUJI WATANABE,KOICHI OZAKI  
PC C12N15/09,C07K14/82,C07K16/32,C12N1/15,C12N1/21, PC  
C12N5/10,C12Q1/68,  
PC G01N33/15,G01N33/50,G01N33/566,G01N33/574//A61K31/713, PC  
A61K35/12,A61K35/76,  
PC A61K39/395,A61K39/395,A61K48/00,A61P35/00,A61P35/04,C12P21/08,  
PC C12N15/00,  
PC C12N5/00  
CC  
FH Key Location/Qualifiers  
FT source 1..16  
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/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 0.3%; Score 14.2; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 3e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2574 TTAAAAAATAAAAAA 2588  
DB 16 TBAATAAAAAAATAAAAA 2  
RESULT 475  
AX406535/C  
LOCUS AX406535 17 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 12 from Patent WO222686.  
ACCESSION AX406535  
VERSION AX406535.1 GI:21439550  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Kwak,L.W. and Biragyn,A.  
TITLE Defensin-antigen fusion proteins  
JOURNAL Patent: WO 0222686-A 12 21-MAR-2002;  
The Secretary, Dept. of Health and Human services, NIH (US)  
FEATURES  
source 1..17  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence; Note =  
Synthetic Construct"  
Query Match 0.3%; Score 14.2; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 3.5e+02;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 974 CCCCCCACCSCCCCC 990  
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Db 17 SCSCCCSCSCSCSCCCC 1  
RESULT 476  
AX721791/c  
LOCUS AX721791 17 bp DNA linear PAT 07-MAY-2003  
DEFINITION Sequence 12 from Patent WO03025002.  
ACCESSION AX721791  
VERSION AX721791.1 GI:30422379  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Biragyn,A. and Kwak,L.W.  
TITLE Method and compositions of defensin-antigen fusion proteins and chemokine-antigen fusion proteins as vaccines for tumors and viral infection  
JOURNAL Patent: WO 03025002-A 12 27-MAR-2003;  
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
FEATURES  
source 1..17  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
Query Match 0.3%; Score 14.2; DB 1; Length 17;  
Best Local Similarity 76.5%; Pred. No. 3.5e+02;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 974 CCCCCCACCSCCCCC 990  
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Db 17 SCSCCCSCSCSCSCCCC 1  
RESULT 477  
A40172/c  
LOCUS A40172 14 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 2 from Patent WO9425588.  
ACCESSION A40172  
VERSION A40172.1 GI:2296326  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR- beta (TGF- beta)  
JOURNAL Patent: WO 9425588-A 2 10-NOV-1994;  
BIOGNOSTIK GES FUER BIOMOLEKUL (DE)  
COMMENT Other publication AU 6794594 941121.  
FEATURES  
source 1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1222 ACTACTGTGTGCTG 1235  
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Db 14 ACTACTGTGTGCTG 1  
RESULT 478  
A40520/c  
LOCUS A40520 14 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 57 from Patent WO9425578.  
ACCESSION A40520  
VERSION A40520.1 GI:2296555

LOCUS BD107505 18 bp DNA linear PAT 18-SEP-2002  
DEFINITION Novel quantitative polymorphism analysis method.  
ACCESSION BD107505  
VERSION BD107505.1 GI:23202323  
KEYWORDS JP 2002000275-A/14.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.  
TITLE Novel quantitative polymorphism analysis method  
JOURNAL Patent: JP 2002000275-A 14 08-JAN-2002;  
& TECHNOL JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE  
COMMENT OS Artificial Sequence  
PN JP 2002000275-A/14  
PD 08-JAN-2002  
PF 27-JUN-2000 JP 2000193133  
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,  
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU  
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base  
sequence was prepared synthetically on the aim of CC  
CC decrease in fluorescence emission of a nucleic acid probe CC  
labeled with  
CC BODIBY FL/C6 upon the hybridization of the  
probe with a target  
CC nucleic  
CC acid.  
FH Key Location/Qualifiers  
FT source 1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

FEATURES  
source  
1..18  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177  
Db 18 ATATATATTTTTTTT 3

RESULT 473  
E52143/c  
LOCUS E52143 16 bp DNA linear PAT 31-JAN-2002  
DEFINITION TSA7005 gene.  
ACCESSION E52143  
VERSION E52143.1 GI:18629626  
KEYWORDS JP 2001025389-A/3.  
SOURCE unidentified  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Ogawara,T., Suzuki,M. and Ozaki,K.  
TITLE TSA7005 gene  
JOURNAL Patent: JP 2001025389-A 3 30-JAN-2001;  
COMMENT OTSUKA PHARMACEUT CO LTD  
OS Unknown  
PN JP 2001025389-A/3  
PD 30-JAN-2001  
PF 15-JUL-1999 JP 1999201279  
PR  
PI TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI  
PC C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21, PC  
C12N5/10//A61K31/00,  
PC A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC

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/db\_xref="taxon:32644"

Query Match 0.3%; Score 14.2; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 3e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAAAAAAAAAA 2588  
Db 16 TDAAAAAAAAAAAAAA 2

RESULT 474  
E53842/c  
LOCUS E53842 16 bp DNA linear PAT 31-JAN-2002

LOCUS BD107505 18 bp DNA linear PAT 18-SEP-2002  
DEFINITION Novel quantitative polymorphism analysis method.  
ACCESSION BD107505  
VERSION BD107505.1 GI:23202323  
KEYWORDS JP 2002000275-A/14.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.  
TITLE Novel quantitative polymorphism analysis method  
JOURNAL Patent: JP 2002000275-A 14 08-JAN-2002;  
& TECHNOL JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE  
COMMENT OS Artificial Sequence  
PN JP 2002000275-A/14  
PD 08-JAN-2002  
PF 27-JUN-2000 JP 2000193133  
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,  
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU  
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base  
sequence was prepared synthetically on the aim of CC  
CC decrease in fluorescence emission of a nucleic acid probe CC  
labeled with  
CC BODIBY FL/C6 upon the hybridization of the  
probe with a target  
CC nucleic  
CC acid.  
FH Key Location/Qualifiers  
FT source 1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

FEATURES  
source  
1..18  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
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QY 1162 ATATATATTTTTTCTT 1177  
Db 18 ATATATATTTTTTTT 3

RESULT 472  
BD107507/c  
LOCUS BD107507 18 bp DNA linear PAT 18-SEP-2002  
DEFINITION Novel quantitative polymorphism analysis method.  
ACCESSION BD107507  
VERSION BD107507.1 GI:23202325  
KEYWORDS JP 2002000275-A/16.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.  
TITLE Novel quantitative polymorphism analysis method  
JOURNAL Patent: JP 2002000275-A 16 08-JAN-2002;  
& TECHNOL JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE  
COMMENT OS Artificial Sequence  
PN JP 2002000275-A/16  
PD 08-JAN-2002  
PF 27-JUN-2000 JP 2000193133  
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,  
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU

|            |   |                  |                    |       |            |                 |        |    |      |    |
|------------|---|------------------|--------------------|-------|------------|-----------------|--------|----|------|----|
| TITLE      | Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method   |                  |                    |       |            |                 |        |    |      |    |
| JOURNAL    | Patent: JP 2001286300-A 18 16-OCT-2001;<br>JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY   |                  |                    |       |            |                 |        |    |      |    |
| COMMENT    | OS Artificial Sequence<br>PN JP 2001286300-A/18<br>PD 16-OCT-2001<br>PF 20-APR-2000 JP 2000120097<br>PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,<br>PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU OSAMU KOYAMA,KENTA FURUSHO<br>PC C1201/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,PC G01N33/566,<br>PC C12N15/00<br>CC The base sequence was prepared synthetically on the aim of CC examining the decrease in fluorescence emission of a nucleic acid probe CC labeled with probe with a target<br>CC nucleic acid.<br>CC acid.<br>FH Key<br>FT source<br>FT Location/Qualifiers<br>FT /organism='Artificial Sequence'.<br>FT Location/Qualifiers<br>FT 1. .18<br>FT /organism="synthetic construct"<br>FT /mol_type="genomic DNA"<br>FT /db_xref="taxon:32630" |                  |                    |       |            |                 |        |    |      |    |
| FEATURES   | source  |                  |                    |       |            |                 |        |    |      |    |
|            | Query Match   | 0.3%;            | Score 14.4;        | DB 1; | Length 18; |                 |        |    |      |    |
|            | Best Local Similarity   | 93.8%;           | Pred. No. 3.6e+02; |       |            |                 |        |    |      |    |
|            | Matches   | 15;              | Conservative       | 0;    | Mismatches | 1;              | Indels | 0; | Gaps | 0; |
| QY         | 1162  | ATATATATTTTTTCTT | 1177               |       |            |                 |        |    |      |    |
| Db         | 18  | ATATATATTTTTTTT  | 3                  |       |            |                 |        |    |      |    |
| RESULT 469 |   |                  |                    |       |            |                 |        |    |      |    |
| BD107503/c |   |                  |                    |       |            |                 |        |    |      |    |
| LOCUS      | BD107503  | 18 bp            |                    | DNA   | linear     | PAT 18-SEP-2002 |        |    |      |    |
| DEFINITION | Novel quantitative polymorphism analysis method.  |                  |                    |       |            |                 |        |    |      |    |
| ACCESSION  | BD107503  |                  |                    |       |            |                 |        |    |      |    |
| VERSION    | BD107503.1  | GI-23202321      |                    |       |            |                 |        |    |      |    |
| KEYWORDS   | JP 2002000275-A/12.   |                  |                    |       |            |                 |        |    |      |    |
| SOURCE     | synthetic construct<br>other sequences; artificial sequences.   |                  |                    |       |            |                 |        |    |      |    |
| ORGANISM   | 1 (bases 1 to 18)   |                  |                    |       |            |                 |        |    |      |    |
| REFERENCE  | Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.   |                  |                    |       |            |                 |        |    |      |    |
| AUTHORS    | Novel quantitative polymorphism analysis method   |                  |                    |       |            |                 |        |    |      |    |
| TITLE      | Patent: JP 2002000275-A 12 08-JAN-2002;   |                  |                    |       |            |                 |        |    |      |    |
| JOURNAL    | JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL   |                  |                    |       |            |                 |        |    |      |    |
| COMMENT    | OS Artificial Sequence<br>PN JP 2002000275-A/12<br>PD 08-JAN-2002<br>PF 27-JUN-2000 JP 2000193133<br>PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,<br>PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU<br>PC C12N15/09,C12M1/00,C12M1/34,C1201/68,C12N15/00 CC The base sequence was prepared synthetically on the aim of CC examining the decrease in fluorescence emission of a nucleic acid probe CC labeled with probe with a target<br>CC BODIBY FL/C6 upon the hybridization of the   |                  |                    |       |            |                 |        |    |      |    |





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/note="Detection oligonucleotide for ELK1"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 935 AAAAAACAAACCTTTC 950
Db 16 AAAAAACAAACCTTTC 1

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16 AAAAAACAAACCTTTC 1

RESULT 464
AX826754
LOCUS
DEFINITION
Sequence 1006 from Patent WO03072821.
ACCESSION
AX826754
VERSION
AX826754.1 GI:39752268
KEYWORDS
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SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Adorjan,P., Burger,M., Maier,S., Nimrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE
Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL
Patent: WO 03072821-A 1006 04-SEP-2003;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for GPIb beta"

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4130 AGTTTGGTTGAGTTT 4145
Db 3 AGTTTGGTTGAGTTT 18

|||||
3 AGTTTGGTTGAGTTT 18

RESULT 465
BD072876/c
LOCUS
DEFINITION
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION
BD072876
VERSION
BD072876.1 GI:22618479
KEYWORDS
JP 2001286300-A/14.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2001286300-A 14 16-OCT-2001;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT
OS Artificial Sequence
PN JP 2001286300-A/14
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53,G01N33/542, PC
G01N33/566,
CC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
```

Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,  
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,  
Pelet,C. and Ziebarth,H.  
Methods and nucleic acids for the analysis of hematopoietic cell  
proliferative disorders  
Patent: WO 0207272-A 652 03-OCT-2002;  
Epigenomics AG (DE)  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for ELK1"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950  
Db 16 AAAAAACAACCTTTC 1

RESULT 458  
AX599726/c  
LOCUS  
DEFINITION  
Sequence 1066 from Patent WO0207272.  
ACCESSION  
AX599726  
VERSION  
AX599726.1 GI:28399874  
KEYWORDS  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1  
AUTHORS  
Berlin,K., Braun,A., Disler,J., Guetig,D., Howe,A., Mueller,J.,  
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,  
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,  
Pelet,C. and Ziebarth,H.  
Methods and nucleic acids for the analysis of hematopoietic cell  
proliferative disorders  
Patent: WO 0207272-A 1066 03-OCT-2002;  
Epigenomics AG (DE)  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for ELK1"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950  
Db 16 AAAAAACAACCTTTC 1

RESULT 459  
AX767728/c  
LOCUS  
DEFINITION  
Sequence 376 from Patent WO03044226.  
ACCESSION  
AX767728  
VERSION  
AX767728.1 GI:32436333  
KEYWORDS  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1  
AUTHORS  
Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and  
Nimmrich,I.  
Method and nucleic acids for the analysis of a lymphoid cell  
proliferative disorder

JOURNAL Patent: WO 03044226-A 376 30-MAY-2003;  
Epigenomics AG (DE)  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for ELK1"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950  
Db 16 AAAAAACAACCTTTC 1

RESULT 460  
AX796166/c  
LOCUS  
DEFINITION  
Sequence 509 from Patent WO03052135.  
ACCESSION  
AX796166  
VERSION  
AX796166.1 GI:37516832  
KEYWORDS  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1  
AUTHORS  
Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.  
and Nimmrich,I.  
Method and nucleic acids for the analysis of a lung cell  
proliferative disorder  
Patent: WO 03052135-A 509 26-JUN-2003;  
Epigenomics AG (DE)  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for ELK1"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950  
Db 16 AAAAAACAACCTTTC 1

RESULT 461  
AX822692/c  
LOCUS  
DEFINITION  
Sequence 584 from Patent EP1340818.  
ACCESSION  
AX822692  
VERSION  
AX822692.1 GI:39749328  
KEYWORDS  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1  
AUTHORS  
Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,  
Rujan,T. and Schmitt,A.  
Method and nucleic acids for the analysis of a colon cell  
proliferative disorder  
Patent: EP 1340818-A 584 03-SEP-2003;  
Epigenomics AG (DE)  
Location/Qualifiers  
1. .18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTTTCTT 1177  
|||||  
Db 18 ATATATATTTTTTTT 3

RESULT 453  
AR478213/c  
LOCUS AR478213 18 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 16 from patent US 6699661.  
ACCESSION AR478213  
VERSION AR478213.1 GI:47236861  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.  
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method  
JOURNAL Patent: US 6699661-A 16 02-MAR-2004;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTTTCTT 1177  
|||||  
Db 18 ATATATATTTTTTTT 3

RESULT 454  
AR478214/c  
LOCUS AR478214 18 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 17 from patent US 6699661.  
ACCESSION AR478214  
VERSION AR478214.1 GI:47236862  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.  
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method  
JOURNAL Patent: US 6699661-A 17 02-MAR-2004;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTTTCTT 1177  
|||||  
Db 18 ATATATATTTTTTTT 3

RESULT 455  
AR478215/c  
LOCUS AR478215 18 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 18 from patent US 6699661.  
ACCESSION AR478215  
VERSION AR478215.1 GI:47236864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.  
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method  
JOURNAL Patent: US 6699661-A 19 02-MAR-2004;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTTTCTT 1177  
|||||  
Db 18 ATATATATTTTTTTT 3

RESULT 456  
AX085253/c  
LOCUS AX085253 18 bp DNA linear PAT 09-MAR-2001  
DEFINITION Sequence 7 from Patent WO0112855.  
ACCESSION AX085253  
VERSION AX085253.1 GI:13275311  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.  
TITLE Binary encoded sequence tags  
JOURNAL Patent: WO 0112855-A 7 22-FEB-2001;  
YALE UNIVERSITY (US)  
FEATURES Location/Qualifiers  
source 1..18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2801 TGAATAAAAAAAAAAACA 2816  
|||||  
Db 18 TGAATAAAAAAAAAAAA 3

RESULT 457  
AX599312/c  
LOCUS AX599312 18 bp DNA linear PAT 14-FEB-2003  
DEFINITION Sequence 652 from Patent WO02077272.  
ACCESSION AX599312  
VERSION AX599312.1 GI:28399454  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Berlin,K., Braun,A., Dietler,J., Guetig,D., Howe,A., Mueller,J.,

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Db      18 ATATATATTTTTTTT 3
|||||
RESULT 448
LOCUS   AR264932/c          18 bp      DNA      linear      PAT 10-APR-2003
DEFINITION   Sequence 16 from patent US 6492121.
ACCESSION   AR264932
VERSION     AR264932.1 GI:29693319
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
TITLE       Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
JOURNAL     Patent: US 6492121-A 16 10-DEC-2002;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1162 ATATATATTTTCTT 1177
|||||
Db      18 ATATATATTTTTTTT 3

RESULT 449
LOCUS   AR264933/c          18 bp      DNA      linear      PAT 10-APR-2003
DEFINITION   Sequence 17 from patent US 6492121.
ACCESSION   AR264933
VERSION     AR264933.1 GI:29693320
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
TITLE       Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
JOURNAL     Patent: US 6492121-A 17 10-DEC-2002;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1162 ATATATATTTTCTT 1177
|||||
Db      18 ATATATATTTTTTTT 3

RESULT 450
LOCUS   AR264935/c          18 bp      DNA      linear      PAT 10-APR-2003
DEFINITION   Sequence 19 from patent US 6492121.
ACCESSION   AR264935
VERSION     AR264935.1 GI:29693322
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
TITLE       Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
JOURNAL     Patent: US 6492121-A 15 02-MAR-2004;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
TITLE       Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
JOURNAL     Patent: US 6492121-A 19 10-DEC-2002;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1162 ATATATATTTTCTT 1177
|||||
Db      18 ATATATATTTTTTTT 3

RESULT 451
LOCUS   AR371952           18 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION   Sequence 19 from patent US 6395545.
ACCESSION   AR371952
VERSION     AR371952.1 GI:34609062
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Monia,B.P. and Cowseert L.M.
TITLE       Antisense modulation of inhibitor-kappa B kinase-alpha expression
JOURNAL     Patent: US 6395545-A 19 28-MAY-2002;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3727 TATTTTATGTTGTC 3742
|||||
Db      1 TATTTTATGTTATTC 16

RESULT 452
LOCUS   AR478212/c          18 bp      DNA      linear      PAT 14-MAY-2004
DEFINITION   Sequence 15 from patent US 6699661.
ACCESSION   AR478212
VERSION     AR478212.1 GI:47236860
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
TITLE       Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
JOURNAL     Patent: US 6699661-A 15 02-MAR-2004;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"
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VERSION      CQ807628.1  GI:47113022
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Fookens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
             Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
             Marx,A.
TITLE        Method and nucleic acids for the improved treatment of breast cell
             proliferative disorders
JOURNAL      Patent: WO 2004035803-A 1078 29-APR-2004;
             Epigenomics AG (DE)
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Detection oligonucleotide for GPIIB"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4130 AGTTGGTTGAGTTT 4145
Db 3 AGTTGGTTGGGTTT 18

RESULT 444
CQ814895/c
LOCUS        CQ814895.1 18 bp DNA linear PAT 24-MAY-2004
DEFINITION   Sequence 18 from Patent WO2004039979.
ACCESSION    CQ814895
VERSION      CQ814895.1 GI:47604062
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Heils,A. and Haug,K.
TITLE        Means and methods for diagnosing and treating idiopathic
             generalized epilepsy (ige)
JOURNAL      Patent: WO 2004039979-A 18 13-MAY-2004;
             Rheinische Friedrich-Wilhelms-Universitaet Bonn (DE)
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Primer for amplifying a fragment of the CLCN-2
               nucleotide sequence"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 96 GAGCTCTGGGGCAGGC 111
Db 18 GAGCTCTGGGGCAGGC 3

RESULT 445
AR196692
LOCUS        AR196692.1 18 bp DNA linear PAT 20-APR-2002
DEFINITION   Sequence 1157 from patent US 6350934.
ACCESSION    AR196692
VERSION      AR196692.1 GI:20246129
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
             Yokomaku,T., Koyama,O. and Furusho,K.
TITLE        Method for determining a concentration of target nucleic acid
             molecules, nucleic acid probes for the method, and method for
             analyzing data obtained by the method
JOURNAL      Patent: US 6492121-A 15 10-DEC-2002;
             Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="genomic DNA"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177

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AUTHORS      Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
             Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE        Nucleic acid encoding delta-9 desaturase
JOURNAL      Patent: US 6350934-A 1157 26-FEB-2002;
             Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 586 CTCCCGCGGCTCGCC 601
Db 2 CTCCCGCGGCTCGCC 17

RESULT 446
AR208427/c
LOCUS        AR208427.1 18 bp DNA linear PAT 20-JUN-2002
DEFINITION   Sequence 7 from patent US 6383754.
ACCESSION    AR208427
VERSION      AR208427.1 GI:21509578
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Kaufman,J.C., Roth,M.E., Lizardi,P.M., Peng,L. and Latimer,D.R.
TITLE        Binary encoded sequence tags
JOURNAL      Patent: US 6383754-A 7 07-MAY-2002;
             Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2801 TGAATAAAAAAAAAACA 2816
Db 18 TGAATAAAAAAAAAAAAA 3

RESULT 447
AR264931/c
LOCUS        AR264931.1 18 bp DNA linear PAT 10-APR-2003
DEFINITION   Sequence 15 from patent US 6492121.
ACCESSION    AR264931
VERSION      AR264931.1 GI:29693318
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
             Yokomaku,T., Koyama,O. and Furusho,K.
TITLE        Method for determining a concentration of target nucleic acid
             molecules, nucleic acid probes for the method, and method for
             analyzing data obtained by the method
JOURNAL      Patent: US 6492121-A 15 10-DEC-2002;
             Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="genomic DNA"
Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTT 1177

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Best Local Similarity 93.8%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177  
|||||  
Db 18 ATATATATTTTTTTT 3

RESULT 438  
BD145039/c  
LOCUS  
DEFINITION  
Method for assaying nucleic acid, nucleic acid probe used therefor,  
and method for analyzing data obtained by that method.

ACCESSION  
BD145039

VERSION  
BD145039.1 GI:27850797

KEYWORDS  
JP 2002119291-A/20.

SOURCE  
synthetic construct

ORGANISM  
other sequences; artificial sequences.

REFERENCE  
1 (bases 1 to 18)

AUTHORS  
Kurane, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,

TITLE  
Method for assaying nucleic acid, nucleic acid probe used therefor,

and method for analyzing data obtained by that method

PATENT: JP 2002119291-A 20 23-APR-2002;

JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED

INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD

OS Artificial Sequence

PN JP 2002119291-A/20

PD 23-APR-2002

PF 27-APR-2001 JP 2001133529

PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI

TORIMURA,

PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC

C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC

53,

PC G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,

PC G01N1/28,

PC G01N1/28,

CC The base sequence was prepared synthetically on the aim of CC

examining the

decrease in fluorescence emission of

a nucleic acid probe labeled with BODIBY FL/C6 upon the CC

hybridization of

the probe with a target nucleic acid.

Key Location/Qualifiers

FT source 1..18

/organism='Artificial Sequence'.

FEATURES

source

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/mol\_type='genomic DNA'

/db\_xref='taxon:32630'

Query Match 0.3%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 3.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177

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Db 18 ATATATATTTTTTTT 3

RESULT 439

BD166035/c

LOCUS

DEFINITION

Novel nucleic acid probes, method for determining concentrations of

nucleic acid by using the probes, and method for analyzing data

obtained by the method.

ACCESSION

BD166035

VERSION

BD166035.1 GI:27871847

KEYWORDS

JP 2002191372-A/15.

SOURCE

unidentified

ORGANISM  
unidentified

REFERENCE

1 (bases 1 to 18)

AUTHORS

Kurane, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,

Yamada, K. and Yokomaku, T.

TITLE

Novel nucleic acid probes, method for determining concentrations of

nucleic acid by using the probes, and method for analyzing data

obtained by the method

PATENT: JP 2002191372-A 15 09-JUL-2002;

NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,

KANKYO ENGINEERING CO LTD

OS Artificial Sequence

PN JP 2002191372-A/15

PD 09-JUL-2002

PF 26-SEP-2001 JP 2001295145

PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI

TORIMURA,

PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC

C12N15/09, C12M1/00, C12Q1/68, G01N33/58//G01N33/53, G01N33/566, PC

C12N15/00

CC The base sequence was prepared synthetically on the aim of CC

examining the

decrease in fluorescence emission of a nucleic acid probe CC

labeled with

BODIBY FL/C6 upon the hybridization of the

probe with a target

nucleic

acid.

Key Location/Qualifiers

FT source 1..18

/organism='Artificial Sequence'.

FEATURES

source

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Best Local Similarity 93.8%; Pred. No. 3.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTTTCTT 1177

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Db 18 ATATATATTTTTTTT 3

RESULT 440

BD166036/c

LOCUS

DEFINITION

Novel nucleic acid probes, method for determining concentrations of

nucleic acid by using the probes, and method for analyzing data

obtained by the method.

ACCESSION

BD166036

VERSION

BD166036.1 GI:27871848

KEYWORDS

JP 2002191372-A/16.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 18)

AUTHORS

Kurane, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,

Yamada, K. and Yokomaku, T.

TITLE

Novel nucleic acid probes, method for determining concentrations of

nucleic acid by using the probes, and method for analyzing data

obtained by the method

PATENT: JP 2002191372-A 16 09-JUL-2002;

NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,

KANKYO ENGINEERING CO LTD

OS Artificial Sequence

PN JP 2002191372-A/16

PD 09-JUL-2002

PF 26-SEP-2001 JP 2001295145

PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI

TORIMURA,



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REFERENCE
AUTHORS      1 (bases 1 to 18)
              Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
              Yamada,K. and Yokomaku,T.
TITLE        Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method
JOURNAL      Patent: JP 2002119291-A 16 23-APR-2002;
              JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
              INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT      OS Artificial Sequence
              PN JP 2002119291-A/16
              PD 23-APR-2002
              PF 27-APR-2001 JP 2001133529
              PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
              TORIMURA,
              PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
              C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
              53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
              PC G01N1/28,
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 436
BD145037/c
LOCUS      18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method.
ACCESSION  BD145037
VERSION     BD145037.1 GI:27850795
KEYWORDS   JP 2002119291-A/18.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
              Yamada,K. and Yokomaku,T.
TITLE        Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method
JOURNAL      Patent: JP 2002119291-A 18 23-APR-2002;
              JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
              INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT      OS Artificial Sequence
              PN JP 2002119291-A/18
              PD 23-APR-2002
              PF 27-APR-2001 JP 2001133529
              PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
              TORIMURA,
              PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
              C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
              53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
              PC G01N1/28,
              PC G01N1/28
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Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 436
BD145036/c
LOCUS      18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method.
ACCESSION  BD145036
VERSION     BD145036.1 GI:27850794
KEYWORDS   JP 2002119291-A/17.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
              Yamada,K. and Yokomaku,T.
TITLE        Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method
JOURNAL      Patent: JP 2002119291-A 17 23-APR-2002;
              JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
              INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT      OS Artificial Sequence
              PN JP 2002119291-A/17
              PD 23-APR-2002
              PF 27-APR-2001 JP 2001133529
              PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
              TORIMURA,
              PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
              C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
              53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
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              PC G01N1/28
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              decrease in fluorescence emission of
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PC G01N1/28,
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decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
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Query Match 0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177
Db 18 ATATATATTTTCTT 3

RESULT 437
BD145037/c
LOCUS      18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method.
ACCESSION  BD145037
VERSION     BD145037.1 GI:27850795
KEYWORDS   JP 2002119291-A/18.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS      Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
              Yamada,K. and Yokomaku,T.
TITLE        Method for assaying nucleic acid, nucleic acid probe used therefor,
              and method for analyzing data obtained by that method
JOURNAL      Patent: JP 2002119291-A 18 23-APR-2002;
              JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
              INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT      OS Artificial Sequence
              PN JP 2002119291-A/18
              PD 23-APR-2002
              PF 27-APR-2001 JP 2001133529
              PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
              TORIMURA,
              PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
              C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
              53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,
              PC G01N1/28,
              PC G01N1/28
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              decrease in fluorescence emission of
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2138 CTACTGCTTTAGAAAT 2153
Db 17 CTACTGCTTTAGAGAT 2

RESULT 431
AX761129/c
LOCUS AX761129 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 4450 from Patent WO03040369.
ACCESSION AX761129
VERSION AX761129.1 GI:32255745
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 4450 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2649 AACTGGCATCTGAGAT 2664
Db 17 AATGGCATCTGAGAT 2

RESULT 432
AX781716
LOCUS AX781716 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 47 from Patent WO03050284.
ACCESSION AX781716
VERSION AX781716.1 GI:32949550
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 47 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
Location/Qualifiers
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Query Match
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 616 CGCGCGGCACGCACG 631
Db 17 TATTTATGTAATATC 16

RESULT 435
BD145035/c
LOCUS BD145035 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145035
VERSION BD145035.1 GI:27850793
KEYWORDS JP 2002119291-A/16.
SOURCE synthetic construct
ORGANISM synthetic sequences; artificial sequences.
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Db 2 CGCGCGGCACGCACG 17

RESULT 433
AX781717
LOCUS AX781717 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 48 from Patent WO03050284.
ACCESSION AX781717
VERSION AX781717.1 GI:32949551
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 48 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
Location/Qualifiers
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Query Match
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 CGCGCGGCACGCACG 16

RESULT 434
AR078640
LOCUS AR078640 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 19 from patent US 5962673.
ACCESSION AR078640
VERSION AR078640.1 GI:10005386
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Monia,B.P. and Cowsert,L.M.
TITLE Antisense modulation of inhibitor-kappa B kinase-alpha expression
JOURNAL Patent: US 5962673-A 19 05-OCT-1999;
Location/Qualifiers
source
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3727 TATTTATGTAATATC 3742
Db 1 TATTTATGTAATATC 16

RESULT 435
BD145035/c
LOCUS BD145035 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145035
VERSION BD145035.1 GI:27850793
KEYWORDS JP 2002119291-A/16.
SOURCE synthetic construct
ORGANISM synthetic sequences; artificial sequences.
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion,  
apoptosis and/or viral resistance phenomena and their use as  
medicines  
JOURNAL Patent: WO 03040369-A 388 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
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Best Local Similarity 93.8%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 833 GATCAGCCACTCCGCA 848  
Db 1 GATCAGCCACCCGCA 16  
RESULT 427  
AX757780  
LOCUS AX757780 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 1101 from Patent WO03040369.  
ACCESSION AX757780  
VERSION AX757780.1 GI:32252396  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion,  
apoptosis and/or viral resistance phenomena and their use as  
medicines  
JOURNAL Patent: WO 03040369-A 1101 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
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Best Local Similarity 93.8%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 821 GATCGGAGTTCAGATC 836  
Db 1 GATCTGAGTTCAGATC 16  
RESULT 428  
AX757892/c  
LOCUS AX757892 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 1213 from Patent WO03040369.  
ACCESSION AX757892  
VERSION AX757892.1 GI:32252508  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion,

apoptosis and/or viral resistance phenomena and their use as  
medicines  
JOURNAL Patent: WO 03040369-A 1213 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2803 AAAAAAACAATC 2818  
Db 16 AAAAAAACAATC 1  
RESULT 429  
AX759064/c  
LOCUS AX759064 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 2385 from Patent WO03040369.  
ACCESSION AX759064  
VERSION AX759064.1 GI:32253680  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion,  
apoptosis and/or viral resistance phenomena and their use as  
medicines  
JOURNAL Patent: WO 03040369-A 2385 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 17 AGCTTTCCATATGAT 2  
RESULT 430  
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LOCUS AX759785 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 3106 from Patent WO03040369.  
ACCESSION AX759785  
VERSION AX759785.1 GI:32254401  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion,  
apoptosis and/or viral resistance phenomena and their use as  
medicines  
JOURNAL Patent: WO 03040369-A 3106 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 821 GATCGAGTTCAGATC 836  
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Db 1 GATCTGAGTTCAGATC 16

RESULT 422  
AX737597/c  
LOCUS AX737597 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 3187 from Patent WO03025177.  
ACCESSION AX737597  
VERSION AX737597.1 GI:30516885  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.  
AUTHORS Sequences involved in phenomena of tumour suppression, tumour  
TITLE reversion, apoptosis and/or resistance to viruses and the use  
thereof as medicaments  
JOURNAL Patent: WO 03025177-A 3187 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 167 TGGCGAGAGGATC 182  
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Db 16 TGGGAGAGGATC 1

RESULT 423  
AX738493/c  
LOCUS AX738493 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 4083 from Patent WO03025177.  
ACCESSION AX738493  
VERSION AX738493.1 GI:30517781  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.  
AUTHORS Sequences involved in phenomena of tumour suppression, tumour  
TITLE reversion, apoptosis and/or resistance to viruses and the use  
thereof as medicaments  
JOURNAL Patent: WO 03025177-A 4083 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACATC 2818  
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Db 16 AAAAAAAAAAAGATC 1

RESULT 424  
AX739553  
LOCUS AX739553 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 5143 from Patent WO03025177.  
ACCESSION AX739553  
VERSION AX739553.1 GI:30518850  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.  
AUTHORS Sequences involved in phenomena of tumour suppression, tumour  
TITLE reversion, apoptosis and/or resistance to viruses and the use  
thereof as medicaments  
JOURNAL Patent: WO 03025177-A 5143 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 821 GATCGAGTTCAGATC 836  
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Db 1 GATCTGAGTTCAGATC 16

RESULT 425  
AX739596/c  
LOCUS AX739596 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 5186 from Patent WO03025177.  
ACCESSION AX739596  
VERSION AX739596.1 GI:30518893  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.  
AUTHORS Sequences involved in phenomena of tumour suppression, tumour  
TITLE reversion, apoptosis and/or resistance to viruses and the use  
thereof as medicaments  
JOURNAL Patent: WO 03025177-A 5186 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 167 TGGCGAGAGGATC 182  
|||  
Db 16 TGAGGAGAGGATC 1

RESULT 426  
AX757067  
LOCUS AX757067 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 388 from Patent WO03040369.  
ACCESSION AX757067  
VERSION AX757067.1 GI:32251683  
KEYWORDS

|                       |            |                                       |                                    |                                    |                                    |
|-----------------------|------------|---------------------------------------|------------------------------------|------------------------------------|------------------------------------|
| AUTHORS               | source     | 1. .17                                | 0.3%; Score 14.4; DB 1; Length 17; | 0.3%; Score 14.4; DB 1; Length 17; | 0.3%; Score 14.4; DB 1; Length 17; |
| TITLE                 |            |                                       |                                    |                                    |                                    |
| JOURNAL               |            |                                       |                                    |                                    |                                    |
| FEATURES              |            |                                       |                                    |                                    |                                    |
| source                |            |                                       |                                    |                                    |                                    |
| Query Match           |            |                                       |                                    |                                    |                                    |
| Best Local Similarity |            |                                       |                                    |                                    |                                    |
| Matches               |            |                                       |                                    |                                    |                                    |
| Indels                |            |                                       |                                    |                                    |                                    |
| Gaps                  |            |                                       |                                    |                                    |                                    |
| QY                    | 2138       | CTACTGCTTTAGAGAT 2153                 | 17 bp DNA                          | linear                             | PAT 08-MAY-2003                    |
| Db                    | 17         | CTACTGCTTTAGAGAT 2                    |                                    |                                    |                                    |
| LOCUS                 | AX736066   | Sequence 1656 from Patent WO03025177. |                                    |                                    |                                    |
| DEFINITION            | AX736066   |                                       |                                    |                                    |                                    |
| ACCESSION             | AX736066   |                                       |                                    |                                    |                                    |
| VERSION               | AX736066.1 | GI:30515343                           |                                    |                                    |                                    |
| KEYWORDS              |            |                                       |                                    |                                    |                                    |
| SOURCE                |            |                                       |                                    |                                    |                                    |
| ORGANISM              |            |                                       |                                    |                                    |                                    |
| REFERENCE             |            |                                       |                                    |                                    |                                    |
| AUTHORS               |            |                                       |                                    |                                    |                                    |
| TITLE                 |            |                                       |                                    |                                    |                                    |
| JOURNAL               |            |                                       |                                    |                                    |                                    |
| FEATURES              |            |                                       |                                    |                                    |                                    |
| source                |            |                                       |                                    |                                    |                                    |
| Query Match           |            |                                       |                                    |                                    |                                    |
| Best Local Similarity |            |                                       |                                    |                                    |                                    |
| Matches               |            |                                       |                                    |                                    |                                    |
| Indels                |            |                                       |                                    |                                    |                                    |
| Gaps                  |            |                                       |                                    |                                    |                                    |
| QY                    | 512        | CCGGCCTCTGTGGATC 527                  | 17 bp DNA                          | linear                             | PAT 08-MAY-2003                    |
| Db                    | 16         | CCGGCCTCTGTGGATC 1                    |                                    |                                    |                                    |
| LOCUS                 | AX736332   | Sequence 1922 from Patent WO03025177. |                                    |                                    |                                    |
| DEFINITION            | AX736332   |                                       |                                    |                                    |                                    |
| ACCESSION             | AX736332   |                                       |                                    |                                    |                                    |
| VERSION               | AX736332.1 | GI:30515609                           |                                    |                                    |                                    |
| KEYWORDS              |            |                                       |                                    |                                    |                                    |
| SOURCE                |            |                                       |                                    |                                    |                                    |
| ORGANISM              |            |                                       |                                    |                                    |                                    |
| REFERENCE             |            |                                       |                                    |                                    |                                    |
| AUTHORS               |            |                                       |                                    |                                    |                                    |
| TITLE                 |            |                                       |                                    |                                    |                                    |
| JOURNAL               |            |                                       |                                    |                                    |                                    |
| FEATURES              |            |                                       |                                    |                                    |                                    |
| source                |            |                                       |                                    |                                    |                                    |
| Query Match           |            |                                       |                                    |                                    |                                    |
| Best Local Similarity |            |                                       |                                    |                                    |                                    |
| Matches               |            |                                       |                                    |                                    |                                    |
| Indels                |            |                                       |                                    |                                    |                                    |
| Gaps                  |            |                                       |                                    |                                    |                                    |
| QY                    | 1727       | GATCCTTAATCCAA 1742                   | 17 bp DNA                          | linear                             | PAT 08-MAY-2003                    |
| Db                    | 1          | GATCCTTAATCCAA 16                     |                                    |                                    |                                    |
| LOCUS                 | AX735212   | Sequence 802 from Patent WO03025177.  |                                    |                                    |                                    |
| DEFINITION            | AX735212   |                                       |                                    |                                    |                                    |
| ACCESSION             | AX735212   |                                       |                                    |                                    |                                    |
| VERSION               | AX735212.1 | GI:30514489                           |                                    |                                    |                                    |
| KEYWORDS              |            |                                       |                                    |                                    |                                    |
| SOURCE                |            |                                       |                                    |                                    |                                    |
| ORGANISM              |            |                                       |                                    |                                    |                                    |
| REFERENCE             |            |                                       |                                    |                                    |                                    |
| AUTHORS               |            |                                       |                                    |                                    |                                    |
| TITLE                 |            |                                       |                                    |                                    |                                    |
| JOURNAL               |            |                                       |                                    |                                    |                                    |
| FEATURES              |            |                                       |                                    |                                    |                                    |
| source                |            |                                       |                                    |                                    |                                    |
| Query Match           |            |                                       |                                    |                                    |                                    |
| Best Local Similarity |            |                                       |                                    |                                    |                                    |
| Matches               |            |                                       |                                    |                                    |                                    |
| Indels                |            |                                       |                                    |                                    |                                    |
| Gaps                  |            |                                       |                                    |                                    |                                    |
| QY                    | 419        | GATCCTTAATCCAA 1742                   | 17 bp DNA                          | linear                             | PAT 08-MAY-2003                    |
| Db                    | 1          | GATCCTTAATCCAA 16                     |                                    |                                    |                                    |
| LOCUS                 | AX735212/c | Sequence 802 from Patent WO03025177.  |                                    |                                    |                                    |
| DEFINITION            | AX735212   |                                       |                                    |                                    |                                    |
| ACCESSION             | AX735212   |                                       |                                    |                                    |                                    |
| VERSION               | AX735212.1 | GI:30514489                           |                                    |                                    |                                    |
| KEYWORDS              |            |                                       |                                    |                                    |                                    |
| SOURCE                |            |                                       |                                    |                                    |                                    |
| ORGANISM              |            |                                       |                                    |                                    |                                    |
| REFERENCE             |            |                                       |                                    |                                    |                                    |
| AUTHORS               |            |                                       |                                    |                                    |                                    |
| TITLE                 |            |                                       |                                    |                                    |                                    |
| JOURNAL               |            |                                       |                                    |                                    |                                    |
| FEATURES              |            |                                       |                                    |                                    |                                    |
| source                |            |                                       |                                    |                                    |                                    |
| Query Match           |            |                                       |                                    |                                    |                                    |
| Best Local Similarity |            |                                       |                                    |                                    |                                    |
| Matches               |            |                                       |                                    |                                    |                                    |
| Indels                |            |                                       |                                    |                                    |                                    |
| Gaps                  |            |                                       |                                    |                                    |                                    |
| QY                    | 3599       | TTTTTTTTTAATGATC 3614                 | 17 bp DNA                          | linear                             | PAT 08-MAY-2003                    |
| Db                    | 16         | TTTTTTTTTAATGATC 1                    |                                    |                                    |                                    |
| LOCUS                 | AX733221   | Sequence 4855 from Patent WO03025175. |                                    |                                    |                                    |
| DEFINITION            | AX733221   |                                       |                                    |                                    |                                    |
| ACCESSION             | AX733221   |                                       |                                    |                                    |                                    |
| VERSION               | AX733221.1 | GI:30512564                           |                                    |                                    |                                    |
| KEYWORDS              |            |                                       |                                    |                                    |                                    |
| SOURCE                |            |                                       |                                    |                                    |                                    |
| ORGANISM              |            |                                       |                                    |                                    |                                    |
| REFERENCE             |            |                                       |                                    |                                    |                                    |
| AUTHORS               |            |                                       |                                    |                                    |                                    |
| TITLE                 |            |                                       |                                    |                                    |                                    |
| JOURNAL               |            |                                       |                                    |                                    |                                    |
| FEATURES              |            |                                       |                                    |                                    |                                    |
| source                |            |                                       |                                    |                                    |                                    |
| Query Match           |            |                                       |                                    |                                    |                                    |

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Db          ||||| ||||| ||||| ||||| |||||
2 ATCTACCTGCCTGTA 17

RESULT 413
AX674166
LOCUS      AX674166          17 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 2611 from Patent WO03004526.
ACCESSION AX674166
VERSION    AX674166.1 GI:29332514
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL    Patent: WO 03004526-A 2611 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1. .17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2798 ATGTGAAAAAATAAAA 2813
Db      ||||| ||||| ||||| ||||| |||||

RESULT 414
AX676082
LOCUS      AX676082          17 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 35 from Patent WO02059381.
ACCESSION AX676082
VERSION    AX676082.1 GI:29333766
KEYWORDS
SOURCE     Mus sp.
ORGANISM   Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Slaugenhaupt,S. and Gusella,J.F.
TITLE      Gene for identifying individuals with familial dysautonomia
JOURNAL    Patent: WO 02059381-A 35 01-AUG-2002;
            The General Hospital Corporation (US)
FEATURES   Location/Qualifiers
            source
            1. .17
                /organism="Mus sp."
                /mol_type="unassigned DNA"
                /db_xref="taxon:10095"

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2745 TTTTCTTTTCTTAAAGGA 2760
Db      TTTTCTTTTCTTAAAGGA 17

RESULT 415
AX724450
LOCUS      AX724450          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2137 from Patent WO03025176.
ACCESSION AX724450
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VERSION
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025176-A 2137 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1. .17
                /organism="Mus musculus"
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Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      821 GATCGGAGTTCAGATC 836
Db      ||||| ||||| ||||| ||||| |||||
            1 GATCTGAGTTCAGATC 16

RESULT 416
AX726113
LOCUS      AX726113          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 3800 from Patent WO03025176.
ACCESSION AX726113
VERSION    AX726113.1 GI:30505456
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025176-A 3800 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
            source
            1. .17
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                /db_xref="taxon:10090"

Query Match      0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2566 ATCAGTGTCTTAAAAAAA 2581
Db      ||||| ||||| ||||| ||||| |||||
            2 ATCAGTCTTTAAAAAAA 17

RESULT 417
AX726611/c
LOCUS      AX726611/c          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 4298 from Patent WO03025176.
ACCESSION AX726611
VERSION    AX726611.1 GI:30505954
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1
```

```
Unclassified.
1 (bases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 656127-A 6425 20-MAY-2003;
Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCACGCGAC 1828
Db 1 TCTCCTTCACGCGAC 16

RESULT 409
AX214791
LOCUS AX214791 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 233 from Patent WO0159103.
ACCESSION AX214791
VERSION AX214791.1 GI:15524834
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Blatt,L., McSwiggen,J. and Chowrira,B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 233 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
1. .17
source
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1587 AGACCTTACTTCAGAA 1602
Db 2 AGATCCTTACTTCAGAA 17

RESULT 410
AX227570
LOCUS AX227570 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 942 from Patent WO0157206.
ACCESSION AX227570
VERSION AX227570.1 GI:15556711
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
AUTHORS Method and reagent for the inhibition of checkpoint kinase-1 (chk
TITLE 1) enzyme
JOURNAL Patent: WO 0157206-A 942 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
1. .17
source
/organism="synthetic construct"
/mol_type="unassigned RNA"

Unclassified.
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 932 AAAAAAAAAACAACCT 947
Db 1 AAAAAAAAAACATACCT 16

RESULT 411
AX671893
LOCUS AX671893 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 338 from Patent WO03004526.
ACCESSION AX671893
VERSION AX671893.1 GI:29330241
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
1 Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 338 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
1. .17
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4072 AGCACCTTTTCTTTTA 4087
Db 2 ATCACCTTTTCTTTTA 17

RESULT 412
AX673880
LOCUS AX673880 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2325 from Patent WO03004526.
ACCESSION AX673880
VERSION AX673880.1 GI:29332228
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
1 Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 2325 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
1. .17
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3713 ATCTTCCTCCTCGTA 3728
Db 3713 ATCTTCCTCCTCGTA 3728
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ACCESSION I37568
VERSION 137568.1 GI:2085528
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
          Stinchcomb,D.T.
TITLE Stromelysin targeted ribozymes
JOURNAL Patent: US 5612215-A 581 18-MAR-1997;
FEATURES Location/Qualifiers
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              /mol_type="unassigned DNA"
          Query Match 0.3%; Score 14.4; DB 1; Length 17;
          Best Local Similarity 93.8%; Pred. No. 3.2e+02;
          Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1034 TTCTTTTAAAGGAA 1049
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      1 TTCAATTTTAAAGGAA 16
Db

RESULT 399
I54412
LOCUS
DEFINITION Sequence 2153 from patent US 5646042.
ACCESSION I54412
VERSION I54412.1 GI:2475615
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2153 08-JUL-1997;
FEATURES Location/Qualifiers
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            1..17
              /organism="unknown"
              /mol_type="unassigned DNA"
          Query Match 0.3%; Score 14.4; DB 1; Length 17;
          Best Local Similarity 93.8%; Pred. No. 3.2e+02;
          Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

I54412
LOCUS
DEFINITION Sequence 2153 from patent US 5646042.
ACCESSION I54412
VERSION I54412.1 GI:2475615
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2153 08-JUL-1997;
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              /organism="unknown"
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AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2159 08-JUL-1997;
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AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
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AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 2161 08-JUL-1997;
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AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
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TITLE Method of reducing stromelysin RNA via ribozymes
JOURNAL Patent: US 5731295-A 578 24-MAR-1998;
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| AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J. |  |  |  |  |  |  |  |  |  |
| TITLE Methods and reagents for HLA DRbeta DNA typing           |  |  |  |  |  |  |  |  |  |
| JOURNAL Patent: US 5567809-A 155 22-OCT-1996;                  |  |  |  |  |  |  |  |  |  |
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| AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and  |  |  |  |  |  |  |  |  |  |
| Stinchcomb,D.T.  |  |  |  |  |  |  |  |  |  |
| TITLE Stromelysin targeted ribozymes                           |  |  |  |  |  |  |  |  |  |
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unclassified.  
1 (bases 1 to 17)  
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
Regulation of repressor genes using nucleic acid molecules  
Patent: JP 2002541795-A 3062 10-DEC-2002;  
RIBOZYME PHARMACEUTICALS INC  
OS Eukaryote  
PN JP 2002541795-A/3062  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
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PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
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PC (C12N5/00,C12R1:91)  
PC Regulation of repressor genes using nucleic acid molecules FH  
CC Regulation of repressor genes using nucleic acid molecules FH  
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DEFINITION Regulation of repressor genes using nucleic acid molecules.  
ACCESSION BD255585  
VERSION BD255585.1 GI:33065355  
KEYWORDS JP 2002541795-A/3378.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
TITLE Regulation of repressor genes using nucleic acid molecules  
JOURNAL Patent: JP 2002541795-A 3378 10-DEC-2002;  
RIBOZYME PHARMACEUTICALS INC  
COMMENT OS Eukaryote  
PN JP 2002541795-A/3378  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC  
C12P21/02,  
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PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
PC A61K37/02,  
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QY 1620 TCAACAATGGAGAAAA 1635  
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LOCUS 17 bp DNA linear PAT 17-JUL-2003  
DEFINITION Regulation of repressor genes using nucleic acid molecules.  
ACCESSION BD257465  
VERSION BD257465.1 GI:33067235  
KEYWORDS JP 2002541795-A/5258.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
TITLE Regulation of repressor genes using nucleic acid molecules  
JOURNAL Patent: JP 2002541795-A 5258 10-DEC-2002;  
RIBOZYME PHARMACEUTICALS INC  
COMMENT OS Eukaryote  
PN JP 2002541795-A/5258  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
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PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
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DEFINITION Regulation of repressor genes using nucleic acid molecules.  
ACCESSION BD258537  
VERSION BD258537.1 GI:33068307  
KEYWORDS JP 2002541795-A/6330.  
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ORGANISM unidentified  
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VERSION AR029903.1 GI:5943117
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 92 19-JAN-1999;
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LOCUS AR029906 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 95 from patent US 5861244.
ACCESSION AR029906
VERSION AR029906.1 GI:5943120
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 95 19-JAN-1999;
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DEFINITION Sequence 2153 from patent US 5817796.
ACCESSION AR047360
VERSION AR047360.1 GI:5968825
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL Patent: US 5817796-A 2153 06-OCT-1998;
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RESULT 389
AR047366
LOCUS AR047366 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2159 from patent US 5817796.
ACCESSION AR047366
VERSION AR047366.1 GI:5968831
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL Patent: US 5817796-A 2159 06-OCT-1998;
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 390
AR047368
LOCUS AR047368 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2161 from patent US 5817796.
ACCESSION AR047368
VERSION AR047368.1 GI:5968833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL Patent: US 5817796-A 2161 06-OCT-1998;
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QY 1156 TTTTATATATATTT 1171
Db 1 TTTTATATATATATGT 16
RESULT 391
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LOCUS BD255269 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255269
VERSION BD255269.1 GI:33065039
KEYWORDS JP 2002541795-A/3062.
SOURCE unidentified
ORGANISM unidentified
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Db 16 CTCCTACAGACTGGAG 1  
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DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD065915  
VERSION BD065915.1 GI:22611518  
KEYWORDS JP 2001511000-A/550.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 550 07-AUG-2001;  
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
OS Unknown  
PN JP 2001511000-A/550  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
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ACCESSION BD066595  
VERSION BD066595.1 GI:22612198  
KEYWORDS JP 2001511000-A/1230.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.

TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 1230 07-AUG-2001;  
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
OS Unknown  
PN JP 2001511000-A/1230  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
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PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
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DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066607  
VERSION BD066607.1 GI:22612210  
KEYWORDS JP 2001511000-A/1242.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 1242 07-AUG-2001;  
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
OS Unknown  
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PD 07-AUG-2001  
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PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
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DEFINITION An antisense oligonucleotide preparation method.  
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REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.

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ACCESSION AX030145
VERSION AX030145.1 GI:10190362
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-52 (tgf-52)
JOURNAL Patent: EP 1008649-A 107 14-JUN-2000;
BIOGNOSTIK GBS (DE)
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DEFINITION Sequence 94 from Patent EP1160319.
ACCESSION AX316453
VERSION AX316453.1 GI:17899626
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 94 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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Db 16 CACCATAAAGACAGCA 1
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AX316466/c
LOCUS AX316466 16 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 107 from Patent EP1160319.
ACCESSION AX316466
VERSION AX316466.1 GI:17899639
KEYWORDS
SOURCE unidentified
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REFERENCE 1
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AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 107 05-DEC-2001;
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AX419943/c
LOCUS AX419943 16 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 280 from Patent WO0198537.
ACCESSION AX419943
VERSION AX419943.1 GI:21524310
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 280 27-DEC-2001;
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Db 16 TGGGAGAGAAACACAG 1
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LOCUS BD065908 16 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065908
VERSION BD065908.1 GI:22611511
KEYWORDS JP 2001511000-A/543.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 543 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/543
PD 07-AUG-2001
PR 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
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AUTHORS Brysch,W.D. and Schlingensiepen,K.D.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: EP 0856579-A 543 05-AUG-1998;  
BIOGNOSTIK GES (DE)  
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ACCESSION A90369  
VERSION A90369.1 GI:6738883  
KEYWORDS  
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REFERENCE 1 (bases 1 to 16)  
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: EP 0856579-A 550 05-AUG-1998;  
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REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
JOURNAL Patent: US 6455689-A 94 24-SEP-2002;  
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ACCESSION AR232850  
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SOURCE Unknown.  
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REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
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Db 16 CCTGCTAAATGTTATTG 1  
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LOCUS AX030132/c  
DEFINITION Sequence 94 from Patent EP1008649.  
ACCESSION AX030132  
VERSION AX030132.1 GI:10190349  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE  
JOURNAL Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2(tgf-b2)  
Patent: EP 1008649-A 94 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
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DEFINITION Sequence 107 from Patent EP1008649.

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RESULT 369
A88395/c
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DEFINITION Sequence 543 from Patent WO9833904.
ACCESSION A88395
VERSION A88395.1 GI:6736965
KEYWORDS
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    Brysch,W. and Schlingensiepen,K.
  TITLE
    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL
    Patent: WO 9833904-A 543 06-AUG-1998;
    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
  FEATURES
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  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2078 CTCTACAGACTGGAG 2093
Db 16 CTCTACAGACTTGAG 1

RESULT 370
A88402/c
LOCUS A88402 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 550 from Patent WO9833904.
ACCESSION A88402
VERSION A88402.1 GI:6736972
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
    Brysch,W. and Schlingensiepen,K.
  TITLE
    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL
    Patent: WO 9833904-A 550 06-AUG-1998;
    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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        /db_xref="taxon:32644"

Query Match
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  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2245 CTAACCTCTGCTGG 2260
Db 16 CCAACTCTGCTGTTG 1
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RESULT 371
A89082/c
LOCUS A89082 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1230 from Patent WO9833904.
ACCESSION A89082
VERSION A89082.1 GI:6737652
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
    Brysch,W. and Schlingensiepen,K.
  TITLE
    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL
    Patent: WO 9833904-A 1230 06-AUG-1998;
    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Qy 1851 CACCACAAGACAGGA 1866
Db 16 CACCATAAGACAGGA 1

RESULT 372
A89094/c
LOCUS A89094 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1242 from Patent WO9833904.
ACCESSION A89094
VERSION A89094.1 GI:6737664
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
    Brysch,W. and Schlingensiepen,K.
  TITLE
    AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL
    Patent: WO 9833904-A 1242 06-AUG-1998;
    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match
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  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2060 CCTGCTAATGTTGTTG 2075
Db 16 CCTGCTAATGTTATTG 1

RESULT 373
A90362/c
LOCUS A90362 16 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 543 from Patent EP0856579.
ACCESSION A90362
VERSION A90362.1 GI:6738876
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unclassified.
  REFERENCE
    1 (bases 1 to 16)
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Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2914 CTGCAGTGGTGCCCTCC 2931
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Db 18 CTGCAGTAGTGCCCAACC 1

RESULT 365
BD107508/c
LOCUS BD107508 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107508
VERSION BD107508.1 GI:23202326
KEYWORDS JP 200200275-A/17,
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 200200275-A 17 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 200200275-A/17
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
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/mol_type='synthetic construct'
/db_xref='taxon:32630'

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179
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Db 18 ATATATATTTTCTTTC 1

RESULT 366
ASE250931/c
LOCUS ASE250931 18 bp RNA linear SYN 17-NOV-1999
DEFINITION Artificial oligonucleotide antisense primer sequence for Homo
sapiens beta3-adrenoceptor.
ACCESSION AJ250931
VERSION AJ250931.1 GI:6453302
KEYWORDS beta3-adrenoceptor; oligonucleotide; primer.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bardou,M.Y. and Loustalot,C.
TITLE Evidence for a role of beta3-adrenoceptor in inhibition of human

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term myometrium spontaneous contractions
Unpublished
REFERENCE 2 (bases 1 to 18)
AUTHORS Bardou,M.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-1999) Bardou M., Lppce, Faculty of Medicine of
Dijon, 7, bd Jeanne d'Arc BP 87900, 21079 Dijon cedex, FRANCE
FEATURES
source 1..18
/organism='synthetic construct'
/mol_type='other RNA'
/db_xref='taxon:32630'
/notes='synthetic oligonucleotide'
misc_feature complement(1..18)
/notes='PCR antisense primer for Homo sapiens
beta3-adrenoceptor'

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 723 AGCCCGCGCGAGCCCGG 740
||||| ||||||| |||
Db 18 AGCCGAGCGAGCCCGG 1

RESULT 367
A40557/c
LOCUS A40557 16 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 94 from Patent WO9425578.
ACCESSION A40557
VERSION A40557.1 GI:2296592
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS
TITLE
JOURNAL
FEATURES
source 1..16
/organism='unidentified'
/mol_type='unassigned DNA'
/db_xref='taxon:32644'

Query Match 0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1851 CACCACAAACAGGAGGA 1866
||||| ||||||| |||
Db 16 CACCATAAGACAGGA 1

RESULT 368
A40570/c
LOCUS A40570 16 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 107 from Patent WO9425578.
ACCESSION A40570
VERSION A40570.1 GI:2296605
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS
TITLE
JOURNAL

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/db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2375 ACCATGACCATTCCTCA 2392
DB 18 ACCTCTAACCATTCCTCA 1

RESULT 362
BD066632/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066632
VERSION     BD066632.1 GI:22612235
KEYWORDS   JP 2001511000-A/1267.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Schlingensiepen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 1267 07-AUG-2001;
          BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
          PN JP 2001511000-A/1267
          PD 07-AUG-2001
          PF 30-JAN-1998 JP 1998532533
          PR 31-JAN-1997 EP 97101531.8
          PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
          PC C12N15/11.C07H21/04.A61K31/70
          CC An antisense oligonucleotide preparation method FH Key
          FT source
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             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTCTTAC 1179
DB 18 ATATATATTTTCTTCTTAC 1

RESULT 364
BD104178/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION  BD104178
VERSION     BD104178.1 GI:22649752
KEYWORDS   WO 0192572-A/282.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
          Nishida,M.
TITLE      Kit and method for determining HLA type
JOURNAL    Patent: WO 0192572-A 282 06-DEC-2001;
          NISHINBO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO
          KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
          NISHIDA
COMMENT    OS Artificial Sequence
          PN WO 0192572-A/282
          PD 06-DEC-2001
          PF 01-JUN-2001 WO 2001JP004662
          PR 01-JUN-2000 JP 00P 164798
          PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI
          MATSUMURA,
          PI SHOGO MORIYA,MICHIO NISHIDA
          PC C12Q1/68.C12M1/00.C12N15/09.G01N33/53
          CC Description of Artificial Sequence:capture
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             Location/Qualifiers
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             /organism='Artificial Sequence'.
FEATURES             source
          source
          1..18
             Location/Qualifiers
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
Query Match      0.3%; Score 14.8; DB 1; Length 18;

QY 2439 GTCAAGTCTTGTAATGC 2456
DB 18 GTAAAGTCTTGCAATGC 1

RESULT 363
BD072881/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
          and method for analyzing data obtained by that method.
ACCESSION  BD072881
VERSION     BD072881.1 GI:22618484
KEYWORDS   JP 2001286300-A/19.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
          Yokomaki,F., Koyama,O. and Furusho,K.
TITLE      Method for assaying nucleic acid, nucleic acid probe used therefor,
          and method for analyzing data obtained by that method
JOURNAL    Patent: JP 2001286300-A 19 16-OCT-2001;
          JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
          NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
          AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT    OS Artificial Sequence
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SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 1221 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Unknown  
PN JP 2001511000-A/1221  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11.C07H21/04.A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
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/db\_xref='taxon:32644'

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGACGTATCAGA 1728  
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Db 18 GGATTGAGCTATATCAGA 1

RESULT 359  
BD066597/c  
LOCUS 18 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066597  
VERSION BD066597.1 GI:22612200  
KEYWORDS JP 2001511000-A/1232.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 1232 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Unknown  
PN JP 2001511000-A/1232  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11.C07H21/04.A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
Location/Qualifiers  
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Location/Qualifiers  
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/mol\_type='genomic DNA'  
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Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTACACTGCC 1897  
||||| ||||| |||||  
Db 18 AATAAGCTTACACTGTCC 1

RESULT 360  
BD066615/c  
LOCUS 18 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066615  
VERSION BD066615.1 GI:22612218  
KEYWORDS JP 2001511000-A/1250.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 1250 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Unknown  
PN JP 2001511000-A/1250  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11.C07H21/04.A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
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Location/Qualifiers  
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/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2175 CGCCCTCTTTACATTGAT 2192  
||||| ||||| |||||  
Db 18 CGTCCACTTTACATTGAT 1

RESULT 361  
BD066628/c  
LOCUS 18 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066628  
VERSION BD066628.1 GI:22612231  
KEYWORDS JP 2001511000-A/1263.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 1263 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Unknown  
PN JP 2001511000-A/1263  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11.C07H21/04.A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
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Location/Qualifiers  
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/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

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/db_xref="taxon:32630"
/note="Detection oligonucleotide for MSH4"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2808 AAAAAACATCAAAACAA 2825
      ||||| ||||| |||||
Db 18 AAAAAACCAACAAACAA 1

RESULT 355
BD064848
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA.
ACCESSION  BD064848
VERSION    BD064848.1 GI:22610451
KEYWORDS   JP 2001275678-A/60.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Kishimoto,I., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and
            Nishikawa,K.
TITLE      Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA
JOURNAL    Patent: JP 2001275678-A 60 09-OCT-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT    OS Artificial Sequence
            PN JP 2001275678-A/60
            PD 09-OCT-2001
            PF 31-MAR-2000 JP 2000096306
            PI TOSHIOKI KISHIMOTO, SHINICHIRO NIWA, YUKO MORI, SACHIYO PI
            MIWAKI, REI FUKUSHIMA,
            PI KAZUKO NISHIKAWA
            PC C12N15/09, C12N5/10, C12Q1/00, C12Q1/68, C12N15/00, C12N5/00 CC
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            FH Key
            FT source
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FEATURES
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 573 GGGGGCGCATCTGCCTCCC 590
      ||||| ||||| |||||
Db 1 GGGGGCGCAGTCGCTGCC 18

RESULT 356
BD066574/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066574
VERSION    BD066574.1 GI:22612177
KEYWORDS   JP 2001511000-A/1209.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Schlingensiepen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 1209 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown

Qy 1527 TATAAAATCGACATGCCG 1544
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Db 18 TACAAATAGACATGCCG 1

RESULT 357
BD066580/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066580
VERSION    BD066580.1 GI:22612183
KEYWORDS   JP 2001511000-A/1215.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Schlingensiepen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 1215 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
            PN JP 2001511000-A/1215
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
            PC C12N15/11, C07H21/04, A61K31/70
            CC An antisense oligonucleotide preparation method FH
            Location/Qualifiers
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            /organism='Unknown'.

FEATURES
    source
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        /organism="unidentified"
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGGTGA 1653
      ||||| ||||| |||||
Db 18 ATGCTTCCAATTGGTGA 1

RESULT 358
BD066586/c
LOCUS      18 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066586
VERSION    BD066586.1 GI:22612189
KEYWORDS   JP 2001511000-A/1221.
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SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE 1
AUTHORS     Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE       Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
JOURNAL     Patent: EP 1160319-A 115 05-DEC-2001;
            BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
  source    Location/Qualifiers
            1..18
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2175 CGCCCTCTTTACATTGAT 2192
Db 18 CGTCCACTTTACATTGAT 1

RESULT 351
AX316487/c
LOCUS      AX316487      18 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 128 from Patent EP1160319.
ACCESSION  AX316487
VERSION     AX316487.1 GI:17899660
KEYWORDS
SOURCE      .
ORGANISM    unidentified
            unclassified.
REFERENCE 1
AUTHORS     Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE       Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
JOURNAL     Patent: EP 1160319-A 128 05-DEC-2001;
            BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
  source    Location/Qualifiers
            1..18
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2375 ACCACTGACCATTTCTTA 2392
Db 18 ACCTTAACCATTTCTTA 1

RESULT 352
AX316491/c
LOCUS      AX316491      18 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 132 from Patent EP1160319.
ACCESSION  AX316491
VERSION     AX316491.1 GI:17899664
KEYWORDS
SOURCE      .
ORGANISM    unidentified
            unclassified.
REFERENCE 1
AUTHORS     Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE       Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
JOURNAL     Patent: EP 1160319-A 132 05-DEC-2001;
            BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
  source    Location/Qualifiers
            1..18
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2375 ACCACTGACCATTTCTTA 2392
Db 18 ACCTTAACCATTTCTTA 1

RESULT 353
AX822988/c
LOCUS      AX822988      18 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 880 from Patent EP1340818.
ACCESSION  AX822988
VERSION     AX822988.1 GI:39749624
KEYWORDS
SOURCE      .
ORGANISM    synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE 1
AUTHORS     Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
TITLE       Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
JOURNAL     Patent: EP 1340818-A 880 03-SEP-2003;
            Epigenomics AG (DE)
FEATURES
  source    Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Detection oligonucleotide for MSH4"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2808 AAAAAACATCAAAACAA 2825
Db 18 AAAAAACCAACCAAAACAA 1

RESULT 354
AX826628/c
LOCUS      AX826628      18 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 880 from Patent WO03072821.
ACCESSION  AX826628
VERSION     AX826628.1 GI:39752142
KEYWORDS
SOURCE      .
ORGANISM    synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE 1
AUTHORS     Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
TITLE       Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
JOURNAL     Patent: WO 03072821-A 880 04-SEP-2003;
            Epigenomics AG (DE)
FEATURES
  source    Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAAATCGACATGCCG 1544  
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Db 18 TACAAAATAGACATGCCG 1

RESULT 346  
AX316431/c  
LOCUS AX316431 18 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 72 from Patent EP1160319.  
ACCESSION AX316431  
VERSION AX316431.1 GI:17899604  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 72 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)

FEATURES  
source  
1..18  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAAATCGACATGCCG 1544  
| | | | | | | | | | | | | | | |  
Db 18 TACAAAATAGACATGCCG 1

RESULT 347  
AX316438/c  
LOCUS AX316438 18 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 79 from Patent EP1160319.  
ACCESSION AX316438  
VERSION AX316438.1 GI:17899611  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 79 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)

FEATURES  
source  
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/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGGTGA 1653  
| | | | | | | | | | | | | | | |  
Db 18 ATGCTTCGAATGGTGA 1

RESULT 348  
AX316444/c  
LOCUS AX316444 18 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 85 from Patent EP1160319.  
ACCESSION AX316444  
VERSION AX316444.1 GI:17899617  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 85 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)

FEATURES  
source  
1..18  
/organism="unidentified"  
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/db\_xref="taxon:32644"  
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAACGTATCAGA 1728  
| | | | | | | | | | | | | | | |  
Db 18 GGATTGAGCTATATCAGA 1

RESULT 349  
AX316455/c  
LOCUS AX316455 18 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 96 from Patent EP1160319.  
ACCESSION AX316455  
VERSION AX316455.1 GI:17899628  
KEYWORDS .  
SOURCE unidentified  
ORGANISM unclassified.

REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 96 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)

FEATURES  
source  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Description of unknown: unknown"

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTTACACTGCC 1897  
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Db 18 AATAAGCTTACACTGCC 1

RESULT 350  
AX316474/c  
LOCUS AX316474 18 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 115 from Patent EP1160319.  
ACCESSION AX316474  
VERSION AX316474.1 GI:17899647  
KEYWORDS .

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TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
JOURNAL    Patent: EP 1008649-A 131 14-JUN-2000;
FEATURES   BIOGNOSTIK GES (DE)
SOURCE     Location/Qualifiers
           1. .18
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2439  GTCAAGTCTTGTAATGC 2456
Db  18  GTAAAGTCTTGCAATGC 1

RESULT 342
AX047272
LOCUS      AX047272                18 bp      DNA      linear      PAT 15-DEC-2000
DEFINITION Sequence 22 from Patent WO0068422.
ACCESSION  AX047272
VERSION     AX047272.1 GI:11876552
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
           Gumbiowski,K. and Zulauf,M.
TITLE      High density labeling of dna with modified or chromophore carrying
           nucleotides and dna polymerases used
JOURNAL    Patent: WO 0068422-A 22 16-NOV-2000;
           Roche Diagnostics GmbH (DE)
FEATURES   Location/Qualifiers
           1. .18
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="second fragment of SEQ ID NO: 6"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  973  CCCCCCCCCACCGCCCC 990
Db  1  CCCCCCCCCCGCCCC 18

RESULT 343
AX047274/c
LOCUS      AX047274                18 bp      DNA      linear      PAT 15-DEC-2000
DEFINITION Sequence 24 from Patent WO0068422.
ACCESSION  AX047274
VERSION     AX047274.1 GI:11876554
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
           Gumbiowski,K. and Zulauf,M.
TITLE      High density labeling of dna with modified or chromophore carrying
           nucleotides and dna polymerases used
JOURNAL    Patent: WO 0068422-A 24 16-NOV-2000;
           Roche Diagnostics GmbH (DE)
FEATURES   Location/Qualifiers
           1. .18
           /organism="synthetic construct"
           /mol_type="unassigned DNA"

TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
JOURNAL    Patent: EP 1008649-A 131 14-JUN-2000;
FEATURES   BIOGNOSTIK GES (DE)
SOURCE     Location/Qualifiers
           1. .18
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  973  CCCCCCCCCACCGCCCC 990
Db  18  CCCCCCCCCCGCCCC 1

RESULT 344
AX191970/c
LOCUS      AX191970                18 bp      DNA      linear      PAT 15-AUG-2001
DEFINITION Sequence 122 from Patent WO0149833.
ACCESSION  AX191970
VERSION     AX191970.1 GI:15210119
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
           Ford,J.D. and Sarkanen,S.
TITLE      Recombinant pinorexinol/laricresinol reductase, recombinant
           dirigent protein, and methods of use
JOURNAL    Patent: WO 0149833-A 122 12-JUL-2001;
           Washington State University Research Foundation (US) ; REGENTS OF
           THE UNIVERSITY OF MINNESOTA (US)
FEATURES   Location/Qualifiers
           1. .18
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="oligonucleotide"
           /misc_feature 1. .18
           /note="Linker primer"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2577  AAAAAAAAAAATTTGGAG 2594
Db  18  AAAAAAAAAAATTCGAG 1

RESULT 345
AX252494/c
LOCUS      AX252494                18 bp      DNA      linear      PAT 05-OCT-2001
DEFINITION Sequence 4 from Patent WO0168146.
ACCESSION  AX252494
VERSION     AX252494.1 GI:15985765
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE      Mixture comprising an inhibitor or suppressor of a gene and a
           molecule binding to an expression product of that gene
JOURNAL    Patent: WO 0168146-A 4 20-SEP-2001;
           Biognostik Gesellschaft fuer biomolekulare Diagnostik mbH (DE)
FEATURES   Location/Qualifiers
           1. .18
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
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/db_xref="taxon:32630"
/note="second fragment of SEQ ID NO: 6"
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy  973  CCCCCCCCCACCGCCCC 990
Db  18  CCCCCCCCCCGCCCC 1
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RESULT 344
AX191970/c
LOCUS      AX191970                18 bp      DNA      linear      PAT 15-AUG-2001
DEFINITION Sequence 122 from Patent WO0149833.
ACCESSION  AX191970
VERSION     AX191970.1 GI:15210119
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
```

```

REFERENCE  1
AUTHORS    Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
           Ford,J.D. and Sarkanen,S.
TITLE      Recombinant pinorexinol/laricresinol reductase, recombinant
           dirigent protein, and methods of use
JOURNAL    Patent: WO 0149833-A 122 12-JUL-2001;
           Washington State University Research Foundation (US) ; REGENTS OF
           THE UNIVERSITY OF MINNESOTA (US)
FEATURES   Location/Qualifiers
           1. .18
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="oligonucleotide"
           /misc_feature 1. .18
           /note="Linker primer"
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy  2577  AAAAAAAAAAATTTGGAG 2594
Db  18  AAAAAAAAAAATTCGAG 1
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RESULT 345
AX252494/c
LOCUS      AX252494                18 bp      DNA      linear      PAT 05-OCT-2001
DEFINITION Sequence 4 from Patent WO0168146.
ACCESSION  AX252494
VERSION     AX252494.1 GI:15985765
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```

REFERENCE  1
AUTHORS    Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE      Mixture comprising an inhibitor or suppressor of a gene and a
           molecule binding to an expression product of that gene
JOURNAL    Patent: WO 0168146-A 4 20-SEP-2001;
           Biognostik Gesellschaft fuer biomolekulare Diagnostik mbH (DE)
FEATURES   Location/Qualifiers
           1. .18
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
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RESULT 337
AX030123/c
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 85 from Patent EP1008649.
ACCESSION  AX030123
VERSION     AX030123.1  GI:10190340
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn, U., Brysch, W., Schlingensiepen, G.F., Schlingensiepen, K.H.
            and Schlingensiepen, R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 85 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source          1..18
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1711 GGATTGAACTGATATCAGA 1728
Db      18  GGATTGAGCTATATCAGA 1
            ||||| || |||||
RESULT 338
AX030134/c
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 96 from Patent EP1008649.
ACCESSION  AX030134
VERSION     AX030134.1  GI:10190351
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn, U., Brysch, W., Schlingensiepen, G.F., Schlingensiepen, K.H.
            and Schlingensiepen, R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 96 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source          1..18
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1880 AATAAGTTTACACTGCC 1897
Db      18  AATAAGCTTACACTGTCC 1
            ||||| |||||
RESULT 339
AX030153/c
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 115 from Patent EP1008649.
ACCESSION  AX030153
VERSION     AX030153.1  GI:10190370
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn, U., Brysch, W., Schlingensiepen, G.F., Schlingensiepen, K.H.
            and Schlingensiepen, R.

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn, U., Brysch, W., Schlingensiepen, G.F., Schlingensiepen, K.H.
            and Schlingensiepen, R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 115 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source          1..18
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2175 GGCCTCTTTTACATTGAT 2192
Db      18  GGTCCACTTTACATTGAT 1
            ||||| |||||
RESULT 340
AX030166/c
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 128 from Patent EP1008649.
ACCESSION  AX030166
VERSION     AX030166.1  GI:10190383
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn, U., Brysch, W., Schlingensiepen, G.F., Schlingensiepen, K.H.
            and Schlingensiepen, R.
TITLE      Antisense-oligonucleotides for the treatment of immuno-suppressive
            effects of transforming growth factor-b2(tgf-b2)
JOURNAL    Patent: EP 1008649-A 128 14-JUN-2000;
            BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source          1..18
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2375 ACCACTGACCATCTCTTA 2392
Db      18  ACCTCTAACCATCTCTTA 1
            ||||| |||||
RESULT 341
AX030169/c
LOCUS      18 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION Sequence 131 from Patent EP1008649.
ACCESSION  AX030169
VERSION     AX030169.1  GI:10190386
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Bogdahn, U., Brysch, W., Schlingensiepen, G.F., Schlingensiepen, K.H.
            and Schlingensiepen, R.

```



```
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
  source
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGCTGA 1653
    ||||| ||||| |||||
Db 18 ATGCTTCCAATTGTGTGA 1

RESULT 333
AX008983/c
LOCUS AX008983 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 16 from Patent WO9963975.
ACCESSION AX008983
VERSION AX008983.1 GI:9996357
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 16 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
  source
    1. .18
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAACTGTATCAGA 1728
    ||||| ||||| |||||
Db 18 GGATTGACTATATCAGA 1

RESULT 334
AX009032/c
LOCUS AX009032 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 65 from Patent WO9963975.
ACCESSION AX009032
VERSION AX009032.1 GI:9996406
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 65 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
  source
    1. .18
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1462 CAAGCCGAGGCGGCGG 1479
    ||||| ||||| |||||
Db 18 CGAGCCGAGGCGGCGG 1

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 335
AX030110/c
LOCUS AX030110 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 72 from Patent EP1008649.
ACCESSION AX030110
VERSION AX030110.1 GI:10190327
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 72 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
  Location/Qualifiers
    source
      1. .18
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATTAATCGACATGCGG 1544
    ||||| ||||| |||||
Db 18 TACAAATAGACATGCGG 1

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 336
AX030117/c
LOCUS AX030117 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 79 from Patent EP1008649.
ACCESSION AX030117
VERSION AX030117.1 GI:10190334
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 79 14-JUN-2000;
BIOGNOSTIK GES (DE)
FEATURES
  Location/Qualifiers
    source
      1. .18
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGCTGA 1653
    ||||| ||||| |||||
Db 18 ATGCTTCCAATTGTGTGA 1
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QY 973 CCCCCCCCACCCGCCGCC 990  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.  
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method  
JOURNAL Patent: US 6492121-A 20 10-DEC-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

RESULT 328  
AR264936/c  
LOCUS AR264936 18 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 20 from patent US 6492121.  
ACCESSION AR264936  
VERSION AR264936.1 GI:29693323  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.  
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method  
JOURNAL Patent: US 6492121-A 20 10-DEC-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179  
Db 18 ATATATATTTTCTTTC 1

RESULT 329  
AR410329/c  
LOCUS AR410329 18 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 122 from patent US 6635459.  
ACCESSION AR410329  
VERSION AR410329.1 GI:40161608  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R., Sarikhan,S. and Ford,J.D.  
TITLE Nucleotide sequences encoding pinorexinol/laricetinol reductase proteins and their methods of use  
JOURNAL Patent: US 6635459-A 122 21-OCT-2003;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAAAAAATGGAG 2594  
Db 18 AAAAAAAAAAATCGAG 1

RESULT 330  
AR478217/c  
LOCUS AR478217 18 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 20 from patent US 6699661.  
ACCESSION AR478217  
VERSION AR478217.1 GI:47236865

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.  
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method  
JOURNAL Patent: US 6699661-A 20 02-MAR-2004;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTTAC 1179  
Db 18 ATATATATTTTCTTTC 1

RESULT 331  
AX008976/c  
LOCUS AX008976 18 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 9 from Patent WO9963975.  
ACCESSION AX008976  
VERSION AX008976.1 GI:9996350  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.  
TITLE A method for stimulating the immune system  
JOURNAL Patent: WO 9963975-A 9 16-DEC-1999;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)  
FEATURES Location/Qualifiers  
source 1..18  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1527 TATAAATCGACATCGCG 1544  
Db 18 TACAAAATAGACATCGCG 1

RESULT 332  
AX008980/c  
LOCUS AX008980 18 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 13 from Patent WO9963975.  
ACCESSION AX008980  
VERSION AX008980.1 GI:9996354  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.  
TITLE A method for stimulating the immune system  
JOURNAL Patent: WO 9963975-A 13 16-DEC-1999;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL

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Db 18 AATAAGCTTACACTGCC 1
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RESULT 323
AR232858/c
LOCUS AR232858 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 115 from patent US 6455689.
ACCESSION AR232858
VERSION AR232858.1 GI:27275196
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 115 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2175 CGCCCTCTTACATTGAT 2192
||| ||||| ||||| |||||
Db 18 CGTCCACTTTACATTGAT 1
RESULT 324
AR232871/c
LOCUS AR232871 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 128 from patent US 6455689.
ACCESSION AR232871
VERSION AR232871.1 GI:27275209
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 128 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2375 ACCACTGACCATTTCTTA 2392
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Db 18 ACCTTAACCATTTCTTA 1
RESULT 325
AR232875/c
LOCUS AR232875 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 132 from patent US 6455689.
ACCESSION AR232875
VERSION AR232875.1 GI:27275213
KEYWORDS
SOURCE
ORGANISM Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL Patent: US 6455689-A 132 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2439 GTCAAGCTTGTAAATGC 2456
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Db 18 GTAAAGCTTTGCAATGC 1
RESULT 326
AR262417
LOCUS AR262417 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 42 from patent US 6323185.
ACCESSION AR262417
VERSION AR262417.1 GI:28073848
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Fennewald,S., Zendegei,J.G., Ojwang,J.O. and Hogan,M.E.
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
JOURNAL Patent: US 6323185-A 42 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 973 CCCCCCCCCCGCCCCCCC 990
||||| ||||| ||||| |||||
Db 1 CCCCCCCCCCGCCCCCCC 18
RESULT 327
AR262418
LOCUS AR262418 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 43 from patent US 6323185.
ACCESSION AR262418
VERSION AR262418.1 GI:28073849
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Fennewald,S., Zendegei,J.G., Ojwang,J.O. and Hogan,M.E.
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
JOURNAL Patent: US 6323185-A 43 27-NOV-2001;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 318
AR200286 LOCUS 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 43 from patent US 6355785.
ACCESSION AR200286
VERSION AR200286.1 GI:20250360
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Fennelwald,S., Zendequi,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
TITLE Guanosine-rich oligonucleotide integrase inhibitors
JOURNAL Patent: US 6355785-A 43 12-MAR-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unassigned DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCCCCCCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 319
AR232815/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 72 from patent US 6455689.
ACCESSION AR232815
VERSION AR232815.1 GI:27275153
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,K. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 72 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATGCCG 1544
Db 18 TACAATAGACATGCCG 1

RESULT 320
AR232822/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 79 from patent US 6455689.
ACCESSION AR232822
VERSION AR232822.1 GI:27275160
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,K. and Bogdahn,U.

RESULT 318
LOCUS 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 43 from patent US 6355785.
ACCESSION AR200286
VERSION AR200286.1 GI:20250360
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Fennelwald,S., Zendequi,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
TITLE Guanosine-rich oligonucleotide integrase inhibitors
JOURNAL Patent: US 6355785-A 43 12-MAR-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unassigned DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCCCCCCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18

RESULT 319
AR232815/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 72 from patent US 6455689.
ACCESSION AR232815
VERSION AR232815.1 GI:27275153
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,K. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 72 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATGCCG 1544
Db 18 TACAATAGACATGCCG 1

RESULT 320
AR232822/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 79 from patent US 6455689.
ACCESSION AR232822
VERSION AR232822.1 GI:27275160
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,K. and Bogdahn,U.
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TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 79 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTCGTGA 1653
Db 18 ATGCTTCGAATTTGTTGA 1

RESULT 321
AR232828/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 85 from patent US 6455689.
ACCESSION AR232828
VERSION AR232828.1 GI:27275166
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,K. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 85 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAACGTATATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 322
AR232839/c LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 96 from patent US 6455689.
ACCESSION AR232839
VERSION AR232839.1 GI:27275177
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,K. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL Patent: US 6455689-A 96 24-SEP-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="genomic DNA"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTTACATGCCCC 1897
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AUTHORS Jun, N., Yusuke, N. and Toshihiro, T.  
 TITLE Mammal-derived tissue specific physiologically active protein  
 JOURNAL Patent: JP 2000037190-A 18 08-FEB-2000;  
 JAPAN TOBACCO INC  
 COMMENT OS Artificial Sequence  
 PN JP 2000037190-A/18  
 PD 08-FEB-2000  
 PF 23-JUL-1998 JP 1998225228  
 PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA  
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC  
 C12N15/02,  
 PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),  
 PC C12N15/00,  
 PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)  
 CC  
 FH Key Location/Qualifiers  
 FT primer\_bind (1)..(18).  
 FEATURES  
 source 1..18  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2801 TGAATAAAAAAAAAACATC 2818  
 Db 18 TGAATAAAAAAAAAAAAAAC 1  
 RESULT 314  
 I27810  
 LOCUS 18 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 42 from patent US 5567604.  
 ACCESSION I27810  
 VERSION I27810.1 GI:1818586  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Rando, R.F., Pennewald, S., Zendeigui, J.G. and Ojwang, J.O.  
 TITLE Anti-viral guanosine-rich oligonucleotides  
 JOURNAL Patent: US 5567604-A 42 22-OCT-1996;  
 FEATURES  
 source 1..18  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 973 CCCCCCCCCACCCGCC 990  
 Db 1 CCCCCCCCCCCCCCCCC 18  
 RESULT 315  
 I27811  
 LOCUS 18 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 43 from patent US 5567604.  
 ACCESSION I27811  
 VERSION I27811.1 GI:1818587  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Rando, R.F., Pennewald, S., Zendeigui, J.G. and Ojwang, J.O.

TITLE Anti-viral guanosine-rich oligonucleotides  
 JOURNAL Patent: US 5567604-A 43 22-OCT-1996;  
 FEATURES  
 source 1..18  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 973 CCCCCCCCCACCCGCC 990  
 Db 1 CCCCCCCCCCCCCCCCC 18  
 RESULT 316  
 I33107/c  
 LOCUS 18 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 21 from patent US 5589585.  
 ACCESSION I33107  
 VERSION I33107.1 GI:1823898  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Mabilat, C. and Pechere, J.-C.  
 TITLE DNA fragments, probes and amplification primers of the 65 kD  
 antigen of mycobacteria  
 JOURNAL Patent: US 5589585-A 21 31-DEC-1996;  
 FEATURES  
 source 1..18  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 359 CTTGGCGCGCTGGAGCA 376  
 Db 18 CTTGGCGCGACTTGAGCA 1  
 RESULT 317  
 AR200285  
 LOCUS 18 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 42 from patent US 6355785.  
 ACCESSION AR200285  
 VERSION AR200285.1 GI:20250359  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Rando, R.F., Pennewald, S., Zendeigui, J.G., Ojwang, J.O., Hogan, M.E.,  
 Pommier, Y., and Mazumder, A.  
 TITLE Guanosine-rich oligonucleotide integrase inhibitors  
 JOURNAL Patent: US 6355785-A 42 12-MAR-2002;  
 FEATURES  
 source 1..18  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 973 CCCCCCCCCACCCGCC 990  
 Db 1 CCCCCCCCCCCCCCCCC 18

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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAAGCTGATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 310
BD234961/c
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234961
VERSION BD234961.1 GI:33044731
KEYWORDS JP 2002517434-A/65.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiefen,K.H., Schlingensiefen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 65 18-JUN-2002;
BIOGOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/65
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7.25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEFEN,REIMAR SCHLINGENSIEFEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..18
/organism="Homo sapiens (human)".
FEATURES
source
1..18
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1462 CAGCCGGAGGGGAGCGG 1479
Db 18 CAGCCGGAGGGGAGCGG 1

RESULT 311
CQ808382
LOCUS
DEFINITION Sequence 1832 from Patent WO2004035803.
ACCESSION CQ808382
VERSION CQ808382.1 GI:47113776
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
Marx,A.
TITLE Method and nucleic acids for the improved treatment of breast cell
proliferative disorders

/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 929 AGAAAAAACAACCAACC 946
Db 18 AGAAAAAACAACCAACC 1

RESULT 313
E32458/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32458
VERSION E32458.1 GI:13018694
KEYWORDS JP 2000037190-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)

JOURNAL Patent: WO 2004035803-A 1832 29-APR-2004;
Epigenomics AG (DE)
FEATURES
source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for BCAR1"

Query Match
Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3275 TTTTAATTGTAATGGTT 3292
Db 1 TTTTGAATTGATAGTGT 18

RESULT 312
E32455/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32455
VERSION E32455.1 GI:13018691
KEYWORDS JP 2000037190-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 15 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/15
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,C12P21/08// (C12N5/10,C12R1:91), (C12P21:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
CC CC
FH Key Location/Qualifiers
FT primer_bind (1)..(18).
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.3%; Score 14.8; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 929 AGAAAAAACAACCAACC 946
Db 18 AGAAAAAACAACCAACC 1

RESULT 313
E32458/c
LOCUS
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32458
VERSION E32458.1 GI:13018694
KEYWORDS JP 2000037190-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
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labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC CC nucleic
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
FEATURES
source
1..18
/organism="Artificial Sequence".
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1162 ATATATATTTTCTTAC 1179
|||||
Db 18 ATATATATTTTCTTTC 1

RESULT 307
BD234905/c
LOCUS BD234905 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234905
VERSION BD234905.1 GI:33044675
KEYWORDS JP 2002517434-A/9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 9 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/9
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCGAATCTGTGA 1653
|||||
Db 18 ATGCTTCCAAATTTGGTGA 1

RESULT 309
BD234912/c
LOCUS BD234912 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234912
VERSION BD234912.1 GI:33044682
KEYWORDS JP 2002517434-A/16.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 16 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/16
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATGCCG 1544
|||||
Db 18 TACAAAATAGACATGCCG 1

RESULT 308
BD234909/c
LOCUS BD234909 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234909

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RESULT 303  
LOCUS AR168816 18 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 42 from patent US 6288042.  
ACCESSION AR168816  
VERSION AR168816.1 GI:17904932  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Rando,R.F., Ojwang,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 42 11-SEP-2001;  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 973 CCCCCCCCCCGCCCC 990  
Db 1 CCCCCCCCCCGCCCC 18

RESULT 304  
LOCUS AR168817 18 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 43 from patent US 6288042.  
ACCESSION AR168817  
VERSION AR168817.1 GI:17904933  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Rando,R.F., Ojwang,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 43 11-SEP-2001;  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 973 CCCCCCCCCCGCCCC 990  
Db 1 CCCCCCCCCCGCCCC 18

RESULT 305  
LOCUS BD145040/c 18 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.  
ACCESSION BD145040  
VERSION BD145040.1 GI:27850798  
KEYWORDS JP 2002119291-A/21.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.  
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,

and method for analyzing data obtained by that method  
Patent: JP 2002119291-A 21 23-APR-2002;  
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD  
OS Artificial Sequence  
PN JP 2002119291-A/21  
PD 23-APR-2002  
PF 27-APR-2001 JP 2001133529  
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI TORIMURA,  
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC  
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/PC  
G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,  
G01N1/28,  
G01N1/28,  
CC The base sequence was prepared synthetically on the aim of CC  
examining the  
decrease in fluorescence emission of  
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC  
hybridization of  
the probe with a target nucleic acid.  
FH key Location/Qualifiers  
FT source 1..18  
/organism='Artificial Sequence'.  
FEATURES  
source Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1162 ATATATATATTTTCTTAC 1179  
Db 18 ATATATATATTTTCTTTC 1

RESULT 306  
LOCUS BD166040/c 18 bp DNA linear PAT 17-JAN-2003  
DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.  
ACCESSION BD166040  
VERSION BD166040.1 GI:27871852  
KEYWORDS JP 2002191372-A/20.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.  
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method  
Patent: JP 2002191372-A 20 09-JUL-2002;  
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD  
OS Artificial Sequence  
PN JP 2002191372-A/20  
PD 09-JUL-2002  
PF 26-SEP-2001 JP 2001295145  
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI TORIMURA,  
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC  
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566,PC  
C12N15/00  
CC The base sequence was prepared synthetically on the aim of CC  
examining the  
decrease in fluorescence emission of a nucleic acid probe CC



Db 18 GTAAAGCTTGGCAATGC 1  
|| |||||  
RESULT 298  
AR034902 AR034902 18 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 24 from patent US 5869643.  
DEFINITION AR034902  
ACCESSION AR034902  
VERSION AR034902.1 GI:5950507  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Chatelain,F. and Kumarev,V.  
TITLE Process for preparing polynucleotides on a solid support in a tightly packed bed  
JOURNAL Patent: US 5869643-A 24 09-FEB-1999;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 973 CCCCCCCCACCCGCCCC 990  
|| |||||  
Db 1 CCCCCCCCACCCGCCCC 18  
|| |||||  
RESULT 299  
AR046298/c AR046298 18 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 21 from patent US 5849901.  
DEFINITION AR046298  
ACCESSION AR066298  
VERSION AR066298.1 GI:5996514  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Mabilat,C. and Pechere,J.-C.  
TITLE DNA fragments of mycobacteria, amplification primers hybridization probes, reagents and method for the detection of mycobacteria  
JOURNAL Patent: US 5849901-A 21 15-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 359 CCTTGGCGCCTGGAGCA 376  
|| |||||  
Db 18 CCTTGGCGGACTTGAGCA 1  
|| |||||  
RESULT 300  
AR084526 AR084526 18 bp DNA linear PAT 01-SEP-2000  
LOCUS Sequence 15 from patent US 5981185.  
DEFINITION AR084526  
ACCESSION AR084526  
VERSION AR084526.1 GI:10011297  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)

AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.  
TITLE Oligonucleotide repeat arrays  
JOURNAL Patent: US 5981185-A 15 09-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2666 ACAGCAACACACACCA 2683  
|| |||||  
Db 1 ACAACAACACACACCA 18  
|| |||||  
RESULT 301  
AR084527 AR084527 18 bp DNA linear PAT 01-SEP-2000  
LOCUS Sequence 16 from patent US 5981185.  
DEFINITION AR084527  
ACCESSION AR084527  
VERSION AR084527.1 GI:10011298  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.  
TITLE Oligonucleotide repeat arrays  
JOURNAL Patent: US 5981185-A 16 09-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2667 CAGCAACAACAACACAA 2684  
|| |||||  
Db 1 CAACAACAACAACACAA 18  
|| |||||  
RESULT 302  
AR144877/c AR144877 18 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 122 from patent US 6210942.  
DEFINITION AR144877  
ACCESSION AR144877  
VERSION AR144877.1 GI:15106744  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Lewis,N.G., Davin,D.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R., Sarkanen,S. and Ford,J.D.  
TITLE Recombinant pinoreisnol/lariciresinol reductase, recombinant dirigent protein, and methods of use  
JOURNAL Patent: US 6210942-A 122 03-APR-2001;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2577 AAAAAAAAAAATGGAG 2594  
|| |||||  
Db 18 AAAAAAAAAAATCGAG 1  
|| |||||

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RESULT 293
A89073/c
LOCUS           A89073           18 bp      DNA           linear           PAT 22-JAN-2000
DEFINITION      Sequence 1221 from Patent WO9833904.
ACCESSION       A89073
VERSION         A89073.1  GI:6737643
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 18)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 1221 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES        Location/Qualifiers
source          1..18
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAAGCTGTATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 294
A89084/c
LOCUS           A89084           18 bp      DNA           linear           PAT 22-JAN-2000
DEFINITION      Sequence 1232 from Patent WO9833904.
ACCESSION       A89084
VERSION         A89084.1  GI:6737654
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 18)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 1232 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES        Location/Qualifiers
source          1..18
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTTACACTGCC 1897
Db 18 AATAAGCTTACACTGTCC 1

RESULT 295
A89102/c
LOCUS           A89102           18 bp      DNA           linear           PAT 22-JAN-2000
DEFINITION      Sequence 1250 from Patent WO9833904.
ACCESSION       A89102
VERSION         A89102.1  GI:6737672
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 18)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
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JOURNAL        Patent: WO 9833904-A 1250 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES        Location/Qualifiers
source          1..18
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2175 GGCCTCTTTTACATTGAT 2192
Db 18 CGTCCACTTTTACATTGAT 1

RESULT 296
A89115/c
LOCUS           A89115           18 bp      DNA           linear           PAT 22-JAN-2000
DEFINITION      Sequence 1263 from Patent WO9833904.
ACCESSION       A89115
VERSION         A89115.1  GI:6737685
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 18)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 1263 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES        Location/Qualifiers
source          1..18
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2375 ACCACTGACCATTTCTCTA 2392
Db 18 ACCTCTAACCATTTCTCTA 1

RESULT 297
A89119/c
LOCUS           A89119           18 bp      DNA           linear           PAT 22-JAN-2000
DEFINITION      Sequence 1267 from Patent WO9833904.
ACCESSION       A89119
VERSION         A89119.1  GI:6737689
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 18)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 1267 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES        Location/Qualifiers
source          1..18
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2439 GTCAAGTCTTGTAAATGC 2456
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SOURCE      unidentified
ORGANISM    unclassified
REFERENCE   1 (bases 1 to 18)
AUTHORS     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
TITLE       EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL     Patent: WO 9425578-A 115 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2175 CGCCCTCTTTACATTGAT 2192
Db 18 CGTCCACTTTACATTGAT 1

RESULT 289
LOCUS      A40591          18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 128 from Patent WO9425578.
ACCESSION  A40591
VERSION     A40591.1 GI:2296626
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     Patent: WO 9425578-A 128 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
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                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2375 ACCACTGACCACTTCTCTA 2392
Db 18 ACCTTAACCACTTCTCTA 1

RESULT 290
LOCUS      A40595          18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 132 from Patent WO9425578.
ACCESSION  A40595
VERSION     A40595.1 GI:2296630
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     .
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     Patent: WO 9425578-A 132 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
              1..18
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

SOURCE      unidentified
ORGANISM    unclassified
REFERENCE   1 (bases 1 to 18)
AUTHORS     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
TITLE       EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL     Patent: WO 9425578-A 115 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2175 CGCCCTCTTTACATTGAT 2192
Db 18 CGTCCACTTTACATTGAT 1

RESULT 289
LOCUS      A40591          18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 128 from Patent WO9425578.
ACCESSION  A40591
VERSION     A40591.1 GI:2296626
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     Patent: WO 9425578-A 128 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
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                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2375 ACCACTGACCACTTCTCTA 2392
Db 18 ACCTTAACCACTTCTCTA 1

RESULT 290
LOCUS      A40595          18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 132 from Patent WO9425578.
ACCESSION  A40595
VERSION     A40595.1 GI:2296630
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     .
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL     Patent: WO 9425578-A 132 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
              1..18
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

SOURCE      unidentified
ORGANISM    unclassified
REFERENCE   1 (bases 1 to 18)
AUTHORS     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
TITLE       EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL     Patent: WO 9425578-A 115 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
              1..18
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2439 GTCAAGTCTTTGTAATGC 2456
Db 18 GTAAAGTCTTTGCAATGC 1

RESULT 291
LOCUS      A89061          18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1209 from Patent WO9833904.
ACCESSION  A89061
VERSION     A89061.1 GI:6737631
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1209 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
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              1..18
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1527 TATAAATCGACATGCCG 1544
Db 18 TACAATAAGACATGCCG 1

RESULT 292
LOCUS      A89067          18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1215 from Patent WO9833904.
ACCESSION  A89067
VERSION     A89067.1 GI:6737637
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1215 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1636 ATGCTTCGAATCTGCTGA 1653
Db 18 ATGCTTCGAATTTGCTGA 1
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SOURCE      unidentified
ORGANISM    unclassified
REFERENCE   1 (bases 1 to 18)
AUTHORS     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
TITLE       EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL     Patent: WO 9425578-A 115 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
              1..18
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2439 GTCAAGTCTTTGTAATGC 2456
Db 18 GTAAAGTCTTTGCAATGC 1

RESULT 291
LOCUS      A89061          18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1209 from Patent WO9833904.
ACCESSION  A89061
VERSION     A89061.1 GI:6737631
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1209 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1527 TATAAATCGACATGCCG 1544
Db 18 TACAATAAGACATGCCG 1

RESULT 292
LOCUS      A89067          18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1215 from Patent WO9833904.
ACCESSION  A89067
VERSION     A89067.1 GI:6737637
KEYWORDS   .
SOURCE     .
ORGANISM   unidentified
            unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1215 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1636 ATGCTTCGAATCTGCTGA 1653
Db 18 ATGCTTCGAATTTGCTGA 1
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FEATURES
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 359 CCTTGGCGCGCTGGACGA 376
Db 18 CCTTGGCGCGACTTGACGA 1

RESULT 284
A40535/c
LOCUS      A40535      18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 72 from Patent WO9425578.
ACCESSION  A40535
VERSION    A40535.1 GI:2296570
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS
TITLE
JOURNAL
FEATURES
  source      Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1527 TATAAATCGACATGCCG 1544
Db 18 TACAAATAGACATGCCG 1

RESULT 285
A40542/c
LOCUS      A40542      18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 79 from Patent WO9425578.
ACCESSION  A40542
VERSION    A40542.1 GI:2296577
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS
TITLE
JOURNAL
FEATURES
  source      Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1636 ATGCTTCCAATCTGGTGA 1653
Db 18 ATGCTTCCAATTTGGTGA 1

RESULT 286
A40548/c
LOCUS      A40548      18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 85 from Patent WO9425578.
ACCESSION  A40548
VERSION    A40548.1 GI:2296583
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS
TITLE
JOURNAL
FEATURES
  source      Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1711 GGATTGAACGTGTATCAGA 1728
Db 18 GGATTGAGCTATATCAGA 1

RESULT 287
A40559/c
LOCUS      A40559      18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 96 from Patent WO9425578.
ACCESSION  A40559
VERSION    A40559.1 GI:2296594
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS
TITLE
JOURNAL
FEATURES
  source      Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1880 AATAAGTTTACTACTGCC 1897
Db 18 AATAAGCTTACTACTGTCC 1

RESULT 288
A40578/c
LOCUS      A40578      18 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 115 from Patent WO9425578.
ACCESSION  A40578
VERSION    A40578.1 GI:2296613
KEYWORDS   .
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Telesman,A., Anson,R. and Tuijinder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL Patent: WO 03025175-A 743 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES Location/Qualifiers  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3922 CTGTGTAACACAGA 3936  
Db 17 CTGTGTAACACAGA 3  
RESULT 280  
E32456/c  
LOCUS E32456 18 bp DNA linear PAT 18-JUN-2001  
DEFINITION Mammal-derived tissue specific physiologically active protein.  
ACCESSION E32456  
VERSION E32456.1 GI:13018692  
KEYWORDS JP 2000037190-A/16.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.  
TITLE Mammal-derived tissue specific physiologically active protein  
JOURNAL Patent: JP 2000037190-A 16 08-FEB-2000;  
JAPAN TOBACCO INC  
COMMENT OS Artificial Sequence  
PN JP 2000037190-A/16  
PD 08-FEB-2000  
PF 23-JUL-1998 JP 1998225228  
PR  
PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA  
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC  
C12N15/02,  
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),  
PC C12N15/00,  
PC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)  
CC  
FH Key Location/Qualifiers  
FT primer\_bind (1)..(18).  
FEATURES source  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 0.4%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2574 TTAATAAAAAAAAAA 2588  
Db 18 TTAATAAAAAAAAAA 4  
RESULT 281  
A28690 18 bp RNA linear PAT 04-JUN-1995  
LOCUS A28690

DEFINITION Oligonucleotide 19 (comp.).  
ACCESSION A28690  
VERSION A28690.1 GI:1248729  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS  
TITLE SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE  
JOURNAL Patent: WO 9014090-A 18 29-NOV-1990;  
FEATURES Location/Qualifiers  
source  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 970 ATTCCCCCCCCACCCCGC 987  
Db 1 ATTCCCCCCCCACCCCGC 18  
RESULT 282  
A28695  
LOCUS A28695 18 bp RNA linear PAT 04-JUN-1995  
DEFINITION Oligonucleotide 17 (comp.).  
ACCESSION A28695  
VERSION A28695.1 GI:1248734  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS  
TITLE SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE  
JOURNAL Patent: WO 9014090-A 23 29-NOV-1990;  
FEATURES Location/Qualifiers  
source  
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/mol\_type="unassigned RNA"  
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Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 970 ATTCCCCCCCCACCCCGC 987  
Db 1 ATTCCCCCCCCACCCCGC 18  
RESULT 283  
A36755/c  
LOCUS A36755 18 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 21 from Patent EP0584023.  
ACCESSION A36755  
VERSION A36755.1 GI:2294022  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Mabilat,C. and Pechere,J.  
TITLE Mycobacteria DNA fragments, amplification primers, hybridization  
probes, reagents and detection process of mycobacteria  
JOURNAL Patent: EP 0584023-A 21 23-FEB-1994;  
BIO MERIEUX (FR)  
COMMENT Other publication CA 2103933 940213  
Other publication FR 2694754 940218.

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JOURNAL macromolecular structures
Patent: US 5571677-A 5 05-NOV-1996;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAA 2814
Db 15 GTGAAAAA 1

RESULT 276
BD065904/c
LOCUS BD065904 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065904
VERSION BD065904.1 GI:22611507
KEYWORDS JP 2001511000-A/539.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 539 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/539
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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FEATURES
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1968 GCAGGTATTGATGCC 1982
Db 15 GCAGGTATTGATGCC 1

RESULT 277
BD065905/c
LOCUS BD065905 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065905
VERSION BD065905.1 GI:22611508
KEYWORDS JP 2001511000-A/540.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 540 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/540
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1968 GCAGGTATTGATGCC 1982
Db 15 GCAGGTATTGATGCC 1

RESULT 277
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LOCUS BD065905 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065905
VERSION BD065905.1 GI:22611508
KEYWORDS JP 2001511000-A/540.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 540 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/540
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
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FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1919 TAATAATTACATCAT 1933
Db 15 TAATAATTACATCAT 1

RESULT 279
AX729109/c
LOCUS AX729109 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 743 from Patent WO03025175.
ACCESSION AX729109
VERSION AX729109.1 GI:30508452
KEYWORDS
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Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Gryaznov,S.M. and Lloyd,D.H.  
TITLE Oligonucleotide clamps having diagnostic and therapeutic applications  
JOURNAL Patent: US 5817795-A 5 06-OCT-1998;  
FEATURES Location/Qualifiers  
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Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814  
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 271  
AR051237/c  
LOCUS AR051237 15 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5830658.  
ACCESSION AR051237  
VERSION AR051237.1 GI:5974601  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Gryaznov,S.M.  
TITLE Convergent synthesis of branched and multiply connected macromolecular structures  
JOURNAL Patent: US 5830658-A 5 03-NOV-1998;  
FEATURES Location/Qualifiers  
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Query Match 0.4%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814  
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 272  
AR084519  
LOCUS AR084519 15 bp DNA linear PAT 01-SEP-2000  
DEFINITION Sequence 8 from patent US 5981185.  
ACCESSION AR084519  
VERSION AR084519.1 GI:10011290  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.  
TITLE Oligonucleotide repeat arrays  
JOURNAL Patent: US 5981185-A 8 09-NOV-1999;  
FEATURES Location/Qualifiers  
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Query Match 0.4%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAAAAAAAAAA 2587

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Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Gryaznov,S.M. and Lloyd,D.H.  
TITLE Oligonucleotide clamps having diagnostic and therapeutic applications  
JOURNAL Patent: US 5817795-A 5 06-OCT-1998;  
FEATURES Location/Qualifiers  
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Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814  
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 273  
AR127784/c  
LOCUS AR127784 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 5 from patent US 6180777.  
ACCESSION AR127784  
VERSION AR127784.1 GI:14114379  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Horn,T.  
TITLE Synthesis of branched nucleic acids  
JOURNAL Patent: US 6180777-A 5 30-JAN-2001;  
FEATURES Location/Qualifiers  
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Query Match 0.4%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814  
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 274  
I16031/c  
LOCUS I16031 15 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 5 from patent US 5473060.  
ACCESSION I16031  
VERSION I16031.1 GI:1250939  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Gryaznov,S.M. and Lloyd,D.H.  
TITLE Oligonucleotide clamps having diagnostic applications  
JOURNAL Patent: US 5473060-A 5 05-DEC-1995;  
FEATURES Location/Qualifiers  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2800 GTGAAAAAAAAAAAAA 2814  
Db 15 GTGAAAAAAAAAAAAA 1

RESULT 275  
I28366/c  
LOCUS I28366 15 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 5 from patent US 5571677.  
ACCESSION I28366  
VERSION I28366.1 GI:1819142  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Gryaznov,S.M.  
TITLE Convergent synthesis of branched and multiply connected

AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 588 06-AUG-1998;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1919 TAATAATTACATCAT 1933  
Db 15 TAATAATTACATCAT 1  
RESULT 266  
A90358/c  
LOCUS A90358 15 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 539 from Patent EP0856579.  
ACCESSION A90358  
VERSION A90358.1 GI:6738872  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: EP 0856579-A 539 05-AUG-1998;  
BIOGNOSTIK GES (DE)  
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1968 GCAGGTATTGATGTC 1982  
Db 15 GCAGGTATTGATGTC 1  
RESULT 267  
A90359/c  
LOCUS A90359 15 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 540 from Patent EP0856579.  
ACCESSION A90359  
VERSION A90359.1 GI:6738873  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: EP 0856579-A 540 05-AUG-1998;  
BIOGNOSTIK GES (DE)  
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Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1971 GGTATTGATGGCACC 1985  
Db 15 GGTATTGATGGCACC 1  
RESULT 268  
A90407/c  
LOCUS A90407 15 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 588 from Patent EP0856579.  
ACCESSION A90407  
VERSION A90407.1 GI:6738921  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: EP 0856579-A 588 05-AUG-1998;  
BIOGNOSTIK GES (DE)  
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1919 TAATAATTACATCAT 1933  
Db 15 TAATAATTACATCAT 1  
RESULT 269  
AR002256/c  
LOCUS AR002256 15 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 5 from patent US 5741643.  
ACCESSION AR002256  
VERSION AR002256.1 GI:3963810  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Gryaznov,S.M. and Lloyd,D.H.  
TITLE Oligonucleotide clamps  
JOURNAL Patent: US 5741643-A 5 21-APR-1998;  
FEATURES  
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Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2800 GTGAAAAA 2814  
Db 15 GTGAAAAA 1  
RESULT 270  
AR045206/c  
LOCUS AR045206 15 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5817795.  
ACCESSION AR045206  
VERSION AR045206.1 GI:5966671  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.



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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdc25 hs ribozyme binding site"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 925 CAGGAGAAAAAAAC 941
DB 19 CAGGAGAAAAAAAC 3

RESULT 261
AX132311/c
LOCUS      AX132311      19 bp      DNA      linear      PAT 15-MAY-2001
DEFINITION Sequence 3529 from Patent WO0130362.
ACCESSION  AX132311
VERSION     AX132311.1 GI:14138616
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Robbins,J.M. and Tritz,R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
JOURNAL     Patent: WO 0130362-A 3529 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES
  source    1..19
            Location/Qualifiers
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Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAAAA 940
DB 17 CCAGGAGAAAAAAAC 1

RESULT 262
AR488890
LOCUS      AR488890      20 bp      DNA      linear      PAT 15-MAY-2004
DEFINITION Sequence 7 from patent US 6709818.
ACCESSION  AR488890
VERSION     AR488890.1 GI:47255117
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Nelson,W.G., Lin,X., Tchou,J.C. and Bakker,J.
TITLE       Methods of diagnosing and treating hepatic cell proliferative
            disorders
JOURNAL     Patent: US 6709818-A 7 23-MAR-2004;
            Location/Qualifiers
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Query Match      0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTCTTTTAAAG 2758
DB 4 ATTTTCTTTTCTTTAAAG 20
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RESULT 263
A88391/c
LOCUS      A88391      15 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 539 from Patent WO9833904.
ACCESSION  A88391
VERSION     A88391.1 GI:6736961
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 539 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match      0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1968 GCAGGTATTGATGCG 1982
DB 15 GCAGGTATTGATGCG 1

RESULT 264
A88392/c
LOCUS      A88392      15 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 540 from Patent WO9833904.
ACCESSION  A88392
VERSION     A88392.1 GI:6736962
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 540 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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            /db_xref="taxon:32644"

Query Match      0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGGCACC 1985
DB 15 GGTATTGATGGCACC 1

RESULT 265
A88440/c
LOCUS      A88440      15 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 588 from Patent WO9833904.
ACCESSION  A88440
VERSION     A88440.1 GI:6737010
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 15)
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Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 256
AR241645
LOCUS AR241645 19 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6472141.
ACCESSION AR241645
VERSION AR241645.1 GI:27287419
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Nikiforov,T.T.
TITLE Kinase assays using polycations
JOURNAL Patent: US 6472141-A 3 29-OCT-2002;
FEATURES
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Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 257
AR292884
LOCUS AR292884 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4619 from patent US 6537751.
ACCESSION AR292884
VERSION AR292884.1 GI:31680168
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4619 25-MAR-2003;
FEATURES
source
Location/Qualifiers
1..19
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/mol_type="genomic DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3126 GTTGTATTAGACTAAG 3142
Db 2 GTTGTATTAGACTAAG 18

RESULT 258
AR473599
LOCUS AR473599 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6689565.

/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 259
AR478107
LOCUS AR478107 19 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 3 from patent US 6699655.
ACCESSION AR478107
VERSION AR478107.1 GI:47236709
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Nikiforov,T.T.
TITLE Fluorescent polarization assays involving multivalent metal ions
JOURNAL Patent: US 6699655-A 3 02-MAR-2004;
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Location/Qualifiers
1..19
/organism="unknown"
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Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCCT 2139
Db 1 CGCTGTGGATGCTGCCT 17

RESULT 260
AX132308/c
LOCUS AX132308/c 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3526 from Patent WO0130362.
ACCESSION AX132308
VERSION AX132308.1 GI:14138613
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 3526 03-MAY-2001;
FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
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FT source 1. .18 /organism='Artificial Sequence'.  
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FT source 0.4%; Score 15.4; DB 1; Length 18;  
CC Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
CC Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 1161 TATATATATTTTCTT 1177  
Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 17 TATATATATTTTCTT 1

RESULT 252  
LOCUS AR167910 19 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 3 from patent US 6287774.  
ACCESSION AR167910  
VERSION AR167910.1 GI:17903721  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Nikiforov,T.T.  
TITLE Assay methods and system  
JOURNAL Patent: US 6287774-A 3 11-SEP-2001;  
FEATURES  
source Location/Qualifiers  
1. .19  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.7e+02;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2123 CGCTTTGGATGCTGCT 2139  
Db 1 CGCTTTGGATGCTGCT 17

RESULT 253  
LOCUS BD211727 19 bp DNA linear PAT 17-JUL-2003  
DEFINITION ALG-2LP and ALG-2-like molecules and utilization thereof.  
ACCESSION BD211727  
VERSION BD211727.1 GI:33021497  
KEYWORDS JP 2002516335-A/10.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Curtis,R.A.J.  
TITLE ALG-2LP and ALG-2-like molecules and utilization thereof  
JOURNAL Patent: JP 2002516335-A 10 04-JUN-2002;  
COMMENT MILLENNIUM PHARMACEUTICALS INC  
OS Unidentified  
FN JP 2002516335-A/10  
PD 04-JUN-2002  
PF 13-MAY-1999 JP 2000550863  
PR 26-MAY-1998 US 09/084749  
PI RORY A J CURTIS  
PC A61K45/00,A61P25/28,A61P35/00,A61P37/02,A61P43/00,A61P43/00,  
PC C07K14/47,  
PC C07K16/18,C07K17/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC  
,C12N5/10,C12N15/09,  
PC C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/574//C12P21/08,  
PC C12N5/00,  
PC C12N5/00,C12N15/00

CC Strandedness: Single;  
CC Topology: Linear;  
CC ALG-2LP and ALG-2-like molecules and utilization thereof FH  
CC Location/Qualifiers  
FT source 1. .19  
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source Location/Qualifiers  
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/organism="unidentified"  
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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 158 CAACCCATCTGCGGAGA 174  
Db 3 CAACCCATCTGCGGAGA 19

RESULT 254  
LOCUS CQ808384 19 bp DNA linear PAT 10-MAY-2004  
DEFINITION Sequence 1834 from Patent WO2004035803.  
ACCESSION CQ808384  
VERSION CQ808384.1 GI:47113778  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 other sequences; artificial sequences.  
AUTHORS Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,P.,  
Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and  
Marx,A.  
TITLE Method and nucleic acids for the improved treatment of breast cell  
proliferative disorders  
JOURNAL Patent: WO 2004035803-A 1834 29-APR-2004;  
FEATURES  
source Location/Qualifiers  
1. .19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for BCAR1"

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2959 GTTATTATTGTGTGTT 2975  
Db 1 GGTATTATTGTGTGTT 17

RESULT 255  
LOCUS CQ829560 19 bp DNA linear PAT 05-JUL-2004  
DEFINITION Sequence 3 from Patent EP1418239.  
ACCESSION CQ829560  
VERSION CQ829560.1 GI:49732871  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 other sequences; artificial sequences.  
AUTHORS Nikiforov,T.T.  
TITLE Fluorescence polarization assays involving polyions  
JOURNAL Patent: EP 1418239-A 3 12-MAY-2004;  
COMMENT Caliper Life Sciences, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. .19  
/organism="synthetic construct"

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| source                   | 1..18<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"<br>/note="Detection oligonucleotide for N-MYC"  |
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| Best Local Similarity    | 94.1%; Pred. No. 2.4e+02;  |
| Matches 16; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;   |
| QY                       | 2807 AAAAAAACATCAAAAC 2823<br>   |
| Db                       | 18 AAAAAAACACCAAAAC 2  |
| RESULT 249               |  |
| BD066612/c               |  |
| LOCUS                    | 18 bp DNA linear PAT 27-AUG-2002   |
| DEFINITION               | An antisense oligonucleotide preparation method.   |
| ACCESSION                | BD066612   |
| VERSION                  | BD066612.1 GI:22612215   |
| KEYWORDS                 | JP 2001511000-A/1247.  |
| SOURCE                   | unidentified   |
| ORGANISM                 | unclassified.  |
| REFERENCE                | 1 (bases 1 to 18)  |
| AUTHORS                  | Schlingensiepen,K.H. and Brysch,W  |
| TITLE                    | An antisense oligonucleotide preparation method  |
| JOURNAL                  | Patent: JP 2001511000-A 1247 07-AUG-2001;  |
| COMMENT                  | BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH<br>OS Unknown<br>PN JP 2001511000-A/1247<br>PD 07-AUG-2001<br>PF 30-JAN-1998 JP 1998532533<br>PR 31-JAN-1997 EP 97101531.8<br>PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH<br>PC C12N15/11,C07H21/04,A61K31/70<br>CC An antisense oligonucleotide preparation method FH Key<br>Location/Qualifiers<br>FT source 1..18<br>FT /organism='Unknown' |
| FEATURES                 | source<br>1..18<br>Location/Qualifiers<br>/organism="unidentified"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:32644"  |
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| Best Local Similarity    | 94.1%; Pred. No. 2.4e+02;  |
| Matches 16; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;   |
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| Db                       | 17 GCCTATTGCTTTAGAAA 1   |
| RESULT 250               |  |
| BD072879/c               |  |
| LOCUS                    | 18 bp DNA linear PAT 27-AUG-2002   |
| DEFINITION               | Method for assaying nucleic acid, nucleic acid probe used therefor,<br>and method for analyzing data obtained by that method.  |
| ACCESSION                | BD072879   |
| VERSION                  | BD072879.1 GI:22618482   |
| KEYWORDS                 | JP 2001286300-A/17.  |
| SOURCE                   | synthetic construct  |
| ORGANISM                 | synthetic construct  |
| REFERENCE                | 1 (bases 1 to 18)  |
| AUTHORS                  | Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,<br>Yokomaku,T., Koyama,O. and Furusho,K.  |
| TITLE                    | Method for assaying nucleic acid, nucleic acid probe used therefor,<br>and method for analyzing data obtained by that method   |
| JOURNAL                  | Patent: JP 2001286300-A 17 16-OCT-2001;  |
| source                   | 1..18<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"<br>/note="Detection oligonucleotide for N-MYC"  |
| Query Match              | 0.4%; Score 15.4; DB 1; Length 18;   |
| Best Local Similarity    | 94.1%; Pred. No. 2.4e+02;  |
| Matches 16; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;   |
| QY                       | 2807 AAAAAAACATCAAAAC 2823<br>   |
| Db                       | 18 AAAAAAACACCAAAAC 2  |
| RESULT 249               |  |
| BD066612/c               |  |
| LOCUS                    | 18 bp DNA linear PAT 27-AUG-2002   |
| DEFINITION               | An antisense oligonucleotide preparation method.   |
| ACCESSION                | BD066612   |
| VERSION                  | BD066612.1 GI:22612215   |
| KEYWORDS                 | JP 2001511000-A/1247.  |
| SOURCE                   | unidentified   |
| ORGANISM                 | unclassified.  |
| REFERENCE                | 1 (bases 1 to 18)  |
| AUTHORS                  | Schlingensiepen,K.H. and Brysch,W  |
| TITLE                    | An antisense oligonucleotide preparation method  |
| JOURNAL                  | Patent: JP 2001511000-A 1247 07-AUG-2001;  |
| COMMENT                  | BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH<br>OS Unknown<br>PN JP 2001511000-A/1247<br>PD 07-AUG-2001<br>PF 30-JAN-1998 JP 1998532533<br>PR 31-JAN-1997 EP 97101531.8<br>PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH<br>PC C12N15/11,C07H21/04,A61K31/70<br>CC An antisense oligonucleotide preparation method FH Key<br>Location/Qualifiers<br>FT source 1..18<br>FT /organism='Unknown' |
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| QY                       | 2136 GCCTACTGCTTTAGAAA 2152<br>  |
| Db                       | 17 GCCTATTGCTTTAGAAA 1   |
| RESULT 250               |  |
| BD072879/c               |  |
| LOCUS                    | 18 bp DNA linear PAT 27-AUG-2002   |
| DEFINITION               | Method for assaying nucleic acid, nucleic acid probe used therefor,<br>and method for analyzing data obtained by that method.  |
| ACCESSION                | BD072879   |
| VERSION                  | BD072879.1 GI:22618482   |
| KEYWORDS                 | JP 2001286300-A/17.  |
| SOURCE                   | synthetic construct  |
| ORGANISM                 | synthetic construct  |
| REFERENCE                | 1 (bases 1 to 18)  |
| AUTHORS                  | Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,<br>Yokomaku,T., Koyama,O. and Furusho,K.  |
| TITLE                    | Method for assaying nucleic acid, nucleic acid probe used therefor,<br>and method for analyzing data obtained by that method   |
| JOURNAL                  | Patent: JP 2001286300-A 17 16-OCT-2001;  |
| source                   | 1..18<br>/organism="synthetic construct"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32630"<br>/note="Detection oligonucleotide for N-MYC"  |
| Query Match              | 0.4%; Score 15.4; DB 1; Length 18;   |
| Best Local Similarity    | 94.1%; Pred. No. 2.4e+02;  |
| Matches 16; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;   |
| QY                       | 2807 AAAAAAACATCAAAAC 2823<br>   |
| Db                       | 18 AAAAAAACACCAAAAC 2  |
| RESULT 249               |  |
| BD066612/c               |  |
| LOCUS                    | 18 bp DNA linear PAT 27-AUG-2002   |
| DEFINITION               | An antisense oligonucleotide preparation method.   |
| ACCESSION                | BD066612   |
| VERSION                  | BD066612.1 GI:22612215   |
| KEYWORDS                 | JP 2001511000-A/1247.  |
| SOURCE                   | unidentified   |
| ORGANISM                 | unclassified.  |
| REFERENCE                | 1 (bases 1 to 18)  |
| AUTHORS                  | Schlingensiepen,K.H. and Brysch,W  |
| TITLE                    | An antisense oligonucleotide preparation method  |
| JOURNAL                  | Patent: JP 2001511000-A 1247 07-AUG-2001;  |
| COMMENT                  | BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH<br>OS Unknown<br>PN JP 2001511000-A/1247<br>PD 07-AUG-2001<br>PF 30-JAN-1998 JP 1998532533<br>PR 31-JAN-1997 EP 97101531.8<br>PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH<br>PC C12N15/11,C07H21/04,A61K31/70<br>CC An antisense oligonucleotide preparation method FH Key<br>Location/Qualifiers<br>FT source 1..18<br>FT /organism='Unknown' |
| FEATURES                 | source<br>1..18<br>Location/Qualifiers<br>/organism="unidentified"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:32644"  |
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| Best Local Similarity    | 94.1%; Pred. No. 2.4e+02;  |
| Matches 16; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;   |
| QY                       | 2136 GCCTACTGCTTTAGAAA 2152<br>  |
| Db                       | 17 GCCTATTGCTTTAGAAA 1   |
| RESULT 250               |  |
| BD072879/c               |  |
| LOCUS                    | 18 bp DNA linear PAT 27-AUG-2002   |
| DEFINITION               | Method for assaying nucleic acid, nucleic acid probe used therefor,<br>and method for analyzing data obtained by that method.  |
| ACCESSION                | BD072879   |
| VERSION                  | BD072879.1 GI:22618482   |
| KEYWORDS                 |  |

LOCUS AR264934 18 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 18 from patent US 6492121.  
ACCESSION AR264934  
VERSION AR264934.1 GI:29693321  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.  
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method  
JOURNAL Patent: US 6492121-A 18 10-DEC-2002;  
FEATURES Location/Qualifiers  
source 1..18  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.4%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
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QY 1161 TATATATATTTTCTT 1177  
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Db 17 TATATATATTTTCTT 1  
RESULT 245  
AX030150/c  
LOCUS AR478215 18 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 18 from patent US 6699661.  
ACCESSION AR478215  
VERSION AR478215.1 GI:47236963  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K., Yokomaku,T., Koyama,O. and Furusho,K.  
TITLE Method for determining a concentration of target nucleic acid molecules, nucleic acid probes for the method, and method for analyzing data obtained by the method  
JOURNAL Patent: US 6699661-A 18 02-MAR-2004;  
FEATURES Location/Qualifiers  
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Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
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QY 1161 TATATATATTTTCTT 1177  
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Db 17 TATATATATTTTCTT 1  
RESULT 246  
AX030150/c  
LOCUS AR478215 18 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 112 from Patent EP1008649.  
ACCESSION AX030150  
VERSION AX030150.1 GI:10190367  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.

and Schlingensiepen,R.  
Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2 (tgf-b2)  
Patent: EP 1008649-A 112 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers  
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QY 2136 GCCTACTGCTTTAGAAA 2152  
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Db 17 GCCTATTGCTTTAGAAA 1  
RESULT 247  
AX316471/c  
LOCUS AX316471 18 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 112 from Patent EP1160319.  
ACCESSION AX316471  
VERSION AX316471.1 GI:17899644  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H., Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 112 05-DEC-2001;  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:32644"  
/note="Description of unknown: unknown"  
Query Match 0.4%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2136 GCCTACTGCTTTAGAAA 2152  
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Db 17 GCCTATTGCTTTAGAAA 1  
RESULT 248  
AX599662/c  
LOCUS AX599662 18 bp DNA linear PAT 14-FEB-2003  
DEFINITION Sequence 1002 from Patent WO02077272.  
ACCESSION AX599662  
VERSION AX599662.1 GI:28399810  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J., Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E., Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T., Pelet,C. and Ziebarth,H.  
TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders  
JOURNAL Patent: WO 02077272-A 1002 03-OCT-2002;  
FEATURES Epigenomics AG (DE)  
Location/Qualifiers

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RESULT 240
BD166038/c
LOCUS
DEFINITION
    18 bp DNA linear PAT 17-JAN-2003
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166038
VERSION
BD166038.1 GI:27871850
KEYWORDS
JP 2002191372-A/18.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL
Patent: JP 2002191372-A 18 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/18
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
source
1..18
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1
RESULT 241
AR232855/c
LOCUS
DEFINITION
Sequence 112 from patent US 6455689.
ACCESSION
AR232855
VERSION
AR232855.1 GI:27275193
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL
Patent: US 6455689-A 112 24-SEP-2002;
FEATURES
Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1
RESULT 242
AR237465/c
LOCUS
DEFINITION
Sequence 3 from patent US 6465628.
ACCESSION
AR237465
VERSION
AR237465.1 GI:27282215
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE
Process for the synthesis of oligomeric compounds
JOURNAL
Patent: US 6465628-A 3 15-OCT-2002;
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Location/Qualifiers
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/mol_type='genomic DNA'
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Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
RESULT 243
AR237467/c
LOCUS
DEFINITION
Sequence 5 from patent US 6465628.
ACCESSION
AR237467
VERSION
AR237467.1 GI:27282217
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE
Process for the synthesis of oligomeric compounds
JOURNAL
Patent: US 6465628-A 5 15-OCT-2002;
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Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
RESULT 244
AR264934/c
LOCUS
DEFINITION
Sequence 112 from patent US 6455689.
ACCESSION
AR232855
VERSION
AR232855.1 GI:27275193
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL
Patent: US 6455689-A 112 24-SEP-2002;
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Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 18 AAAAAAAAAAATTGGGG 2
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/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2136 GCCTACTGCTTTAGAAA 2152
Db 17 GCCTATTGCTTTAGAAA 1
RESULT 242
AR237465/c
LOCUS
DEFINITION
Sequence 3 from patent US 6465628.
ACCESSION
AR237465
VERSION
AR237465.1 GI:27282215
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE
Process for the synthesis of oligomeric compounds
JOURNAL
Patent: US 6465628-A 3 15-OCT-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
RESULT 243
AR237467/c
LOCUS
DEFINITION
Sequence 5 from patent US 6465628.
ACCESSION
AR237467
VERSION
AR237467.1 GI:27282217
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
Guzaev,A.
TITLE
Process for the synthesis of oligomeric compounds
JOURNAL
Patent: US 6465628-A 5 15-OCT-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
RESULT 244
AR264934/c
LOCUS
DEFINITION
Sequence 112 from patent US 6455689.
ACCESSION
AR232855
VERSION
AR232855.1 GI:27275193
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
JOURNAL
Patent: US 6455689-A 112 24-SEP-2002;
FEATURES
Location/Qualifiers
source
1..18
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2578 AAAAAAAAAAATTGGAG 2594
Db 18 AAAAAAAAAAATTGGGG 2
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DEFINITION Sequence 1219 from Patent WO03025177.
ACCESSION AX736539
VERSION AX736539.1 GI:30515827
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2129 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3598 TTTTCTTTTAAATGATC 3614
Db 17 TTTCTTTTAAATGATC 1
RESULT 237
A40575/c
LOCUS A40575 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 112 from Patent WO9425578.
ACCESSION A40575
VERSION A40575.1 GI:2296610
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 112 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
source
1. .18
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2136 GCCTACTGCTTTAGAAA 2152
Db 17 GCCTATTGCTTTAGAAA 1
RESULT 238
A89099/c
LOCUS A89099 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1247 from Patent WO9833904.
ACCESSION A89099
VERSION A89099.1 GI:6737669
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 1247 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1. .18
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2136 GCCTACTGCTTTAGAAA 2152
Db 17 GCCTATTGCTTTAGAAA 1
RESULT 239
BD145038/c
LOCUS BD145038 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD145038
VERSION BD145038.1 GI:27850796
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kurane,R., Kanagawa,T., Kanagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaki,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 19 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/19
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAWAGATA, MASAKI PI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N1/28, G01N33/ PC
53, G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00.
PC G01N1/28'
PC G01N1/28'
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .18
/organism='Artificial Sequence'.
FEATURES
source
1. .18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1161 TATATATATTTTCTT 1177
Db 17 TATATATTTTCTT 1

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|                       |  |
|-----------------------|--|
| DEFINITION            | Sequence 2155 from patent US 5646042.  |
| ACCESSION             | I54414   |
| VERSION               | I54414.1 GI:2475617  |
| KEYWORDS              | .  |
| SOURCE                | Unknown.   |
| ORGANISM              | Unknown.   |
| REFERENCE             | Unclassified.  |
| AUTHORS               | 1 (bases 1 to 17)  |
| TITLE                 | Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.   |
| JOURNAL               | C-myb targeted ribozymes   |
| FEATURES              | Patent: US 5646042-A 2155 08-JUL-1997;<br>Location/Qualifiers<br>1..17<br>/organism="unknown"<br>/mol_type="unassigned DNA"  |
| Query Match           | 0.4%; Score 15.4; DB 1; Length 17;   |
| Best Local Similarity | 94.1%; Pred. No. 2.1e+02;  |
| Matches               | 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  |
| Qy                    | 1152 TTTCCTTTTATATATA 1168<br>     <br>1 TTTATTTTTATATATA 17   |
| Db                    |  |
| RESULT 232            |  |
| I54416                |  |
| LOCUS                 | I54416 17 bp DNA linear PAT 07-OCT-1997  |
| DEFINITION            | Sequence 2157 from patent US 5646042.  |
| ACCESSION             | I54416   |
| VERSION               | I54416.1 GI:2475619  |
| KEYWORDS              | .  |
| SOURCE                | Unknown.   |
| ORGANISM              | Unclassified.  |
| REFERENCE             | 1 (bases 1 to 17)  |
| AUTHORS               | Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.   |
| TITLE                 | C-myb targeted ribozymes   |
| JOURNAL               | Patent: US 5646042-A 2157 08-JUL-1997;   |
| FEATURES              | Location/Qualifiers<br>1..17<br>/organism="unknown"<br>/mol_type="unassigned DNA"  |
| Query Match           | 0.4%; Score 15.4; DB 1; Length 17;   |
| Best Local Similarity | 94.1%; Pred. No. 2.1e+02;  |
| Matches               | 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  |
| Qy                    | 1153 TTCTTTTTATATATAT 1169<br>     <br>1 TTATTTTATATATAT 17  |
| Db                    |  |
| RESULT 233            |  |
| I54416                |  |
| LOCUS                 | I54416 17 bp DNA linear PAT 01-DEC-1998  |
| DEFINITION            | Sequence 579 from patent US 5731295.   |
| ACCESSION             | I54416   |
| VERSION               | I54416.1 GI:3938886  |
| KEYWORDS              | .  |
| SOURCE                | Unknown.   |
| ORGANISM              | Unclassified.  |
| REFERENCE             | 1 (bases 1 to 17)  |
| AUTHORS               | Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.  |
| TITLE                 | Method of reducing stromelysin RNA via ribozymes   |
| JOURNAL               | Patent: US 5731295-A 579 24-MAR-1998;  |
| FEATURES              | Location/Qualifiers<br>1..17<br>/organism="unknown"<br>/mol_type="unassigned DNA"  |
| Query Match           | 0.4%; Score 15.4; DB 1; Length 17;   |
| Best Local Similarity | 94.1%; Pred. No. 2.1e+02;  |
| Matches               | 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  |
| Qy                    | 1153 TTCTTTTAAAGGAA 1048<br>     <br>1 TTTCATTTTAAAGGA 17  |
| Db                    |  |
| RESULT 234            |  |
| I54417                |  |
| LOCUS                 | I54417 17 bp DNA linear PAT 01-DEC-1998  |
| DEFINITION            | Sequence 580 from patent US 5731295.   |
| ACCESSION             | I54417   |
| VERSION               | I54417.1 GI:3938887  |
| KEYWORDS              | .  |
| SOURCE                | Unknown.   |
| ORGANISM              | Unclassified.  |
| REFERENCE             | 1 (bases 1 to 17)  |
| AUTHORS               | Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.  |
| TITLE                 | Method of reducing stromelysin RNA via ribozymes   |
| JOURNAL               | Patent: US 5731295-A 580 24-MAR-1998;  |
| FEATURES              | Location/Qualifiers<br>1..17<br>/organism="unknown"<br>/mol_type="unassigned DNA"  |
| Query Match           | 0.4%; Score 15.4; DB 1; Length 17;   |
| Best Local Similarity | 94.1%; Pred. No. 2.1e+02;  |
| Matches               | 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  |
| Qy                    | 1033 TTTCTTTTAAAGGAA 1049<br>     <br>1 TTTCATTTTAAAGGA 17   |
| Db                    |  |
| RESULT 235            |  |
| AX009039/c            |  |
| LOCUS                 | AX009039 17 bp DNA linear PAT 06-SEP-2000  |
| DEFINITION            | Sequence 72 from Patent WO9963975.   |
| ACCESSION             | AX009039   |
| VERSION               | AX009039.1 GI:9996413  |
| KEYWORDS              | .  |
| SOURCE                | Homo sapiens (human)   |
| ORGANISM              | Homo sapiens   |
| REFERENCE             | 1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.<br>A method for stimulating the immune system<br>Patent: WO 9963975-A 72 16-DEC-1999;<br>BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)<br>Location/Qualifiers<br>1..17<br>/organism="Homo sapiens"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:9606" |
| Query Match           | 0.4%; Score 15.4; DB 1; Length 17;   |
| Best Local Similarity | 94.1%; Pred. No. 2.1e+02;  |
| Matches               | 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  |
| Qy                    | 2349 CCTTGCTGTGTGCCCA 2365<br>     <br>17 CCTTGCTGTGTGCCCA 1   |
| Db                    |  |
| RESULT 236            |  |
| AX736539/c            |  |
| LOCUS                 | AX736539 17 bp DNA linear PAT 08-MAY-2003  |

[illegible][illegible]



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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTCTCTTTTATATATA 1168
DB 1 TTTATTTTATATATA 17

RESULT 227
LOCUS AR047364 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2157 from patent US 5817796.
ACCESSION AR047364
VERSION AR047364.1 GI:5968829
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J., and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL Patent: US 5817796-A 2157 06-OCT-1998;
FEATURES Location/Qualifiers
source 1..17
organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTCTTTTATATATAT 1169
DB 1 TTATTTTATATATAT 17

RESULT 228
LOCUS BD234968/c 17 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234968
VERSION BD234968.1 GI:33044738
KEYWORDS JP 2002517434-A/72.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 17)
JOURNAL Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
PATENT: JP 2002517434-A 72 18-JUN-2002;
COMMENT BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/72
PD 18-JUN-2002
PP 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00.
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES source 1..17
Location/Qualifiers
/organism="Homo sapiens"

/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2349 CCTGCTGTGTGTCCTCA 2365
DB 17 CCTGCTGCTGTGTCCTCA 1

RESULT 229
LOCUS I37566 17 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 579 from patent US 5612215.
ACCESSION I37566
VERSION I37566.1 GI:2085526
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
Stinchcomb,D.T.
TITLE Stromelysin targeted ribozymes
JOURNAL Patent: US 5612215-A 579 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..17
organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1032 TTTCTCTTTTAAAGGA 1048
DB 1 TTTTCATTTTAAAGGA 17

RESULT 230
LOCUS I37567 17 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 580 from patent US 5612215.
ACCESSION I37567
VERSION I37567.1 GI:2085527
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
Stinchcomb,D.T.
TITLE Stromelysin targeted ribozymes
JOURNAL Patent: US 5612215-A 580 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..17
organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1033 TTTCTCTTTTAAAGGA 1049
DB 1 TTTTCATTTTAAAGGA 17

RESULT 231
LOCUS I54414 17 bp DNA linear PAT 07-OCT-1997
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|                                     |   |                         |      |  |  |
|-------------------------------------|---|-------------------------|------|--|--|
| Sequence 32 from patent US 6635422. |   |                         |      |  |  |
| DEFINITION                          |   |                         |      |  |  |
| ACCESSION                           | AR409919  |                         |      |  |  |
| VERSION                             | AR409919.1 GI:40161054  |                         |      |  |  |
| KEYWORDS                            | Unknown.  |                         |      |  |  |
| SOURCE                              | Unknown.  |                         |      |  |  |
| ORGANISM                            | Unclassified.   |                         |      |  |  |
| REFERENCE                           | 1 (bases 1 to 22)   |                         |      |  |  |
| AUTHORS                             | Keene,J.D., Tenenbaum,S.A. and Carson,C.C.  |                         |      |  |  |
| TITLE                               | Methods for isolating and characterizing endogenous mRNA-protein (mRNP) complexes |                         |      |  |  |
| JOURNAL                             | Patent: US 6635422-A 32 21-OCT-2003;  |                         |      |  |  |
| FEATURES                            | Location/Qualifiers   |                         |      |  |  |
| source                              | 1..22   |                         |      |  |  |
|                                     | /organism="unknown"   |                         |      |  |  |
|                                     | /mol_type="unassigned RNA"  |                         |      |  |  |
| Query Match                         | 0.4%; Score 15.6; DB 1; Length 22;  |                         |      |  |  |
| Best Local Similarity               | 81.8%; Pred.No.3.4e+02;   |                         |      |  |  |
| Matches                             | 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;                               |                         |      |  |  |
| <br>                                |   |                         |      |  |  |
| QY                                  | 2578  | AAAAAAAAAATTGGAGAAAAA   | 2599 |  |  |
|                                     |   |                         |      |  |  |
| Db                                  | 22  | AAAAAAAACCCAATTAAGAAAAA | 1    |  |  |
| <br>                                |   |                         |      |  |  |
| RESULT 225                          |   |                         |      |  |  |
| AX404674/c                          |   |                         |      |  |  |
| LOCUS                               | AX404674 22 bp DNA linear PAT 14-JUN-2002   |                         |      |  |  |
| DEFINITION                          | Sequence 48 from Patent WO0224745.  |                         |      |  |  |
| ACCESSION                           | AX404674  |                         |      |  |  |
| VERSION                             | AX404674.1 GI:21437955  |                         |      |  |  |
| KEYWORDS                            | synthetic construct   |                         |      |  |  |
| SOURCE                              | synthetic construct   |                         |      |  |  |
| ORGANISM                            | other sequences; artificial sequences.  |                         |      |  |  |
| REFERENCE                           | 1   |                         |      |  |  |
| AUTHORS                             | Abken,H. and Schinkoethe,T.   |                         |      |  |  |
| TITLE                               | Method for detecting tumor cells  |                         |      |  |  |
| JOURNAL                             | Patent: WO 0224745-A 48 28-MAR-2002;  |                         |      |  |  |
|                                     | Abken, Hinrich (DE)   |                         |      |  |  |
| FEATURES                            | Location/Qualifiers   |                         |      |  |  |
| source                              | 1..22   |                         |      |  |  |
|                                     | /organism="synthetic construct"   |                         |      |  |  |
|                                     | /mol_type="unassigned DNA"  |                         |      |  |  |
|                                     | /db_xref="taxon:32630"  |                         |      |  |  |
|                                     | /note="Sonde"   |                         |      |  |  |
| Query Match                         | 0.4%; Score 15.6; DB 1; Length 22;  |                         |      |  |  |
| Best Local Similarity               | 81.8%; Pred.No.3.4e+02;   |                         |      |  |  |
| Matches                             | 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;                               |                         |      |  |  |
| <br>                                |   |                         |      |  |  |
| QY                                  | 3795  | TCATTTTCCAAAGATAAAAA    | 3816 |  |  |
|                                     |   |                         |      |  |  |
| Db                                  | 22  | TTTTTTTTCCAAAAAA        | 1    |  |  |
| <br>                                |   |                         |      |  |  |
| RESULT 226                          |   |                         |      |  |  |
| AR047362                            |   |                         |      |  |  |
| LOCUS                               | AR047362 17 bp DNA linear PAT 29-SEP-1999   |                         |      |  |  |
| DEFINITION                          | Sequence 2155 from patent US 5817796.   |                         |      |  |  |
| ACCESSION                           | AR047362  |                         |      |  |  |
| VERSION                             | AR047362.1 GI:5968827   |                         |      |  |  |
| KEYWORDS                            | Unknown.  |                         |      |  |  |
| SOURCE                              | Unknown.  |                         |      |  |  |
| ORGANISM                            | Unclassified.   |                         |      |  |  |
| REFERENCE                           | 1 (bases 1 to 17).  |                         |      |  |  |
| AUTHORS                             | Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.                            |                         |      |  |  |
| TITLE                               | C-myp ribozymes having 2'-5'-linked adenylyate residues                           |                         |      |  |  |
| JOURNAL                             | Patent: US 5817796-A 2155 06-OCT-1998;  |                         |      |  |  |
| FEATURES                            | Location/Qualifiers   |                         |      |  |  |
| source                              | 1..17   |                         |      |  |  |

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Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCAGCAGCGCG 633
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Db 1 GCGCGCGCGCGCGCGCGCG 19

RESULT 218
AX355314/c
LOCUS AX355314 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 342 from Patent WO0197843.
ACCESSION AX355314
VERSION AX355314.1 GI:18619982
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 138 11-JUL-2002;
FEATURES Location/Qualifiers
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            /note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CCGCGCGCGCAGCAGCGCG 634
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Db 19 CCGCGCGCGCGCGCGCGCG 1

RESULT 219
AX546999
LOCUS AX546999 19 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 138 from Patent WO02053141.
ACCESSION AX546999
VERSION AX546999.1 GI:25812143
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 138 11-JUL-2002;
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            /note="Synthetic Sequence"

Query Match      0.4%; Score 15.8; DB 1; Length 19;
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RESULT 220
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LOCUS AX546999 19 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 138 from Patent WO02053141.
ACCESSION AX546999
VERSION AX546999.1 GI:25812143
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 138 11-JUL-2002;
FEATURES Location/Qualifiers
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QY 3162 TCAAGAGCCCCCAGCAACAC 3180
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Db 1 TCACGTGCCCCCAGCAACAC 19

RESULT 222
BD065893/c
LOCUS BD065893 19 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065893
VERSION BD065893.1 GI:22611496
KEYWORDS JP 2001511000-A/528.
SOURCE unidentified
ORGANISM unidentified
          unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Schlingensiepen,K.H. and Brysch,W.

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ACCESSION AX008974
VERSION AX008974.1 GI:9996348
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 993975-A 7 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1520 GGAGGTTTATAAATCGAC 1538
Db 19 GGAGGTTTACAAATAGAC 1
RESULT 214
AX103946
LOCUS AX103946 19 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 138 from Patent WO0122972.
ACCESSION AX103946
VERSION AX103946.1 GI:13920143
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
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Db 1 GCGGCGCGCGCGCGCGC 19
RESULT 215
AX103946/c
LOCUS AX103946/c 19 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 138 from Patent WO0122972.
ACCESSION AX103946
VERSION AX103946.1 GI:13920143
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 138 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3591 TTTGGACTTTTCTTTTAA 3609
Db 19 TTTGGACTTTATCTTTAA 1
RESULT 217
AX355314
LOCUS AX355314 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 342 from Patent WO0197843.
ACCESSION AX355314
VERSION AX355314.1 GI:18619982
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 342 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
Location/Qualifiers
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/Note="Synthetic oligonucleotide-phosphodiester backbone"
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCACGCGCGC 634
Db 19 CGCGCGCGCGCGCGCGC 1
RESULT 216
AX132849/c
LOCUS AX132849 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 4067 from Patent WO0130362.
ACCESSION AX132849
VERSION AX132849.1 GI:14139159
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 4067 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
Location/Qualifiers
source 1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/Note="PCNA HH ribozyme binding site"
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3591 TTTGGACTTTTCTTTTAA 3609
Db 19 TTTGGACTTTATCTTTAA 1
RESULT 217
AX355314
LOCUS AX355314 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 342 from Patent WO0197843.
ACCESSION AX355314
VERSION AX355314.1 GI:18619982
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 342 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/Note="Synthetic oligonucleotide-phosphodiester backbone"
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAATCGAC 1538
Db 19 GGAGGTTTACAAAATAGAC 1

RESULT 209
A88400/c
LOCUS
DEFINITION Sequence 548 from Patent WO9833904.
ACCESSION A88400
VERSION A88400.1 GI:6736970
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 548 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2212 GGAATGGATCCATGAACC 2230
Db 19 GGAATGGATACACGAACC 1

RESULT 212
BD234903/c
LOCUS
DEFINITION A method for stimulating the immune system.
ACCESSION BD234903
VERSION BD234903.1 GI:33044673
KEYWORDS JP 2002517434-A/7.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 7 18-JUN-2002;
BIOGHOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/7
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 9810709.7, 25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
BRYSCH
PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61P31/
PC A61P35/00,
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Homo sapiens (human)'

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Query Match 0.4%; Score 15.8; DB 1; Length 19;
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAATCGAC 1538
Db 19 GGAGGTTTACAAAATAGAC 1

RESULT 211
A90367/c
LOCUS
DEFINITION Sequence 548 from Patent EP0856579.
ACCESSION A90367
VERSION A90367.1 GI:6738881
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 528 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
Location/Qualifiers
source
1..19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAATCGAC 1538
Db 19 GGAGGTTTACAAAATAGAC 1

RESULT 211
A90367/c
LOCUS
DEFINITION Sequence 548 from Patent EP0856579.
ACCESSION A90367
VERSION A90367.1 GI:6738881
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Query Match 0.4%; Score 16; DB 1; Length 24;  
Best Local Similarity 79.2%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT 2754  
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Db 24 AAAAAAAAAAGGGTTTTTTT 1

RESULT 204  
I35523/c  
LOCUS I35523 24 bp DNA linear PAT 13-MAY-1997  
DEFINITION Sequence 13 from patent US 5599922.  
ACCESSION I35523  
VERSION I35523.1 GI:2088491  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.  
TITLE Oligonucleotide N3'-p5', phosphoramidates: hybridization and  
nuclease resistance properties  
JOURNAL Patent: US 5599922-A 13 04-FEB-1997;  
FEATURES Location/Qualifiers  
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Query Match 0.4%; Score 16; DB 1; Length 24;  
Best Local Similarity 79.2%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT 2754  
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Db 24 AAAAAAAAAAGGGTTTTTTT 1

RESULT 205  
I43133/c  
LOCUS I43133 24 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 13 from patent US 5631135.  
ACCESSION I43133  
VERSION I43133.1 GI:2468377  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.  
TITLE Oligonucleotide N3'.fwdw.p5', phosphoramidates: hybridization and  
nuclease resistance properties  
JOURNAL Patent: US 5631135-A 13 20-MAY-1997;  
FEATURES Location/Qualifiers  
source 1..24  
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Query Match 0.4%; Score 16; DB 1; Length 24;  
Best Local Similarity 79.2%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT 2754  
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Db 24 AAAAAAAAAAGGGTTTTTTT 1

RESULT 206  
I92011/c  
LOCUS I92011 24 bp DNA linear PAT 01-DEC-1998  
DEFINITION Sequence 13 from patent US 5726297.  
ACCESSION I92011  
VERSION I92011.1 GI:3936481

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.  
TITLE Oligodeoxyribonucleotide N3', P5', phosphoramidates  
JOURNAL Patent: US 5726297-A 13 10-MAR-1998;  
FEATURES Location/Qualifiers  
source 1..24  
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Query Match 0.4%; Score 16; DB 1; Length 24;  
Best Local Similarity 79.2%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT 2754  
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Db 24 AAAAAAAAAAGGGTTTTTTT 1

RESULT 207  
A05202  
LOCUS A05202 19 bp DNA linear PAT 07-MAY-1993  
DEFINITION Oligonucleotide primer 1.  
ACCESSION A05202  
VERSION A05202.1 GI:345043  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Patent: WO 8803807-A 2 02-JUN-1988;  
JOURNAL Location/Qualifiers  
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Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2268 CCATATCTATGAGTTCAG 2286  
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Db 1 CCGTATTATGAGTTCAG 19

RESULT 208  
A88380/c  
LOCUS A88380 19 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 528 from Patent WO9833904.  
ACCESSION A88380  
VERSION A88380.1 GI:6736950  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 528 06-AUG-1998;  
FEATURES Location/Qualifiers  
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/organism="unidentified"  
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Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.3e+02;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTTTTT 2754  
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Db 24 AAAAAAAAAAGGGGTTTTTTTTT 1

RESULT 200  
BD123295/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 24)  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

AR123295 24 bp DNA linear PAT 16-MAY-2001  
Sequence 13 from patent US 6169170.  
ACCESSION  
AR123295.1 GI:14108261  
Unknown.  
Unknow.  
Unclassified.  
Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.  
Oligonucleotide N3'.fwdarw.N5'.Phosphoramidate Duplexes  
Patent: US 6169170-A 13 02-JAN-2001;  
Location/Qualifiers  
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QY 2731 AAAAGAAAAACATCTTTTTTTT 2754  
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Db 24 AAAAAAAAAAGGGGTTTTTTTTT 1

RESULT 201  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 24)  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD175807 24 bp DNA linear PAT 18-MAR-2003  
2'-4'-RNA oligonucleotide having N3'-P5' binding.  
BD175807  
BD175807.1 GI:29121509  
JP 2002255990-A/10.  
synthetic construct  
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other sequences; artificial sequences.  
1 (bases 1 to 24)  
Imanishi,T. and Kohiga,S.  
2'-4'-RNA oligonucleotide having N3'-P5' binding  
Patent: JP 2002255990-A 10 11-SEP-2002;  
SANKYO CO LTD  
OS Artificial Sequence  
PN JP 2002255990-A/10  
PD 11-SEP-2002  
PF 19-NOV-2001 JP 2001352543  
PI TAKESHI IMANISHI,SATOSHI KOHIGA  
PC C07H19/06,A61K31/712,A61K48/00,A61P31/18,C07H19/16,C07H21/00,  
PC C12N15/09,  
PC C12N15/00  
CC Description of Artificial Sequence: Synthesized and hairpin-  
formed  
CC oligonucleotide  
CC key Location/Qualifiers  
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FT source /organism='Artificial Sequence'.  
FT Location/Qualifiers  
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Query Match 0.4%; Score 16; DB 1; Length 24;  
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Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 24 AAAAAAAAAAGGGGTTTTTTTTT 1

RESULT 202  
BD188897/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 24)  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD188897 24 bp DNA linear PAT 17-JUL-2003  
Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;  
hybridization and nuclease tolerant characteristics.  
BD188897  
BD188897.1 GI:32998636  
JP 2003012688-A/13.  
unidentified  
unclassified.  
1 (bases 1 to 24)  
Gryaznov,S.M., Schultz,R.G. and Chen,J.  
Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound  
hybridization and nuclease tolerant characteristics  
Patent: JP 2003012688-A 13 15-JAN-2003;  
LYNX THERAPEUTICS INC  
OS Unidentified  
PN JP 2003012688-A/13  
PD 15-JAN-2003  
PF 12-JUN-2002 JP 2002171743  
PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI  
SERGEI M GRYAZNOV,RONALD G SCHULTZ,JER-KANG CHEN PC  
C07H19/16//C12Q1/02,C12Q1/68  
CC Strandedness: Both;  
CC Topology: Linear;  
CC Oligonucleotide N3' to P5' phosphoramidate: synthesis and CC  
compound;  
hybridization and nuclease tolerant characteristics FH Key  
CC Location/Qualifiers  
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FT Location/Qualifiers  
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Query Match 0.4%; Score 16; DB 1; Length 24;  
Best Local Similarity 79.2%; Pred. No. 3.4e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2731 AAAAGAAAAACATCTTTTTTTT 2754  
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Db 24 AAAAAAAAAAGGGGTTTTTTTTT 1

RESULT 203  
I33258/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 24)  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

I33258 24 bp DNA linear PAT 06-FEB-1997  
Sequence 13 from patent US 5591607.  
I33258  
I33258.1 GI:1824049  
Unknown.  
Unknow.  
Unclassified.  
1 (bases 1 to 24)  
Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.  
Oligonucleotide N3'.fwdarw.P5' phosphoramidates: triplex DNA  
formation  
Patent: US 5591607-A 13 07-JAN-1997;  
Location/Qualifiers  
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/mol\_type="unassigned DNA"

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DEFINITION Sequence 40 from Patent WO0071747.
ACCESSION AX048441
VERSION AX048441.1 GI:12225605
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 40 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
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/note="Beschreibung der kunstlichen
Sequenz:Erkennungssystem"
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1
RESULT 196
AX048442/c
LOCUS AX048442 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 41 from Patent WO0071747.
ACCESSION AX048442
VERSION AX048442.1 GI:12225606
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 41 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
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source
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Sequenz:Erkennungssystem"
Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1
RESULT 197
AX048443/c
LOCUS AX048443 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 42 from Patent WO0071747.
ACCESSION AX048443
VERSION AX048443.1 GI:12225607
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 42 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
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Sequenz:Erkennungssystem"
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QY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1
RESULT 198
AX058881/c
LOCUS AX058881 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5837835.
ACCESSION AR058881
VERSION AR058881.1 GI:5984458
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 13 17-NOV-1998;
Aventis Research & Technologies GmbH & Co. KG (DE)
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2731 AAAAGAAAACATCTTTT 2754
Db 24 AAAAGAAAAGGGTTT 1
RESULT 199
AR079586/c
LOCUS AR079586 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 13 from patent US 5965720.
ACCESSION AR079586
VERSION AR079586.1 GI:10006330
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 13 12-OCT-1999;
Aventis Research & Technologies GmbH & Co. KG (DE)
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Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2731 AAAAGAAAACATCTTTT 2754
Db 24 AAAAGAAAAGGGTTT 1
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PD 12-FEB-2002
PR 18-FEB-1999 JP 2000532549
PR 20-FEB-1998 US 09/026601
PI JAMES JOSEPH BECK
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: primer JB659 FH key
FT source 1..19
FT Location/Qualifiers
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   1..19
   /organism="Artificial Sequence".

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Length 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3190 GAAGCTTCATGGACGC 3205
Db 1 GAAGCTTCATGGACGC 16

RESULT 191
AR200636
LOCUS AR200636 19 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 25 from patent US 6358680.
ACCESSION AR200636
VERSION AR200636.1 GI:20251524
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Beck,J.Joseph.
TITLE Detection of wheat and barley fungal pathogens using the polymerase
JOURNAL chain reaction
FEATURES
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   Location/Qualifiers
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   /organism="unknown"
   /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3190 GAAGCTTCATGGACGC 3205
Db 1 GAAGCTTCATGGACGC 16

RESULT 192
AR116691
LOCUS AR116691 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6133434.
ACCESSION AR116691
VERSION AR116691.1 GI:14097013
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buell,G.Nutter., Surprenant,A. and Kawashima,E.
TITLE Purinergic receptor
JOURNAL Patent: US 6133434-A 4 17-OCT-2000;
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Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2102 GTCCAGCCGCGGAAG 2117
Db 1 GTCCAGCCGCGGAAG 16

RESULT 193
AR275649
LOCUS AR275649 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 4 from patent US 6509163.
ACCESSION AR275649
VERSION AR275649.1 GI:29709100
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buell,G.N., Surprenant,A. and Kawashima,E.
TITLE Methods of screening modulators of mammalian P2X7 purinergic
JOURNAL receptors
FEATURES
   source
   Location/Qualifiers
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   /organism="unknown"
   /mol_type="genomic DNA"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2102 GTCCAGCCGCGGAAG 2117
Db 1 GTCCAGCCGCGGAAG 16

RESULT 194
AX048440/c
LOCUS AX048440 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 39 from Patent WO0071747.
ACCESSION AX048440
VERSION AX048440.1 GI:12225604
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
JOURNAL production and use of the same
FEATURES
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   Location/Qualifiers
   1..20
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Beschreibung der kunstlichen
   Sequenz:Erkennungssystem"

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2588
Db 16 TTTAAAAA 1

RESULT 195
AX048441/c
LOCUS AX048441 20 bp DNA linear PAT 12-JAN-2001

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thioredoxin reductase genes and methods of using same to modulate cell growth

JOURNAL  
Patent: US 6566514-A 2 20-MAY-2003;  
Location/Qualifiers

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Query Match 0.4%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2209 GATGGAATGGATCCA 2224  
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Db 1 GATGGAATGGATCCA 16

RESULT 187  
AX009027/c  
LOCUS 17 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 60 from Patent WO963975.  
ACCESSION AX009027  
VERSION AX009027.1 GI:9996401  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1  
AUTHORS Brysch, W., Schlingensiepen, K.H. and Schlingensiepen, R.  
TITLE A method for stimulating the immune system  
JOURNAL Patent: WO 9963975-A 60 16-DEC-1999;  
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL  
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)  
Location/Qualifiers

FEATURES  
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1. .17  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1806 GAATGGCTCTCCTTCG 1821  
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Db 16 GAATGGCTCTCCTTCG 1

RESULT 188  
BD131940  
LOCUS 17 bp DNA linear PAT 18-SEP-2002  
DEFINITION Oligonucleotide sequence complementary to thioredoxin gene or  
thioredoxin reductase gene and utilization thereof for controlling  
cell proliferation.  
ACCESSION BD131940  
VERSION BD131940.1 GI:23226885  
KEYWORDS JP 2002501743-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS Wright, J.A., Young, A.H. and Lee, Y.S.  
TITLE Oligonucleotide sequence complementary to thioredoxin gene or  
thioredoxin reductase gene and utilization thereof for controlling  
JOURNAL Patent: JP 2002501743-A 2 22-JAN-2002;  
GENSENSE TECHNOLOGIES INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002501743-A/2  
PD 22-JAN-2002  
PR 29-JAN-1999 JP 2000529423  
PR 30-JAN-1998 US 60/073196

JIM A WRIGHT, AIPING H YOUNG, YOON S LEE  
C12N15/09, A61K31/711, A61K48/00, A61P35/00, A61P35/04, C07H21/04//  
PC (A61K31/711, A61K45/00), (A61K48/00, A61K45/00), C12N15/00 CC  
Oligonucleotide sequence complementary to thioredoxin gene or CC  
thioredoxin  
CC reductase gene and utilization thereof for controlling cell  
proliferation  
FH Key Location/Qualifiers  
FT source 1. .17  
/organism="Homo sapiens (human)"  
/db\_xref="taxon:9606"

FEATURES  
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Location/Qualifiers

Query Match 0.4%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2209 GATGGAATGGATCCA 2224  
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Db 1 GATGGAATGGATCCA 16

RESULT 189  
I73187/c  
LOCUS 18 bp DNA linear PAT 03-APR-1998  
DEFINITION Sequence 1 from patent US 5686242.  
ACCESSION I73187  
VERSION I73187.1 GI:3009326  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Bruice, T.W. and Lima, W.F.  
TITLE Determination of oligonucleotides for therapeutics, diagnostics and  
research reagents  
JOURNAL Patent: US 5686242-A 1 11-NOV-1997;  
Location/Qualifiers

FEATURES  
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Query Match 0.4%; Score 16; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2803 AAAAAAAAAAACATC 2818  
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Db 17 AAAAAAAAAAACATC 2

RESULT 190  
BD137911  
LOCUS 19 bp DNA linear PAT 18-SEP-2002  
DEFINITION Detection of wheat and barley fungal pathogens using the polymerase  
chain reaction.  
ACCESSION BD137911  
VERSION BD137911.1 GI:23232856  
KEYWORDS JP 2002504347-A/25.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Beck, J.J.  
TITLE Detection of wheat and barley fungal pathogens using the polymerase  
chain reaction  
JOURNAL Patent: JP 2002504347-A 25 12-FEB-2002;  
NOVARTIS AG  
COMMENT OS Artificial Sequence  
PN JP 2002504347-A/25

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QY      2156 GCAGGATAATTGCTGC 2171
Db      16 GCAGGATAATTGCTGC 1

RESULT 183
BD066606/c
LOCUS   An antisense oligonucleotide preparation method.
DEFINITION
ACCESSION BD066606
VERSION   BD066606.1 GI:22612209
KEYWORDS JP 2001511000-A/1241.
SOURCE   unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE    An antisense oligonucleotide preparation method
JOURNAL  Patent: JP 2001511000-A 1241 07-AUG-2001;
        BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT  OS Unknown
        PN JP 2001511000-A/1241
        PD 07-AUG-2001
        PF 30-JAN-1998 JP 1998532533
        PR 31-JAN-1997 EP 97101531.8
        PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
        PC C12N15/11,C07H21/04,A61K31/70
        CC An antisense oligonucleotide preparation method FH Key
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Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2020 AGTCCACTAGGAAAAA 2035
Db      16 AGTCCACTAGGAAAAA 1

RESULT 184
BD066613/c
LOCUS   An antisense oligonucleotide preparation method.
DEFINITION
ACCESSION BD066613
VERSION   BD066613.1 GI:22612216
KEYWORDS JP 2001511000-A/1248.
SOURCE   unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE    An antisense oligonucleotide preparation method
JOURNAL  Patent: JP 2001511000-A 1248 07-AUG-2001;
        BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT  OS Unknown
        PN JP 2001511000-A/1248
        PD 07-AUG-2001
        PF 30-JAN-1998 JP 1998532533
        PR 31-JAN-1997 EP 97101531.8
        PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
        PC C12N15/11,C07H21/04,A61K31/70
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Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2153 TGTGCAGGATAATTGC 2168
Db      16 TGTGCAGGATAATTGC 1

RESULT 185
BD234956/c
LOCUS   A method for stimulating the immune system.
DEFINITION
ACCESSION BD234956
VERSION   BD234956.1 GI:33044726
KEYWORDS JP 2002517434-A/60.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schlengensiepen,K.H., Schlengensiepen,R. and Brysch,W.
TITLE    A method for stimulating the immune system
JOURNAL  Patent: JP 2002517434-A 60 18-JUN-2002;
        BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT  OS Homo sapiens (human)
        PN JP 2002517434-A/60
        PD 18-JUN-2002
        PF 10-JUN-1999 JP 2000553044
        PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
        PI KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG BRYSCH
        PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
        PC 00,A61P35/00,
        PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
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Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1806 GAATGGCTCTCCTTCG 1821
Db      16 GAATGGCTCTCCTTCG 1

RESULT 186
AR337667
LOCUS   Sequence 2 from patent US 6566514.
DEFINITION
ACCESSION AR337667
VERSION   AR337667.1 GI:33724235
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE    Oligonucleotide sequences complementary to thioredoxin or

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Query Match  
Best Local Similarity 0.4%; Score 16; DB 1; Length 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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/db\_xref="taxon:9606"

Qy 2020 AGTCCACTAGGAAAA 2035  
Db 16 AGTCCACTAGGAAAA 1

RESULT 179  
AX30151/c  
LOCUS AX30151 16 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 113 from Patent EP1008649.  
ACCESSION AX30151  
VERSION AX30151.1 GI:10190368  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2 (tgf-b2)  
JOURNAL Patent: EP 1008649-A 113 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match  
Best Local Similarity 0.4%; Score 16; DB 1; Length 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2153 TGTGCAGGATAATGC 2168  
Db 16 TGTGCAGGATAATGC 1

RESULT 180  
AX316464/c  
LOCUS AX316464 16 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 105 from Patent EP1160319.  
ACCESSION AX316464  
VERSION AX316464.1 GI:17899637  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 105 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Description of unknown: unknown"

Query Match  
Best Local Similarity 0.4%; Score 16; DB 1; Length 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2020 AGTCCACTAGGAAAA 2035  
Db 16 AGTCCACTAGGAAAA 1

RESULT 181  
AX316472/c  
LOCUS AX316472 16 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 113 from Patent EP1160319.  
ACCESSION AX316472  
VERSION AX316472.1 GI:17899645  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 113 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
FEATURES  
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1. .16  
Location/Qualifiers  
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/note="Description of unknown: unknown"

Query Match  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2153 TGTGCAGGATAATGC 2168  
Db 16 TGTGCAGGATAATGC 1

RESULT 182  
BD065911/c  
LOCUS BD065911 16 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD065911  
VERSION BD065911.1 GI:22611514  
KEYWORDS JP 2001511000-A/546.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 546 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Unknown  
PN JP 2001511000-A/546  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
Location/Qualifiers  
FT source  
1. .16  
Location/Qualifiers  
/organism="Unknown"

Query Match  
Best Local Similarity 0.4%; Score 16; DB 1; Length 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 174
AR367888
LOCUS          AR367888          16 bp      DNA          linear          PAT 12-SEP-2003
DEFINITION     Sequence 17 from patent US 6376199.
ACCESSION      AR367888
VERSION        AR367888.1  GI:34601344
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 16)
AUTHORS       Caniggia,I., Post,M. and Lye,S.
TITLE         Methods to diagnose a required regulation of trophoblast invasion
JOURNAL       Patent: US 6376199-A 17 23-APR-2002;
FEATURES       Location/Qualifiers
source        1..16
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match    0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACTACTGTGTG 1232
Db 1 CATGCACTACTGTGTG 16

RESULT 175
ARX008985/c
LOCUS          AX008985          16 bp      DNA          linear          PAT 06-SEP-2000
DEFINITION     Sequence 18 from Patent WO9963975.
ACCESSION      AX008985
VERSION        AX008985.1  GI:9996359
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS       Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE         A method for stimulating the immune system
JOURNAL       Patent: WO 9963975-A 18 16-DEC-1999;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
              HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES       Location/Qualifiers
source        1..16
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match    0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAAA 2035
Db 16 AGTCCACTAGGAAAAA 1

RESULT 176
ARX008987/c
LOCUS          AX008987          16 bp      DNA          linear          PAT 06-SEP-2000
DEFINITION     Sequence 20 from Patent WO9963975.
ACCESSION      AX008987
VERSION        AX008987.1  GI:9996361
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS       Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
              and Schlingensiepen,R.
TITLE         Antisense-oligonucleotides for the treatment of immuno-suppressive
              effects of transforming growth factor-b2 (tgf-b2)
JOURNAL       Patent: EP 1008649-A 105 14-JUN-2000;
              BIOGNOSTIK GES (DE)
FEATURES       Location/Qualifiers
source        1..16
              /organism="Homo sapiens"
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AUTHORS       Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE         A method for stimulating the immune system
JOURNAL       Patent: WO 9963975-A 20 16-DEC-1999;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
              HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES       Location/Qualifiers
source        1..16
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match    0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATTGC 2168
Db 16 TGTGCAGGATAATTGC 1

RESULT 177
ARX008988/c
LOCUS          AX008988          16 bp      DNA          linear          PAT 06-SEP-2000
DEFINITION     Sequence 21 from Patent WO9963975.
ACCESSION      AX008988
VERSION        AX008988.1  GI:9996362
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS       Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE         A method for stimulating the immune system
JOURNAL       Patent: WO 9963975-A 21 16-DEC-1999;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
              HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES       Location/Qualifiers
source        1..16
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match    0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2156 GCAGGATAATTGCTGC 2171
Db 16 GCAGGATAATTGCTGC 1

RESULT 178
ARX030143/c
LOCUS          AX030143          16 bp      DNA          linear          PAT 16-SEP-2000
DEFINITION     Sequence 105 from Patent EP1008649.
ACCESSION      AX030143
VERSION        AX030143.1  GI:10190360
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS       Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
              and Schlingensiepen,R.
TITLE         Antisense-oligonucleotides for the treatment of immuno-suppressive
              effects of transforming growth factor-b2 (tgf-b2)
JOURNAL       Patent: EP 1008649-A 105 14-JUN-2000;
              BIOGNOSTIK GES (DE)
FEATURES       Location/Qualifiers
source        1..16
              /organism="Homo sapiens"
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(TGF-.beta.)

JOURNAL Patent: US 6455689-A 105 24-SEP-2002;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGCAGGATAATTGC 2168  
|||||  
16 TGTGCAGGATAATTGC 1

Db 16 AGTCCACTAGGAAAA 1

RESULT 170  
BD234917/c 16 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION A method for stimulating the immune system.  
ACCESSION BD234917  
VERSION BD234917.1 GI:33044687  
KEYWORDS JP 2002517434-A/21.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,K.-F., Brysch,W., Schlingensiepen,K.-H.,  
TITLE A method for stimulating the immune system  
JOURNAL Patent: JP 2002517434-A 21 18-JUN-2002;  
COMMENT BIOLOGIST GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH  
OS Homo sapiens (human)  
PN JP 2002517434-A/21  
PD 18-JUN-2002  
PF 10-JUN-1999 JP 2000553044  
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI  
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI  
BRYSCH  
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/  
PC 00,A61P35/00.  
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A  
method for stimulating the immune system  
FH Key Location/Qualifiers  
FT source 1..16  
FT Location/Qualifiers  
source 1..16  
/organism="Homo sapiens (human)".  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 0.4%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2156 GCAGGATAATTGCTGC 2171  
|||||  
16 GCAGGATAATTGCTGC 1

Db 16 GCAGGATAATTGCTGC 1

RESULT 171  
AR232848/c 16 bp DNA linear PAT 20-DEC-2002  
LOCUS  
DEFINITION Sequence 105 from patent US 6455689.  
ACCESSION AR232848  
VERSION AR232848.1 GI:27275186  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,K.-F., Brysch,W., Schlingensiepen,K.-H.,  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.

Query Match 0.4%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACACTACTGTGTG 1232  
|||||  
16 CATGCACACTACTGTGTG 1

Db 16 CATGCACACTACTGTGTG 1

(TGF-.beta.)

JOURNAL Patent: US 6455689-A 105 24-SEP-2002;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 AGTCCACTAGGAAAA 2035  
|||||  
16 AGTCCACTAGGAAAA 1

Db 16 AGTCCACTAGGAAAA 1

RESULT 172  
AR232856/c 16 bp DNA linear PAT 20-DEC-2002  
LOCUS  
DEFINITION Sequence 113 from patent US 6455689.  
ACCESSION AR232856  
VERSION AR232856.1 GI:27275194  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Schlingensiepen,K.-F., Brysch,W., Schlingensiepen,K.-H.,  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.

QY 2153 TGTGCAGGATAATTGC 2168  
|||||  
16 TGTGCAGGATAATTGC 1

Db 16 TGTGCAGGATAATTGC 1

RESULT 173  
AR367887/c 16 bp DNA linear PAT 12-SEP-2003  
LOCUS  
DEFINITION Sequence 16 from patent US 6376199.  
ACCESSION AR367887  
VERSION AR367887.1 GI:34601343  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Caniggia,I., Post,M. and Lye,S.  
TITLE Methods to diagnose a required regulation of trophoblast invasion  
JOURNAL Patent: US 6376199-A 16 23-APR-2002;  
FEATURES Location/Qualifiers  
source 1..16  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 CATGCACACTACTGTGTG 1232  
|||||  
16 CATGCACACTACTGTGTG 1

Db 16 CATGCACACTACTGTGTG 1

[illegible]

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Db          2 GCCAGGGACGTTTCTTA 19

RESULT 161
AX613450
LOCUS      AX613450          20 bp    DNA          linear    PAT 17-FEB-2003
DEFINITION Sequence 4475 from Patent WO02072882.
ACCESSION  AX613450
VERSION     AX613450.1  GI:28408879
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Cullen,P. and Seedorf,U.
TITLE     Coronary chip
JOURNAL   Patent: WO 02072882-A 4475 19-SEP-2002;
          OGHAM GmbH (DE)
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  935 AAAAAACAAACCTTCTT 952
      ||||| ||||| ||||| |||||
Db   3 AAAAAAACCCTTCTT 20

RESULT 162
A40568/c
LOCUS      A40568          16 bp    DNA          linear    PAT 05-MAR-1997
DEFINITION Sequence 105 from Patent WO9425578.
ACCESSION  A40568
VERSION     A40568.1  GI:2296603
KEYWORDS   .
SOURCE     unidentified
            unclassified.
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   .
TITLE     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL   EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
          Patent: WO 9425578-A 105 10-NOV-1994;
          BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source          1..16
                        /organism="unidentified"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2020 AGTCCACTAGGAAAAA 2035
      ||||| ||||| ||||| |||||
Db   16 AGTCCACTAGGAAAAA 1

RESULT 163
A40576/c
LOCUS      A40576          16 bp    DNA          linear    PAT 05-MAR-1997
DEFINITION Sequence 113 from Patent WO9425578.
ACCESSION  A40576
VERSION     A40576.1  GI:2296611
KEYWORDS   .
SOURCE     unidentified
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ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   .
TITLE     ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL   EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
          Patent: WO 9425578-A 113 10-NOV-1994;
          BIOGNOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source          1..16
                        /organism="unidentified"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2153 TGTGCAGGATAATTGC 2168
      ||||| ||||| ||||| |||||
Db   16 TGTGCAGGATAATTGC 1

RESULT 164
A88398/c
LOCUS      A88398          16 bp    DNA          linear    PAT 22-JAN-2000
DEFINITION Sequence 546 from Patent WO9833904.
ACCESSION  A88398
VERSION     A88398.1  GI:6736968
KEYWORDS   .
SOURCE     unidentified
            unclassified.
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Brysch,W. and Schlingensiepen,K.
TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL   Patent: WO 9833904-A 546 06-AUG-1998;
          BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
            source          1..16
                        /organism="unidentified"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2156 GCAGGATAATTGCTGC 2171
      ||||| ||||| ||||| |||||
Db   16 GCAGGATAATTGCTGC 1

RESULT 165
A89093/c
LOCUS      A89093          16 bp    DNA          linear    PAT 22-JAN-2000
DEFINITION Sequence 1241 from Patent WO9833904.
ACCESSION  A89093
VERSION     A89093.1  GI:6737663
KEYWORDS   .
SOURCE     unidentified
            unclassified.
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Brysch,W. and Schlingensiepen,K.
TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL   Patent: WO 9833904-A 1241 06-AUG-1998;
          BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
            source          1..16
                        /organism="unidentified"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32644"
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ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS 1 Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F., Nimrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and Marx,A.  
TITLE Method and nucleic acids for the improved treatment of breast cell proliferative disorders  
JOURNAL Patent: WO 2004035803-A 1676 29-APR-2004;  
Epigenomics AG (DE)  
FEATURES Location/Qualifiers  
source 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Detection oligonucleotide for HSPB1"  
Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2745 TTTTTCCTTTTAAAGGAAA 2762  
|||||  
Db 1 TTTTTCCTTTTAAAGGAAA 18  
|||||  
RESULT 157  
AX132309/c 19 bp DNA linear PAT 15-MAY-2001  
LOCUS Sequence 3527 from Patent WO0130362.  
DEFINITION AX132309  
ACCESSION AX132309.1 GI:14138614  
VERSION  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Robbins,J.M. and Tritz,R.  
AUTHORS Ribozyme therapy for the treatment of proliferative skin and eye diseases  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 3527 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES Location/Qualifiers  
source 1..19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Cdc25 hs ribozyme binding site"  
Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 924 CCAGGAGAAAAAAAAC 941  
|||||  
Db 19 CCAGGAGAAAAACAAAAC 2  
|||||  
RESULT 158  
AX132310/c 19 bp DNA linear PAT 15-MAY-2001  
LOCUS Sequence 3528 from Patent WO0130362.  
DEFINITION AX132310  
ACCESSION AX132310.1 GI:14138615  
VERSION  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 Robbins,J.M. and Tritz,R.  
AUTHORS Ribozyme therapy for the treatment of proliferative skin and eye diseases  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases

diseases  
JOURNAL Patent: WO 0130362-A 3528 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES Location/Qualifiers  
source 1..19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Cdc25 hs ribozyme binding site"  
Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 924 CCAGGAGAAAAAAAAC 941  
|||||  
Db 18 CCAGGAGAAAAACAAAAC 1  
|||||  
RESULT 159  
AR207116 20 bp DNA linear PAT 20-JUN-2002  
LOCUS Sequence 10 from patent US 6372492.  
DEFINITION AR207116  
ACCESSION AR207116  
VERSION AR207116.1 GI:21505925  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett,C.Frank. and Cowsett,L.M.  
TITLE Antisense modulation of talin expression  
JOURNAL Patent: US 6372492-A 10 16-APR-2002;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3393 TCCTTTGCTCTGGTATAT 3410  
|||||  
Db 2 TCCTTCGCTCTGGTATAT 19  
|||||  
RESULT 160  
AR312091 20 bp DNA linear PAT 12-JUN-2003  
LOCUS Sequence 2628 from patent US 6559294.  
DEFINITION AR312091  
ACCESSION AR312091  
VERSION AR312091.1 GI:31705517  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Griffais,R., Hoiseh,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.  
TITLE Chlamydia pneumoniae polynucleotides and uses thereof  
JOURNAL Patent: US 6559294-A 2628 06-MAY-2003;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1055 GCCAGGAACGTTTCTTA 1072  
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REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
        Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
        effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 76 05-DEC-2001;
        BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
        1..18
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"
        /note="Description of unknown: unknown"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCTACTTCAGAAATCGT 1606
Db 18 ACCCTACTTCAGAAATGTT 1

RESULT 153
AX316492/c
LOCUS AX316492 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 133 from Patent EP1160319.
ACCESSION AX316492
VERSION AX316492.1 GI:17899665
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
        Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
        effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 133 05-DEC-2001;
        BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES
source Location/Qualifiers
        1..18
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"
        /note="Description of unknown: unknown"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463
Db 18 CTTGCAATGCAGCTAAA 1

RESULT 154
BD066577/c
LOCUS BD066577 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066577
VERSION BD066577.1 GI:22612180
KEYWORDS JP 2001511000-A/1212.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1212 07-AUG-2001;
        BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
        FN JP 2001511000-A/1212

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PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source Location/Qualifiers
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        /Location/Qualifiers
        1..18
        /organism="unidentified"
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        /db_xref="taxon:32644"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCTACTTCAGAAATCGT 1606
Db 18 ACCCTACTTCAGAAATGTT 1

RESULT 155
BD066633/c
LOCUS BD066633 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066633
VERSION BD066633.1 GI:22612236
KEYWORDS JP 2001511000-A/1268.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1268 07-AUG-2001;
        BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
        FN JP 2001511000-A/1268
        PD 07-AUG-2001
        PF 30-JAN-1998 JP 1998532533
        PR 31-JAN-1997 EP 97101531.8
        PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
        PC C12N15/11,C07H21/04,A61K31/70
        CC An antisense oligonucleotide preparation method FH Key
        FT source Location/Qualifiers
        1..18
        /organism="Unknown"
        /Location/Qualifiers
        1..18
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463
Db 18 CTTGCAATGCAGCTAAA 1

RESULT 156
CQ808226
LOCUS CQ808226 19 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 1676 from Patent WO2004035803.
ACCESSION CQ808226
VERSION CQ808226.1 GI:47113620
KEYWORDS
SOURCE synthetic construct

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QY 1589 ACCCTACTTCAGAAATCGT 1606
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Db 18 ACCCTACTTCAGAAATGTT 1

RESULT 148
LOCUS AX008993/c
DEFINITION Sequence 26 from Patent WO9963975.
ACCESSION AX008993
VERSION AX008993.1 GI:9996367
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 26 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
    Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463
    |||||
Db 18 CTTGCAATGCAGCTAAA 1

RESULT 149
LOCUS AX009037/c
DEFINITION Sequence 70 from Patent WO9963975.
ACCESSION AX009037
VERSION AX009037.1 GI:9996411
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 70 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
    Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2237 GTACATGCTACTTCTG 2254
    |||||
Db 18 GTACAATGCCAATCTCTG 1

RESULT 150
LOCUS AX030114/c
DEFINITION Sequence 76 from Patent EP1008649.
ACCESSION AX030114
VERSION AX030114.1 GI:10190331
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 76 14-JUN-2000;
BIOGOSTIK GES (DE)
FEATURES
    Location/Qualifiers
    source 1..18
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGAAATCGT 1606
    |||||
Db 18 ACCCTACTTCAGAAATGTT 1

RESULT 151
LOCUS AX030171/c
DEFINITION Sequence 133 from Patent EP1008649.
ACCESSION AX030171
VERSION AX030171.1 GI:10190388
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 133 14-JUN-2000;
BIOGOSTIK GES (DE)
FEATURES
    Location/Qualifiers
    source 1..18
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463
    |||||
Db 18 CTTGCAATGCAGCTAAA 1

RESULT 152
LOCUS AX316435/c
DEFINITION Sequence 76 from Patent EP160319.
ACCESSION AX316435
VERSION AX316435.1 GI:17899608
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified
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|-----------------------|--|---|--|
| TITLE                 |  | Antisense-oligonucleotides for transforming growth factor- $\beta$ . (TGF- $\beta$ ).   |  |
| JOURNAL               |  | Patent: US 6455689-A 76 24-SEP-2002;  |  |
| FEATURES              |  | Location/Qualifiers   |  |
| source                |  | 1..18   |  |
|                       |  | /organism="unknown"   |  |
|                       |  | /mol_type="genomic DNA"   |  |
| Query Match           |  | 0.4%; Score 16.4; DB 1; Length 18;  |  |
| Best Local Similarity |  | 94.4%; Pred. No. 1.5e+02;   |  |
| Matches               |  | 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   |  |
| QY                    |  | 2446 CTTGTAATGCAGCTAAA 2463   |  |
| Db                    |  | 18 CTTGCAATGCAGCTAAA 1  |  |
| RESULT 144            |  | BD234966 18 bp DNA linear PAT 17-JUL-2003   |  |
| LOCUS                 |  | A method for stimulating the immune system.   |  |
| DEFINITION            |  | BD234966  |  |
| ACCESSION             |  | BD234966.1 GI:33044736  |  |
| VERSION               |  | JP 2002517434-A/70.   |  |
| KEYWORDS              |  | Homo sapiens (human)  |  |
| SOURCE                |  | Homo sapiens  |  |
| ORGANISM              |  | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 18) |  |
| REFERENCE             |  | Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W. A method for stimulating the immune system                                   |  |
| AUTHORS               |  | Patent: JP 2002517434-A 70 18-JUN-2002;   |  |
| TITLE                 |  | BIOGENOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH  |  |
| JOURNAL               |  | OS Homo sapiens (human)   |  |
| COMMENT               |  | PN JP 2002517434-A/70   |  |
|                       |  | PD 18-JUN-2002  |  |
|                       |  | PF 10-JUN-1999 JP 2000553044  |  |
|                       |  | PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI   |  |
|                       |  | KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI   |  |
|                       |  | BRYSCH  |  |
|                       |  | PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/00,A61P35/00.   |  |
|                       |  | PC 00,A61P35/00.  |  |
|                       |  | PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A   |  |
|                       |  | method for stimulating the immune system  |  |
| FH Key                |  | Location/Qualifiers   |  |
| FT source             |  | 1..18   |  |
| FT                    |  | /organism='Homo sapiens (human)'  |  |
| FEATURES              |  | Location/Qualifiers   |  |
| source                |  | 1..18   |  |
|                       |  | /organism="Homo sapiens"  |  |
|                       |  | /mol_type="genomic DNA"   |  |
|                       |  | /db_xref="taxon:9606"   |  |
| Query Match           |  | 0.4%; Score 16.4; DB 1; Length 18;  |  |
| Best Local Similarity |  | 94.4%; Pred. No. 1.5e+02;   |  |
| Matches               |  | 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   |  |
| QY                    |  | 2237 GTACAATGTAATCTCTG 2254   |  |
| Db                    |  | 18 GTACAATGCAACTCTG 1   |  |
| RESULT 145            |  | AR232819/c 18 bp DNA linear PAT 20-DEC-2002   |  |
| LOCUS                 |  | Sequence 76 from patent US 6455689.   |  |
| DEFINITION            |  | AR232819  |  |
| ACCESSION             |  | AR232819.1 GI:27275157  |  |
| VERSION               |  | Unknown.  |  |
| KEYWORDS              |  | Unclassified.   |  |
| SOURCE                |  | 1 (bases 1 to 18)   |  |
| REFERENCE             |  | Schlingensiepen,K.H., Brysch,W., Schlingensiepen,R. and Bogdahn,U. A method for stimulating the immune system                       |  |
| AUTHORS               |  | Patent: WO 9963975-A 12 16-DEC-1999;  |  |
| TITLE                 |  | BIOGENOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)                          |  |
| JOURNAL               |  | 1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R. A method for stimulating the immune system                                 |  |
| FEATURES              |  | Location/Qualifiers   |  |
| source                |  | 1..18   |  |
|                       |  | /organism="Homo sapiens"  |  |
|                       |  | /mol_type="unassigned DNA"  |  |
|                       |  | /db_xref="taxon:9606"   |  |
| Query Match           |  | 0.4%; Score 16.4; DB 1; Length 18;  |  |
| Best Local Similarity |  | 94.4%; Pred. No. 1.5e+02;   |  |
| Matches               |  | 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   |  |
| QY                    |  | 2445 CTTGTAATGCAGCTAAA 2463   |  |
| Db                    |  | 18 CTTGCAATGCAGCTAAA 1  |  |
| RESULT 147            |  | AX008979/c 18 bp DNA linear PAT 06-SEP-2000   |  |
| LOCUS                 |  | Sequence 12 from Patent WO9963975.  |  |
| DEFINITION            |  | AX008979  |  |
| ACCESSION             |  | AX008979.1 GI:9996353   |  |
| VERSION               |  | Homo sapiens (human)  |  |
| KEYWORDS              |  | Homo sapiens  |  |
| SOURCE                |  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1       |  |
| ORGANISM              |  | Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R. A method for stimulating the immune system                                   |  |
| REFERENCE             |  | Patent: WO 9963975-A 12 16-DEC-1999;  |  |
| AUTHORS               |  | BIOGENOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)                          |  |
| TITLE                 |  | 1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R. A method for stimulating the immune system                                 |  |
| JOURNAL               |  | 1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R. A method for stimulating the immune system                                 |  |
| FEATURES              |  | Location/Qualifiers   |  |
| source                |  | 1..18   |  |
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|                       |  | /mol_type="unassigned DNA"  |  |
|                       |  | /db_xref="taxon:9606"   |  |
| Query Match           |  | 0.4%; Score 16.4; DB 1; Length 18;  |  |
| Best Local Similarity |  | 94.4%; Pred. No. 1.5e+02;   |  |
| Matches               |  | 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   |  |
| QY                    |  | 2445 CTTGTAATGCAGCTAAA 2463   |  |
| Db                    |  | 18 CTTGCAATGCAGCTAAA 1  |  |
| RESULT 147            |  | AX008979/c 18 bp DNA linear PAT 06-SEP-2000   |  |
| LOCUS                 |  | Sequence 12 from Patent WO9963975.  |  |
| DEFINITION            |  | AX008979  |  |
| ACCESSION             |  | AX008979.1 GI:9996353   |  |
| VERSION               |  | Homo sapiens (human)  |  |
| KEYWORDS              |  | Homo sapiens  |  |
| SOURCE                |  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1       |  |
| ORGANISM              |  | Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R. A method for stimulating the immune system                                   |  |
| REFERENCE             |  | Patent: WO 9963975-A 12 16-DEC-1999;  |  |
| AUTHORS               |  | BIOGENOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)                          |  |
| TITLE                 |  | 1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R. A method for stimulating the immune system                                 |  |
| JOURNAL               |  | 1 Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R. A method for stimulating the immune system                                 |  |
| FEATURES              |  | Location/Qualifiers   |  |
| source                |  | 1..18   |  |
|                       |  | /organism="Homo sapiens"  |  |
|                       |  | /mol_type="unassigned DNA"  |  |
|                       |  | /db_xref="taxon:9606"   |  |

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/db_xref="taxon:32644"
Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463
DB 18 CTTGCAATGCAGCTAAA 1

RESULT 140
A89064/c
LOCUS A89064 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1212 from Patent W09833904.
ACCESSION A89064
VERSION A89064.1 GI:6737634
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1212 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGAAATCGT 1606
DB 18 ACCCTACTTCAGAAATGT 1

RESULT 141
A89120/c
LOCUS A89120 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1268 from Patent W09833904.
ACCESSION A89120
VERSION A89120.1 GI:6737690
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1268 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAATGCAGCTAAA 2463
DB 18 CTTGCAATGCAGCTAAA 1

RESULT 142
BD234908/c
LOCUS BD234908 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234908
VERSION BD234908.1 GI:33044678
KEYWORDS JP 2002517434-A/12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 12 18-JUN-2002;
BIOGOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/12
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7.25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FT Key Location/Qualifiers
FT source 1..18
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGAAATCGT 1606
DB 18 ACCCTACTTCAGAAATGT 1

RESULT 143
BD234922/c
LOCUS BD234922 18 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234922
VERSION BD234922.1 GI:33044692
KEYWORDS JP 2002517434-A/26.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
TITLE A method for stimulating the immune system
JOURNAL Patent: JP 2002517434-A 26 18-JUN-2002;
BIOGOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Homo sapiens (human)
PN JP 2002517434-A/26
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7.25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FT Key Location/Qualifiers
FT source 1..18
/organism="Homo sapiens (human)"
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 629 ACGCGCGCACACGCCACAC 648
    |||||
Db 21 ACGCGCGCACACGCCACAC 2

RESULT 136
ATH523738/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 21 bp DNA linear PLN 29-MAR-2003
ACCESSION 060H10
VERSION AJ523738
KEYWORDS 1 GI:26791974
SOURCE left border; T-DNA flanking sequence.
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
REFERENCE
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 21)
AUTHORS Balzerque, S.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
source
    1..21
        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /cultivar="Wassilewskija"
        /db_xref="taxon:3702"
        /clone="060H10"
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misc_feature
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Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2808 AAAAAACATCAAAACAAA 2827
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Db 21 AAACAACATCAAAACAGA 2

RESULT 137
AR306126/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 24 bp DNA linear PAT 12-JUN-2003
ACCESSION AR306126
VERSION AR306126
KEYWORDS 1 GI:31695813

Query Match 0.4%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2732 AAAAGAAAACATCTTTTTTTT 2754
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Db 24 AAAAAAAAAGTGTTTTTTTT 2

RESULT 138
A40539/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION Sequence 76 from Patent WO9425578.
ACCESSION A40539
VERSION A40539.1 GI:2296574
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 76 10-NOV-1994;
BIOGNOSTIK GES (DE)
FEATURES
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        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGATCGT 1606
    |||||
Db 18 ACCCTACTTCAGATTGT 1

RESULT 139
A40596/c
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION Sequence 133 from Patent WO9425578.
ACCESSION A40596
VERSION A40596.1 GI:2296631
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL Patent: WO 9425578-A 133 10-NOV-1994;
BIOGNOSTIK GES (DE)
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PR 31-JAN-1997 BP 97101531.8
PI KARL HERMANN SCHLINGENSIBPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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FT source 1..20
FT /Organism='Unknown'.

FEATURES
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Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAAGCG 1947
Db 20 CATCATCCCAATAAAAGTG 1

RESULT 133
LOCUS BD069970
DEFINITION Use of nucleic acids containing unmethylated CPG dinucleotide in
the treatment of LPS-associated disorders.
ACCESSION BD069970.1 GI:22615573
VERSION JP 2001513776-A/59.
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM 1 (bases 1 to 20)
AUTHORS Schwartz,D.A. and Krieg,A.M.
TITLE Use of nucleic acids containing unmethylated CPG dinucleotide in
the treatment of LPS-associated disorders
JOURNAL Patent: JP 2001513776-A 59 04-SEP-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2001513776-A/59
PD 04-SEP-2001
PF 25-FEB-1998 JP 1998537810
PR 28-FEB-1997 US 60/039405
PI DAVID A SCHWARTZ,ARTHUR M KRIEG
PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
CC synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1..20
FT /Organism='Artificial Sequence'.

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Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 134
LOCUS BD069970/c
DEFINITION Use of nucleic acids containing unmethylated CPG dinucleotide in
the treatment of LPS-associated disorders.
ACCESSION BD069970
VERSION BD069970.1 GI:22615573
KEYWORDS synthetic construct
SOURCE JP 2001513776-A/59.

FEATURES
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    20 bp DNA linear PAT 27-AUG-2002
    Use of nucleic acids containing unmethylated CPG dinucleotide in
    the treatment of LPS-associated disorders.
    Patent: JP 2001513776-A 59 04-SEP-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION
    OS Artificial Sequence
    PN JP 2001513776-A/59
    PD 04-SEP-2001
    PF 25-FEB-1998 JP 1998537810
    PR 28-FEB-1997 US 60/039405
    PI DAVID A SCHWARTZ,ARTHUR M KRIEG
    PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
    CC synthetic oligonucleotide
    FH Key Location/Qualifiers
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FEATURES
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    /mol_type="genomic DNA"
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Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 134
LOCUS BD069970/c
DEFINITION Use of nucleic acids containing unmethylated CPG dinucleotide in
the treatment of LPS-associated disorders.
ACCESSION BD069970
VERSION BD069970.1 GI:22615573
KEYWORDS synthetic construct
SOURCE JP 2001513776-A/59.

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Schwartz,D.A. and Krieg,A.M.
TITLE Use of nucleic acids containing unmethylated CPG dinucleotide in
the treatment of LPS-associated disorders
JOURNAL Patent: JP 2001513776-A 59 04-SEP-2001;
COMMENT OS Artificial Sequence
UNIVERSITY OF IOWA RESEARCH FOUNDATION
PN JP 2001513776-A/59
PD 04-SEP-2001
PF 25-FEB-1998 JP 1998537810
PR 28-FEB-1997 US 60/039405
PI DAVID A SCHWARTZ,ARTHUR M KRIEG
PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
CC synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1..20
FT /Organism='Artificial Sequence'.

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    /db_xref="taxon:32630"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 135
LOCUS E08187/c
DEFINITION Primer for isolation of the promoter in rice starch-branching
enzyme.
ACCESSION E08187
VERSION E08187.1 GI:2176308
KEYWORDS JP 1994261767-A/5.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Baba,T. and Shimada,H.
TITLE NEW RICE PLANT STARCH-BRANCHED ENZYMIC GENE
JOURNAL Patent: JP 1994261767-A 5 20-SEP-1994;
COMMENT MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1994261767-A/5
PD 20-SEP-1994
PF 22-OCT-1993 JP 1993265171
PR 29-OCT-1992 JP 92P 291719
PI BABA TADASHI, SHIMADA HIROAKI
PC C12N15/54,A01H5/00,C12N5/10,C12P19/16//A2311/10,C12N9/10; CC
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..21
FT /Organism='Artificial sequences'.

FEATURES
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    Location/Qualifiers
    1..21
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 520 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..20
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic Sequence"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 129
BD065894/c
LOCUS      BD065894      20 bp      DNA      linear      PAT 01-MAR-2003
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065894
VERSION    BD065894.1 GI:25812774
KEYWORDS   JP 2001511000-A/529
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
  AUTHORS  Schlingensiepen,K.H. and Brysch,W.
  TITLE    An antisense oligonucleotide preparation method
  JOURNAL  Patent: JP 2001511000-A 529 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
          PN JP 2001511000-A/529
          PD 07-AUG-2001
          PF 30-JAN-1998 JP 1998532533
          PR 31-JAN-1997 EP 97101531.8
          PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
          PC C12N15/11,C07H21/04,A61K31/70
          CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
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Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1523 GGTATTATAAATCGACATGC 1542
Db 20 GGTATTATAAATAGACATGC 1

RESULT 132
BD066600/c
LOCUS      BD066600      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066600
VERSION    BD066600.1 GI:22612203
KEYWORDS   JP 2001511000-A/1235.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
  AUTHORS  Schlingensiepen,K.H. and Brysch,W.
  TITLE    An antisense oligonucleotide preparation method
  JOURNAL  Patent: JP 2001511000-A 1235 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
          PN JP 2001511000-A/1235
          PD 07-AUG-2001
          PF 30-JAN-1998 JP 1998532533

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 520 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES   Location/Qualifiers
            source
              1..20
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic Sequence"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 129
AX547630
LOCUS      AX547630      20 bp      DNA      linear      PAT 01-MAR-2003
DEFINITION Sequence 769 from Patent WO02053141.
ACCESSION  AX547630
VERSION    AX547630.1 GI:25812774
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
  AUTHORS  Bratzler,R.L.
  TITLE    Inhibition of angiogenesis by nucleic acids
  JOURNAL  Patent: WO 02053141-A 769 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 130
AX547630/c
LOCUS      AX547630      20 bp      DNA      linear      PAT 01-MAR-2003
DEFINITION Sequence 769 from Patent WO02053141.
ACCESSION  AX547630
VERSION    AX547630.1 GI:25812774
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
  AUTHORS  Bratzler,R.L.
  TITLE    Inhibition of angiogenesis by nucleic acids
  JOURNAL  Patent: WO 02053141-A 769 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES   Location/Qualifiers
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                /note="Synthetic Sequence"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 130
AX547630/c
LOCUS      AX547630      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066600
VERSION    BD066600.1 GI:22612203
KEYWORDS   JP 2001511000-A/1235.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
  AUTHORS  Schlingensiepen,K.H. and Brysch,W.
  TITLE    An antisense oligonucleotide preparation method
  JOURNAL  Patent: JP 2001511000-A 1235 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
          PN JP 2001511000-A/1235
          PD 07-AUG-2001
          PF 30-JAN-1998 JP 1998532533
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
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Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 124
AX355165/c
LOCUS AX355165 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 193 from Patent WO0197843.
ACCESSION AX355165
VERSION AX355165.1 GI:18619832
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Weiner,G. and Hartmann,G.
AUTHORS Methods for enhancing antibody-induced cell lysis and treating
TITLE cancer
JOURNAL Patent: WO 0197843-A 193 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
|||||
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 125
AX441509
LOCUS AX441509 20 bp DNA linear PAT 02-JUL-2002
DEFINITION Sequence 13 from Patent WO0206531.
ACCESSION AX441509
VERSION AX441509.1 GI:21690470
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Dattagupta,N.
AUTHORS Nucleic acid hairpin probes and uses thereof
TITLE Patent: WO 0206531-A 13 24-JAN-2002;
JOURNAL Applied Gene Technologies, Inc. (US)
FEATURES
source
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="Oligo AGT02020"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTTGAGAAAAA 2599
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Db 1 AAAAAAATTTGAGAAAAA 20

RESULT 126
AX441510
LOCUS AX441510 20 bp DNA linear PAT 02-JUL-2002
DEFINITION Sequence 14 from Patent WO0206531.
ACCESSION AX441510
VERSION AX441510.1 GI:21690471
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Dattagupta,N.
AUTHORS Nucleic acid hairpin probes and uses thereof
TITLE Patent: WO 0206531-A 14 24-JAN-2002;
JOURNAL Applied Gene Technologies, Inc. (US)
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Location/Qualifiers
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Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAATTTGAGAAAAA 2599
|||||
Db 1 AAAAAAATTTGAGAAAAA 20

RESULT 127
AX547381
LOCUS AX547381 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 520 from Patent WO02053141.
ACCESSION AX547381
VERSION AX547381.1 GI:25812525
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Bratzler,R.L.
AUTHORS Inhibition of angiogenesis by nucleic acids
TITLE Patent: WO 02053141-A 520 11-JUL-2002;
JOURNAL Coley Pharmaceutical Group, Inc. (US)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
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Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
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Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 128
AX547381/c
LOCUS AX547381 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 520 from Patent WO02053141.
ACCESSION AX547381
VERSION AX547381.1 GI:25812525
KEYWORDS
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LOCUS AX104577 20 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 769 from Patent WO0122972.  
ACCESSION AX104577  
VERSION AX104577.1 GI:13920774  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.  
TITLE Immunostimulatory nucleic acids  
JOURNAL Patent: WO 0122972-A 769 05-APR-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
GmbH (DE)  
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/db\_xref="taxon:32630"  
Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 616 CGCGCGCGCACGCGCGCG 635  
Db 20 CGCGCGCGCGCGCGCGCG 1  
RESULT 120  
AX316458/c  
LOCUS AX316458 20 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 99 from Patent EP1160319.  
ACCESSION AX316458  
VERSION AX316458.1 GI:17899631  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 99 05-DEC-2001;  
BIOGNOSTIK GESSELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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/db\_xref="taxon:32644"  
/note="Description of unknown: unknown"  
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Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1928 CATCATCCCGCAATAAAGCG 1947  
Db 20 CATCATCCCAATAAAGTG 1  
RESULT 121  
AX355164  
LOCUS AX355164 20 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 192 from Patent WO0197843.  
ACCESSION AX355164  
VERSION AX355164.1 GI:18619831  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 193 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES  
source  
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AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 192 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES  
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1. .20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide-phosphorothioate  
backbone"  
Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 616 CGCGCGCGCACGCGCGCG 635  
Db 1 CGCGCGCGCGCGCGCGCG 20  
RESULT 122  
AX355164/c  
LOCUS AX355164 20 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 192 from Patent WO0197843.  
ACCESSION AX355164  
VERSION AX355164.1 GI:18619831  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 192 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
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backbone"  
Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 616 CGCGCGCGCACGCGCGCG 635  
Db 20 CGCGCGCGCGCGCGCGCG 1  
RESULT 123  
AX355165  
LOCUS AX355165 20 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 193 from Patent WO0197843.  
ACCESSION AX355165  
VERSION AX355165.1 GI:18619832  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 193 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES  
source  
1. .20

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JOURNAL Patent: WO 9963975-A 8 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSTIEPEN KARL
HERMANN (DE); SCHLINGENSTIEPEN REIMAR (DE)
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1523 GGTATTATAAAATCGACATGC 1542
DB 20 GGTTTACAAATAGACATGC 1

RESULT 115
AX030137/c
LOCUS AX030137 20 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 99 from Patent EP1008649.
ACCESSION AX030137
VERSION AX030137.1 GI:10190354
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,K.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2(tgf-b2)
JOURNAL Patent: EP 1008649-A 99 14-JUN-2000;
BIOGOSTIK GES (DE)
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAAGCG 1947
DB 20 CATCATCCCAATAAAAGTG 1

RESULT 116
AX104328
LOCUS AX104328 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 520 from Patent WO0122972.
ACCESSION AX104328
VERSION AX104328.1 GI:13920525
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 520 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 20

RESULT 117
AX104328/c
LOCUS AX104328 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 520 from Patent WO0122972.
ACCESSION AX104328
VERSION AX104328.1 GI:13920525
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 520 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 20

RESULT 118
AX104577
LOCUS AX104577 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 769 from Patent WO0122972.
ACCESSION AX104577
VERSION AX104577.1 GI:13920774
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
REFERENCE
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 769 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
    source
        Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCAGCAGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 119
AX104577/c
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TITLE      Methods and compositions for analyzing nucleotide sequence
JOURNAL    mismatches using RNase H
PATENT     Patent: US 6596489-A 14 22-JUL-2003;
FEATURES   Location/Qualifiers
SOURCE     1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
      |||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 110
AR360425
LOCUS     AR360425
DEFINITION Sequence 13 from patent US 6596490.
ACCESSION AR360425
VERSION   AR360425.1 GI:33767455
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Dattagupta,N.
TITLE     Nucleic acid hairpin probes and uses thereof
JOURNAL   Patent: US 6596490-A 13 22-JUL-2003;
FEATURES  Location/Qualifiers
SOURCE    1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
      |||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 111
AR360426
LOCUS     AR360426
DEFINITION Sequence 14 from patent US 6596490.
ACCESSION AR360426
VERSION   AR360426.1 GI:33767456
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Dattagupta,N.
TITLE     Nucleic acid hairpin probes and uses thereof
JOURNAL   Patent: US 6596490-A 14 22-JUL-2003;
FEATURES  Location/Qualifiers
SOURCE    1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599
      |||||
Db 1 AAAAAAAAAATTGTAAGAAAAA 20

RESULT 112
AR363652/c
LOCUS     AR363652/c
DEFINITION Sequence 13 from patent US 5221620.
ACCESSION AR363652
VERSION   AR363652.1 GI:34425532
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Purchio,A.F., Madisen,L. and Webb,N.
TITLE     Cloning and expression of transforming growth factor .beta.2
JOURNAL   Patent: US 5221620-A 13 22-JUN-1993;
FEATURES  Location/Qualifiers
SOURCE    1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2211 TCGAATGGATCCATGAACC 2230
      |||||
Db 20 TCGAATGGATACACGAACC 1

RESULT 113
AR478239/c
LOCUS     AR478239
DEFINITION Sequence 42 from patent US 6699661.
ACCESSION AR478239
VERSION   AR478239.1 GI:47236887
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Kurane,R., Kanagawa,T., Kanagata,Y., Kurata,S., Yamada,K.,
           Yokomaki,T., Koyama,O. and Furusho,K.
TITLE     Method for determining a concentration of target nucleic acid
           molecules, nucleic acid probes for the method, and method for
           analyzing data obtained by the method
JOURNAL   Patent: US 6699661-A 42 02-MAR-2004;
FEATURES  Location/Qualifiers
SOURCE    1..20
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATATTT 1171
      |||
Db 20 TTTTATATATATATATAT 1

RESULT 114
AX008975/c
LOCUS     AX008975
DEFINITION Sequence 8 from Patent WO963975.
ACCESSION AX008975
VERSION   AX008975.1 GI:9996349
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE     A method for stimulating the immune system
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TITLE      Vectors and methods for immunization or therapeutic protocols
JOURNAL    Patent: US 6339068-A 76 15-JAN-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCGCGCGCGC 634
Db 1 GCGCGCGCGCGCGCGCGC 20

RESULT 105
AR182904/c
LOCUS      AR182904      20 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 76 from patent US 6339068.
ACCESSION  AR182904
VERSION     AR182904.1 GI:20226111
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE     Vectors and methods for immunization or therapeutic protocols
JOURNAL   Patent: US 6339068-A 76 15-JAN-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCGCGCGCGC 634
Db 20 GCGCGCGCGCGCGCGCGC 1

RESULT 106
AR232842/c
LOCUS      AR232842      20 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 99 from patent US 6455689.
ACCESSION  AR232842
VERSION     AR232842.1 GI:27275180
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE     Antisense-oligonucleotides for transforming growth factor-.beta.
            (TGF-.beta.)
JOURNAL   Patent: US 6455689-A 99 24-SEP-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1928 CATCATCCCGAATAAAAGCG 1947
Db 20 CATCATCCCGAATAAAAGTG 1
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RESULT 107
AR264958/c
LOCUS      AR264958      20 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 42 from patent US 6492121.
ACCESSION  AR264958
VERSION     AR264958.1 GI:29693345
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Kurane,R., Kanagawa,T., Kanagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
            Patent: US 6492121-A 42 10-DEC-2002;
JOURNAL   Patent: US 6492121-A 42 10-DEC-2002;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1152 TTCTTTTTTATATATATTT 1171
Db 20 TTTTTTTTTATATATATAT 1

RESULT 108
AR360398/c
LOCUS      AR360398      20 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 13 from patent US 6596489.
ACCESSION  AR360398
VERSION     AR360398.1 GI:33767428
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dattagupta,N. and Tseng,T.-C.
TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
JOURNAL   Patent: US 6596489-A 13 22-JUL-2003;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATTGGAGAAAAA 2599
Db 1 AAAAAAAATTGGAGAAAAA 20

RESULT 109
AR360399/c
LOCUS      AR360399      20 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6596489.
ACCESSION  AR360399
VERSION     AR360399.1 GI:33767429
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dattagupta,N. and Tseng,T.-C.
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QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 100
LOCUS AR084562 20 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 51 from patent US 5981185.
ACCESSION AR084562
VERSION AR084562.1 GI:10011333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays.
JOURNAL Patent: US 5981185-A 51 09-NOV-1999;
FEATURES
    Location/Qualifiers
        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 101
LOCUS BD234904/c 20 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234904
VERSION BD234904.1 GI:33044674
KEYWORDS JP 2002517434-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 20)
JOURNAL Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
PATENT: JP 2002517434-A 8 18-JUN-2002;
FEATURES BIOLOGISTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
    OS Homo sapiens (human)
    PN JP 2002517434-A/8
    PD 18-JUN-2002
    PF 10-JUN-1999 JP 2000553044
    PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
    PC A61K37/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
    KY KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
    BRYSCH
    PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
    PC 00,A61P35/00.
    PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
    ME method for stimulating the immune system
    PH Key Location/Qualifiers
    FT source 1..20
    FT /organism='Homo sapiens (human)'.
    FT Location/Qualifiers
        source
            1..20
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 102
LOCUS AR182850 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 22 from patent US 6339068.
ACCESSION AR182850
VERSION AR182850.1 GI:20226057
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6339068-A 22 15-JAN-2002;
FEATURES
    Location/Qualifiers
        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 103
LOCUS AR182850/c 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 22 from patent US 6339068.
ACCESSION AR182850
VERSION AR182850.1 GI:20226057
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6339068-A 22 15-JAN-2002;
FEATURES
    Location/Qualifiers
        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 104
LOCUS AR182904 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 76 from patent US 6339068.
ACCESSION AR182904
VERSION AR182904.1 GI:20226111
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
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|                          |  |
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| ORGANISM                 | unidentified<br>unclassified.  |
| REFERENCE                | 1 (bases 1 to 20)  |
| AUTHORS                  | Brysch,W.D. and Schlingensiepen,K.D.   |
| TITLE                    | An antisense oligonucleotide preparation method  |
| JOURNAL                  | Patent: EP 0856579-A 529 05-AUG-1998;  |
| FEATURES                 | BIOGNOSTIK GES (DE)<br>Location/Qualifiers<br>source 1..20<br>/organism="unidentified"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:32644" |
| Query Match              | 0.4%; Score 16.8; DB 1; Length 20;   |
| Best Local Similarity    | 90.0%; Pred. No. 1.6e+02;  |
| Matches 18; Conservative | 0; Mismatches 2; Indels 0; Gaps 0;   |
| Qy                       | 1523 GGTTTATAAATCGACATGC 1542<br>  |
| Db                       | 20 GGTTTACAATAAGACATGC 1   |
| RESULT 98                |  |
| LOCUS                    | AR030495 20 bp DNA linear PAT 29-SEP-1999  |
| DEFINITION               | Sequence 68 from patent US 5861273.  |
| ACCESSION                | AR030495   |
| VERSION                  | AR030495.1 GI:5943709  |
| KEYWORDS                 |  |
| SOURCE                   | Unknown.<br>Unclassified.  |
| REFERENCE                | 1 (bases 1 to 20)  |
| AUTHORS                  | Olson,P.S. and Mascarenhas,D.  |
| TITLE                    | Chromosomal expression of heterologous genes in bacterial cells  |
| JOURNAL                  | Patent: US 5861273-A 68 19-JAN-1999;   |
| FEATURES                 | Location/Qualifiers<br>source 1..20<br>/organism="unknown"<br>/mol_type="unassigned DNA"   |
| Query Match              | 0.4%; Score 16.8; DB 1; Length 20;   |
| Best Local Similarity    | 90.0%; Pred. No. 1.6e+02;  |
| Matches 18; Conservative | 0; Mismatches 2; Indels 0; Gaps 0;   |
| Qy                       | 2212 GGAATGGATCCCATGACC 2231<br>   |
| Db                       | 1 GGAATGGATACGAAACC 20   |
| RESULT 99                |  |
| LOCUS                    | AR084562 20 bp DNA linear PAT 01-SEP-2000  |
| DEFINITION               | Sequence 51 from patent US 5981185.  |
| ACCESSION                | AR084562   |
| VERSION                  | AR084562.1 GI:10011333   |
| KEYWORDS                 |  |
| SOURCE                   | Unknown.<br>Unclassified.  |
| REFERENCE                | 1 (bases 1 to 20)  |
| AUTHORS                  | Matson,R.S., Coassin,F.J., Rampal,J.B. and Caskey,C.Thomas.  |
| TITLE                    | Oligonucleotide repeat arrays  |
| JOURNAL                  | Patent: US 5981185-A 51 09-NOV-1999;   |
| FEATURES                 | Location/Qualifiers<br>source 1..20<br>/organism="unknown"<br>/mol_type="unassigned DNA"   |
| Query Match              | 0.4%; Score 16.8; DB 1; Length 20;   |
| Best Local Similarity    | 90.0%; Pred. No. 1.6e+02;  |
| Matches 18; Conservative | 0; Mismatches 2; Indels 0; Gaps 0;   |

JOURNAL Patent: WO 9963975-A 3 16-DEC-1999;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL  
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)  
FEATURES  
source  
Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.4%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1343 GCAGATCCTTGAGCAAGC 1359  
Db 17 GCAGATCCTTGAGCAAGC 1  
RESULT 91  
AX009035/c  
LOCUS 17 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 68 from Patent WO9963975.  
ACCESSION AX009035  
VERSION AX009035.1 GI:9996409  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.  
TITLE A method for stimulating the immune system  
JOURNAL Patent: WO 9963975-A 68 16-DEC-1999;  
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL  
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)  
FEATURES  
source  
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/organism="Homo sapiens"  
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Query Match 0.4%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1509 TACTACGCCAAGGAGGT 1525  
Db 17 TACTACGCCAAGGAGGT 1  
RESULT 92  
BD065887/c  
LOCUS 17 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD065887  
VERSION BD065887.1 GI:22611490  
KEYWORDS JP 2001511000-A/522.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 522 07-AUG-2001;  
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Unknown  
PN JP 2001511000-A/522  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key

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/db\_xref="taxon:32644"  
Query Match 0.4%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1343 GCAGATCCTTGAGCAAGC 1359  
Db 17 GCAGATCCTTGAGCAAGC 1  
RESULT 93  
AR488890/c  
LOCUS 20 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 7 from patent US 6709818.  
ACCESSION AR488890  
VERSION AR488890.1 GI:47255117  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Nelson,W.G., Lin,X., Tchou,J.C. and Bakker,J.  
TITLE Methods of diagnosing and treating hepatic cell proliferative disorders  
JOURNAL Patent: US 6709818-A 7 23-MAR-2004;  
FEATURES  
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Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2574 TTAAAAAAAATAATT 2590  
Db 19 TTAAAAAAAATAATT 3  
RESULT 94  
A40562/c  
LOCUS 20 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 99 from Patent WO9425578.  
ACCESSION A40562  
VERSION A40562.1 GI:2296597  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 20)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))  
JOURNAL Patent: WO 9425578-A 99 10-NOV-1994;  
BIOGNOSTIK GES (DE)  
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/db\_xref="taxon:32644"  
Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



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QY 1343 GCAGATCTGTGACGACG 1359
Db 17 GCAGATCTGTGACGACG 1

RESULT 87
BD234899/c
LOCUS BD234899 17 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234899
VERSION BD234899.1 GI:330444669
KEYWORDS JP 2002517434-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 3 18-JUN-2002;
BIOLOGISTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/3
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61P31/
PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
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Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 TACTACGCCAAGGAGGT 1525
Db 17 TACTACGCCAAGGAGGT 1

RESULT 89
CO778290
LOCUS CO778290 17 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 1976 from Patent EP1394274.
ACCESSION CO778290
VERSION CO778290.1 GI:45381008
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
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REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuwara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
pulmonary disease
JOURNAL Patent: EP 1394274-A 1976 03-MAR-2004;
Genox Research, Inc. (JP)
FEATURES
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/db_xref='taxon:33630'
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TAMRA(6-carboxy-N,N,NH-tetramethylrhodamine)'.

Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 CGCAGCCACGCGCCCA 308
Db 1 CGCAGCCACGCGCCCA 17

RESULT 90
AX008970/c
LOCUS AX008970 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9963975.
ACCESSION AX008970
VERSION AX008970.1 GI:9996344
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system

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            /mol_type="genomic DNA"

Query Match      0.4%; Score 17.4; DB 1; Length 21;
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Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 588 CCCCGGGCTCGCAGGCTCG 608
Db 21 CCCCGGGCTCYCCAGGCTCG 1

RESULT 83
AX096770/c
LOCUS      21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1948 from Patent WO0118250.
ACCESSION  AX096770
VERSION     AX096770.1 GI:13513024
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Lander, E.S., Gargill, M., Ireland, J.S., Bolck, S., Daley, G.Q. and
            McCarthy, J.J.
TITLE       Single nucleotide polymorphisms in genes
            Patent: WO 0118250-A 1948 15-MAR-2001.
JOURNAL     WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
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source      1. .21
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            /db_xref="taxon:9606"

Query Match      0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 588 CCCCGGGCTCGCAGGCTCG 608
Db 21 CCCCGGGCTCYCCAGGCTCG 1

RESULT 84
BD129806
LOCUS      21 bp DNA linear PAT 18-SEP-2002
DEFINITION Asthma-associated gene.
ACCESSION  BD129806
VERSION     BD129806.1 GI:23224751
KEYWORDS    JP 2002500895-A/96.
SOURCE      unidentified
            unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Wilson, A.R.B., Buckler, A., Cardon, L., Carey, A.H., Galvin, M.,
            Miller, A. and North, M.
TITLE       Asthma-associated gene
            Patent: JP 2002500895-A 96 15-JAN-2002;
            AXYS PHARMACEUTICALS INC
COMMENT     OS Unidentified
            PN JP 2002500895-A/96
            PD 15-JAN-2002
            PF 21-JAN-1998 JP 2000528715
            PI ANGELA R BROOKS WILSON, ALAN BUCKLER, LON
            CARDON, ALI SOUN H CAREY,
            PI MARGARET GALVIN, ANDREW MILLER, MICHAEL NORTH
            PC C12Q1/68, A01K67/027, C07K14/47, C12N15/09, C12N15/00 CC
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            CC Topology: Linear;
            CC Asthma-associated gene
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Query Match      0.4%; Score 17.4; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTTCCTTAAAGGAAAAA 2765
Db 2 TTTTTCCTTAAAGGAAAAA 21

RESULT 85
A88374/c
LOCUS      17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 522 from Patent WO9833904.
ACCESSION  A88374
VERSION     A88374.1 GI:6736944
KEYWORDS
SOURCE      unidentified
            unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Brysch, W. and Schlingensiepen, K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
            Patent: WO 9833904-A 522 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1343 GCAGATCCTGAGCAAGC 1359
Db 17 GCAGATCCTGAGCAAGC 1

RESULT 86
A90341/c
LOCUS      17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 522 from Patent EP0856579.
ACCESSION  A90341
VERSION     A90341.1 GI:6738855
KEYWORDS
SOURCE      unidentified
            unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Brysch, W.D. and Schlingensiepen, K.D.
TITLE       An antisense oligonucleotide preparation method
            Patent: EP 0856579-A 522 05-AUG-1998;
            BIOGNOSTIK GES (DE)
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source      1. .17
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Query Match      0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 555 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2383 CCATTCTCTATTACATTGG 2401
Db 19 CCATTCTCTACTACATTGG 1

RESULT 79
BD065899/c
LOCUS BD065899 19 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065899
VERSION BD065899.1 GI:22611502
KEYWORDS JP 2001511000-A/534.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 534 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
  OS Unknown
  PN JP 2001511000-A/534
  PD 07-AUG-2001
  PF 30-JAN-1998 JP 1998532533
  PR 31-JAN-1997 EP 97101531.8
  PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
  PC C12N15/11,C07H21/04,A61K31/70
  CC An antisense oligonucleotide preparation method FH Key
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2383 CCATTCTCTATTACATTGG 2401
Db 19 CCATTCTCTACTACATTGG 1

RESULT 81
AR103576
LOCUS AR103576 21 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 100 from patent US 6087485.
ACCESSION AR103576
VERSION AR103576.1 GI:12815164
KEYWORDS
  SOURCE Unknown.
  ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brooks-Wilson,A.R., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
  Miller,A. and North,M.
TITLE Asthma related genes
JOURNAL Patent: US 6087485-A 100 11-JUL-2000;
FEATURES
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTTCCTTTTAAGGAAAAA 2765
Db 2 TTTTTCCTTTTAAGGAAAAA 21

RESULT 82
AR530745/c
LOCUS AR530745 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1948 from patent US 6727063.
ACCESSION AR530745
VERSION AR530745.1 GI:53919182
KEYWORDS
  SOURCE Unknown.
  ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
  McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: US 6727063-A 1948 27-APR-2004;
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  Location/Qualifiers

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/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1

RESULT 74
AX404674 22 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 48 from Patent WO224745.
ACCESSION AX404674
VERSION AX404674.1 GI:21437955
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Abken,H. and Schinkoethe,T.
TITLE Method for detecting tumor cells
JOURNAL Patent: WO 0224745-A 48 28-MAR-2002;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match 0.4%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.3e+02;
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QY 2746 TTTTCTTTTAAAGGAAAAA 2766
Db 1 TTTTCTTTTAAAGGAAAAA 21

RESULT 75
A88386/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 534 from Patent WO9833904.
ACCESSION A88386
VERSION A88386.1 GI:6736956
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 534 06-AUG-1998;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCAAGACTTAACATCTCC 1756
Db 19 CCAAGACTTAACATCTCC 1

RESULT 76
A88407/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 555 from Patent WO9833904.
ACCESSION A88407
VERSION A88407.1 GI:6736977
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 555 06-AUG-1998;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2383 CCATTCTCTATTACATTGG 2401
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RESULT 77
A90353/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 534 from Patent EP0856579.
ACCESSION A90353
VERSION A90353.1 GI:6738867
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 534 05-AUG-1998;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCAAGACTTAACATCTCC 1756
Db 19 CCAAGACTTAACATCTCC 1

RESULT 78
A90374/c 19 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 555 from Patent EP0856579.
ACCESSION A90374
VERSION A90374.1 GI:6738888
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
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| BD066569/c            | LOCUS  | BD066569            | 18 bp DNA linear PAT 27-AUG-2002 |
| DEFINITION            | An antisense oligonucleotide preparation method.   |                     |                                  |
| ACCESSION             | BD066569   |                     |                                  |
| VERSION               | BD066569.1 GI:22612172   |                     |                                  |
| KEYWORDS              | JP 2001511000-A/1204.  |                     |                                  |
| SOURCE                | unidentified   |                     |                                  |
| ORGANISM              | unclassified   |                     |                                  |
| REFERENCE             | 1 (bases 1 to 18)  |                     |                                  |
| AUTHORS               | Schlingensiepen,K.H. and Brysch,W.   |                     |                                  |
| TITLE                 | An antisense oligonucleotide preparation method  |                     |                                  |
| JOURNAL               | Patent: JP 2001511000-A 1204 07-AUG-2001;  |                     |                                  |
| COMMENT               | BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH   |                     |                                  |
| OS                    | Unknown  |                     |                                  |
| PN                    | JP 2001511000-A/1204   |                     |                                  |
| PD                    | 07-AUG-2001  |                     |                                  |
| PF                    | 30-JAN-1998 JP 1998532533  |                     |                                  |
| PR                    | 31-JAN-1997 EP 97101531.8  |                     |                                  |
| PI                    | KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH   |                     |                                  |
| PC                    | C12N15/11,C07H21/04,A61K31/70  |                     |                                  |
| CC                    | An antisense oligonucleotide preparation method FH   |                     | Key                              |
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| Db                    | 18   | AGGTGATTTCATCTACA   | 1                                |
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| BD066605/c            | LOCUS  | BD066605            | 18 bp DNA linear PAT 27-AUG-2002 |
| DEFINITION            | An antisense oligonucleotide preparation method.   |                     |                                  |
| ACCESSION             | BD066605   |                     |                                  |
| VERSION               | BD066605.1 GI:22612208   |                     |                                  |
| KEYWORDS              | JP 2001511000-A/1240.  |                     |                                  |
| SOURCE                | unidentified   |                     |                                  |
| ORGANISM              | unclassified   |                     |                                  |
| REFERENCE             | 1 (bases 1 to 18)  |                     |                                  |
| AUTHORS               | Schlingensiepen,K.H. and Brysch,W.   |                     |                                  |
| TITLE                 | An antisense oligonucleotide preparation method  |                     |                                  |
| JOURNAL               | Patent: JP 2001511000-A 1240 07-AUG-2001;  |                     |                                  |
| COMMENT               | BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH   |                     |                                  |
| OS                    | Unknown  |                     |                                  |
| PN                    | JP 2001511000-A/1240   |                     |                                  |
| PD                    | 07-AUG-2001  |                     |                                  |
| PF                    | 30-JAN-1998 JP 1998532533  |                     |                                  |
| PR                    | 31-JAN-1997 EP 97101531.8  |                     |                                  |
| PI                    | KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH   |                     |                                  |
| PC                    | C12N15/11,C07H21/04,A61K31/70  |                     |                                  |
| CC                    | An antisense oligonucleotide preparation method FH   |                     | Key                              |
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| Matches               | 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |                     |                                  |
| Qy                    | 2014   | CTATAAAAGTCCACTAGGA | 2031                             |
| Db                    | 18   | CTATAAAAGTCCACTAGGA | 1                                |
| RESULT 71             |  |                     |                                  |
| BD065907/c            | LOCUS  | BD065907            | 18 bp DNA linear PAT 27-AUG-2002 |
| DEFINITION            | An antisense oligonucleotide preparation method.   |                     |                                  |
| ACCESSION             | BD065907   |                     |                                  |
| VERSION               | BD065907.1 GI:22611510   |                     |                                  |
| KEYWORDS              | JP 2001511000-A/542.   |                     |                                  |
| SOURCE                | unidentified   |                     |                                  |
| ORGANISM              | unclassified   |                     |                                  |
| REFERENCE             | 1 (bases 1 to 18)  |                     |                                  |
| AUTHORS               | Schlingensiepen,K.H. and Brysch,W.   |                     |                                  |
| TITLE                 | An antisense oligonucleotide preparation method  |                     |                                  |
| JOURNAL               | Patent: JP 2001511000-A 542 07-AUG-2001;   |                     |                                  |
| COMMENT               | BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH   |                     |                                  |
| OS                    | Unknown  |                     |                                  |
| PN                    | JP 2001511000-A/542  |                     |                                  |
| PD                    | 07-AUG-2001  |                     |                                  |
| PF                    | 30-JAN-1998 JP 1998532533  |                     |                                  |
| PR                    | 31-JAN-1997 EP 97101531.8  |                     |                                  |
| PI                    | KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH   |                     |                                  |
| PC                    | C12N15/11,C07H21/04,A61K31/70  |                     |                                  |
| CC                    | An antisense oligonucleotide preparation method FH   |                     | Key                              |
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| Qy                    | 2014   | CTATAAAAGTCCACTAGGA | 2031                             |
| Db                    | 18   | CTATAAAAGTCCACTAGGA | 1                                |
| RESULT 70             |  |                     |                                  |
| AX316463/c            | LOCUS  | AX316463            | 18 bp DNA linear PAT 14-DEC-2001 |
| DEFINITION            | Sequence 104 from Patent EP1160319.  |                     |                                  |
| ACCESSION             | AX316463   |                     |                                  |
| VERSION               | AX316463.1 GI:17899636   |                     |                                  |
| KEYWORDS              | unidentified   |                     |                                  |
| SOURCE                | unclassified   |                     |                                  |
| ORGANISM              | unclassified   |                     |                                  |
| REFERENCE             | 1  |                     |                                  |
| AUTHORS               | Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,<br>Schlingensiepen,R. and Bogdahn,U.                                |                     |                                  |
| TITLE                 | Antisense-oligonucleotides for the treatment of immunosuppressive<br>effects of transforming growth factor-beta (tgf-beta) |                     |                                  |
| JOURNAL               | Patent: EP 1160319-A 104 05-DEC-2001;  |                     |                                  |
| COMMENT               | BIOGNOSTIK   |                     |                                  |

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Unclassified.
1 (bases 1 to 18)
Caniggia,I., Post,M. and Lye,S.
Methods to diagnose a required regulation of trophoblast invasion
Patent: US 6376199-A 9 23-APR-2002;
JOURNAL
FEATURES
Location/Qualifiers
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Query Match
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 CCTACTTCAGATCGTC 1607
Db 18 CCTACTTCAGATCGTC 1

RESULT 66
AX008984/c
LOCUS AX008984 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 17 from Patent WO9963975.
ACCESSION AX008984
VERSION AX008984.1 GI:9996358
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 17 16-DEC-1999;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
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QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1

RESULT 67
AX030105/c
LOCUS AX030105 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 67 from Patent EP1008649.
ACCESSION AX030105
VERSION AX030105.1 GI:10190322
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2 (tgf-b2)
JOURNAL Patent: EP 1008649-A 67 14-JUN-2000;
BIOGNOSTIK GES (DE)
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Unclassified.
1 (bases 1 to 18)
Caniggia,I., Post,M. and Lye,S.
Methods to diagnose a required regulation of trophoblast invasion
Patent: US 6376199-A 9 23-APR-2002;
JOURNAL
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Location/Qualifiers
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Query Match
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCTACTACA 1431
Db 18 AGGTGATTTCCTACTACA 1

RESULT 68
AX030142/c
LOCUS AX030142 18 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 104 from Patent EP1008649.
ACCESSION AX030142
VERSION AX030142.1 GI:10190359
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.
and Schlingensiepen,R.
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive
effects of transforming growth factor-b2 (tgf-b2)
JOURNAL Patent: EP 1008649-A 104 14-JUN-2000;
BIOGNOSTIK GES (DE)
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Query Match
Best Local Similarity 0.4%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031
Db 18 CTATAAGTCCACTAGGA 1

RESULT 69
AX316426/c
LOCUS AX316426 18 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 67 from Patent EP1160319.
ACCESSION AX316426
VERSION AX316426.1 GI:17899599
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 67 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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Query Match
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QY 1414 AGGTGATTTCCTACTACA 1431
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RESULT 61  
A90361/c  
LOCUS  
DEFINITION  
Sequence 542 from Patent EP0856579.  
ACCESSION  
A90361  
VERSION  
A90361.1 GI:6738875  
KEYWORDS  
unidentified  
ORGANISM  
unclassified.  
REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Brysch,W.D. and Schlingensiepen,K.D.  
TITLE  
An antisense oligonucleotide preparation method  
JOURNAL  
Patent: EP 0856579-A 542 05-AUG-1998;  
BIOGOSTIK GES (DB)  
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2007 CAGAAAACCTATAAGTCC 2024  
DB 18 CAGAAAACCTATAAGTCC 1  
RESULT 62  
BD234913/c  
LOCUS  
DEFINITION  
A method for stimulating the immune system.  
ACCESSION  
BD234913  
VERSION  
BD234913.1 GI:33044683  
KEYWORDS  
JP 2002517434-A/17.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.  
TITLE  
A method for stimulating the immune system  
JOURNAL  
Patent: JP 2002517434-A 17 18-JUN-2002;  
BIOGOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002517434-A/17  
PD 18-JUN-2002  
PF 10-JUN-1999 JP 2000553044  
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI  
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI  
BRYSCH  
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/00,A61P35/00,  
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A  
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QY 2014 CTATAAGTCCACTAGGA 2031

DB 18 CTATAAGTCCACTAGGA 1  
RESULT 63  
AR232810/c  
LOCUS  
DEFINITION  
Sequence 67 from patent US 6455689.  
ACCESSION  
AR232810  
VERSION  
AR232810.1 GI:27275148  
KEYWORDS  
Unknown.  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE  
Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
JOURNAL  
Patent: US 6455689-A 67 24-SEP-2002;  
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QY 1414 AGTGATTTCCTACATACA 1431  
DB 18 AGTGATTTCCTACATACA 1  
RESULT 64  
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LOCUS  
DEFINITION  
Sequence 104 from patent US 6455689.  
ACCESSION  
AR232847  
VERSION  
AR232847.1 GI:27275185  
KEYWORDS  
Unknown.  
SOURCE  
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ORGANISM  
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REFERENCE  
1 (bases 1 to 18)  
AUTHORS  
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE  
Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
JOURNAL  
Patent: US 6455689-A 104 24-SEP-2002;  
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QY 2014 CTATAAGTCCACTAGGA 2031  
DB 18 CTATAAGTCCACTAGGA 1  
RESULT 65  
AR367880/c  
LOCUS  
DEFINITION  
Sequence 9 from patent US 6376199.  
ACCESSION  
AR367880  
VERSION  
AR367880.1 GI:34601336  
KEYWORDS  
Unknown.  
SOURCE  
Unknown.  
ORGANISM  
Unknown.

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ACCESSION A40530
VERSION A40530.1 GI:2296565
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
PATENT: WO 9425578-A 67 10-NOV-1994;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1414 AGTGATTTCCATCTACA 1431
DB 18 AGTGATTTCCATCTACA 1
RESULT 57
A88394/c
LOCUS 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 104 from Patent WO9425578.
ACCESSION A40567
VERSION A40567.1 GI:2296602
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 9425578-A 104 10-NOV-1994;
BIOGHOSTIK GES (DE)
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 104 from Patent WO9425578.
ACCESSION A40567
VERSION A40567.1 GI:2296602
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 9425578-A 104 10-NOV-1994;
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Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A88394
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 542 from Patent WO9833904.
ACCESSION A88394
VERSION A88394.1 GI:6736964
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 9833904-A 542 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
QY 2014 CTATAAGTCCACTAGGA 2031
DB 18 CTATAAGTCCACTAGGA 1
RESULT 58
A88394/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 542 from Patent WO9833904.
ACCESSION A88394
VERSION A88394.1 GI:6736964
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 9833904-A 542 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
QY 2014 CTATAAGTCCACTAGGA 2031
DB 18 CTATAAGTCCACTAGGA 1
RESULT 59
A89056/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1204 from Patent WO9833904.
ACCESSION A89056
VERSION A89056.1 GI:6737626
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 9833904-A 1204 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Best Local Similarity 100.0%; Pred. No. 73;
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DEFINITION Sequence 1204 from Patent WO9833904.
ACCESSION A89056
VERSION A89056.1 GI:6737626
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 9833904-A 1204 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A89092
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1240 from Patent WO9833904.
ACCESSION A89092
VERSION A89092.1 GI:6737662
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 9833904-A 1240 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Best Local Similarity 100.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 1240 from Patent WO9833904.
ACCESSION A89092
VERSION A89092.1 GI:6737662
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL PATENT: WO 9833904-A 1240 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Query Match 0.4%; Score 18; DB 1; Length 18;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CTATAAGTCCACTAGGA 2031
DB 18 CTATAAGTCCACTAGGA 1
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RESULT 52
BD065901/c
LOCUS          BD065901          20 bp      DNA          linear          PAT 27-AUG-2002
DEFINITION     An antisense oligonucleotide preparation method.
ACCESSION      BD065901
VERSION        BD065901.1  GI:22611504
KEYWORDS       JP 2001511000-A/536.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Schlingensiepen,K.H. and Brysch,W.
TITLE          An antisense oligonucleotide preparation method
JOURNAL        Patent: JP 2001511000-A 536 07-AUG-2001;
                BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT        OS      Unknown
                PN      JP 2001511000-A/536
                PD      07-AUG-2001
                PF      30-JAN-1998  JP 1998532533
                PR      31-JAN-1997  EP 97101531.8
                PI      KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
                PC      C12N15/11,C07H21/04,A61K31/70
                CC      An antisense oligonucleotide preparation method FH      Key
                CQ      Location/Qualifiers
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Query Match          0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1853 CCACAAGACAGGACCTGG 1872
DB 20 CCATAAGACAGGACCTGG 1

RESULT 53
A87861/c
LOCUS          A87861          23 bp      DNA          linear          PAT 22-JAN-2000
DEFINITION     Sequence 9 from Patent WO9833904.
ACCESSION      A87861
VERSION        A87861.1  GI:6736431
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 9 06-AUG-1998;
                BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
COMMENT        Location/Qualifiers
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                /organism='unidentified'
                /mol_type='unassigned DNA'
                /db_xref='taxon:32644'

Query Match          0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1333 CCATCGCGGGCAGATCCTG 1352
DB 23 CCATCGCGGGCAGATCCTG 4

RESULT 54
A89828/c
LOCUS          A89828          23 bp      DNA          linear          PAT 22-JAN-2000
DEFINITION     Sequence 9 from Patent EP0856579.
ACCESSION      A89828
VERSION        A89828.1  GI:6738342
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Brysch,W.D. and Schlingensiepen,K.D.
TITLE          An antisense oligonucleotide preparation method
JOURNAL        Patent: EP 0856579-A 9 05-AUG-1998;
                BIOGNOSTIK GES (DE)
COMMENT        Location/Qualifiers
                1..23
                /organism='unidentified'
                /mol_type='unassigned DNA'
                /db_xref='taxon:32644'

Query Match          0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1333 CCATCGCGGGCAGATCCTG 1352
DB 23 CCATCGCGGGCAGATCCTG 4

RESULT 56
A40530/c
LOCUS          A40530          18 bp      DNA          linear          PAT 05-MAR-1997
DEFINITION     Sequence 67 from Patent WO9425578.
```

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LOCUS          A89828          23 bp      DNA          linear          PAT 22-JAN-2000
DEFINITION     Sequence 9 from Patent EP0856579.
ACCESSION      A89828
VERSION        A89828.1  GI:6738342
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Brysch,W.D. and Schlingensiepen,K.D.
TITLE          An antisense oligonucleotide preparation method
JOURNAL        Patent: EP 0856579-A 9 05-AUG-1998;
                BIOGNOSTIK GES (DE)
COMMENT        Location/Qualifiers
                1..23
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Query Match          0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1333 CCATCGCGGGCAGATCCTG 1352
DB 23 CCATCGCGGGCAGATCCTG 4

RESULT 55
BD065374/c
LOCUS          BD065374          23 bp      DNA          linear          PAT 27-AUG-2002
DEFINITION     An antisense oligonucleotide preparation method.
ACCESSION      BD065374
VERSION        BD065374.1  GI:22610977
KEYWORDS       JP 2001511000-A/9.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Schlingensiepen,K.H. and Brysch,W.
TITLE          An antisense oligonucleotide preparation method
JOURNAL        Patent: JP 2001511000-A 9 07-AUG-2001;
                BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT        OS      Unknown
                PN      JP 2001511000-A/9
                PD      07-AUG-2001
                PF      30-JAN-1998  JP 1998532533
                PR      31-JAN-1997  EP 97101531.8
                PI      KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
                PC      C12N15/11,C07H21/04,A61K31/70
                CC      An antisense oligonucleotide preparation method FH      Key
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Query Match          0.4%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1333 CCATCGCGGGCAGATCCTG 1352
DB 23 CCATCGCGGGCAGATCCTG 4

RESULT 56
A40530/c
LOCUS          A40530          18 bp      DNA          linear          PAT 05-MAR-1997
DEFINITION     Sequence 67 from Patent WO9425578.
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LOCUS      A88388                20 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 536 from Patent WO9833904.
ACCESSION  A88388
VERSION     A88388.1  GI:6736958
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 20)
AUTHORS     Brysch W. and Schlingensiepen K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 536 06-AUG-1998;
            BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1853  CCACAAAGACAGGACCTGG 1872
Db      20  CCATAAAGACAGGACCTGG 1

RESULT 48
A90355/c
LOCUS      A90355                20 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 536 from Patent EP0856579.
ACCESSION  A90355
VERSION     A90355.1  GI:6738869
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 20)
AUTHORS     Brysch W.D. and Schlingensiepen, K.D.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: EP 0856579-A 536 05-AUG-1998;
            BIOGHOSTIK GES (DE)
FEATURES   Location/Qualifiers
            source
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Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A90355      Sequence 536 from Patent EP0856579.
A90355      0.4%; Score 18.4; DB 1; Length 20;
A90355      Best Local Similarity 95.0%; Pred. No. 79;
A90355      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1853  CCACAAAGACAGGACCTGG 1872
Db      20  CCATAAAGACAGGACCTGG 1

RESULT 49
A90355/c
LOCUS      A90355                20 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 536 from Patent EP0856579.
ACCESSION  A90355
VERSION     A90355.1  GI:6738869
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 20)
AUTHORS     Brysch W.D. and Schlingensiepen, K.D.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: EP 0856579-A 536 05-AUG-1998;
            BIOGHOSTIK GES (DE)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A90355      Sequence 536 from Patent EP0856579.
A90355      0.4%; Score 18.4; DB 1; Length 20;
A90355      Best Local Similarity 95.0%; Pred. No. 79;
A90355      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1853  CCACAAAGACAGGACCTGG 1872
Db      20  CCATAAAGACAGGACCTGG 1

RESULT 49
A90355/c
LOCUS      A90355                20 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 15 from patent US 6596489.
ACCESSION  A90355
VERSION     A90355.1  GI:33767430
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dattagupta, N. and Tseng, T.-C.
TITLE       Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
JOURNAL     Patent: US 6596489-A 15 22-JUL-2003;

LOCUS      A88388                20 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 536 from Patent WO9833904.
ACCESSION  A88388
VERSION     A88388.1  GI:6736958
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 20)
AUTHORS     Brysch W. and Schlingensiepen K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 536 06-AUG-1998;
            BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2580  AAAAAAAATTGGAGAAAAA 2599
Db      1  AAAAAAAATTGGAGAAAAA 20

RESULT 50
AR360427
LOCUS      AR360427              20 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 15 from patent US 6596490.
ACCESSION  AR360427
VERSION     AR360427.1  GI:33767457
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dattagupta, N.
TITLE       Nucleic acid hairpin probes and uses thereof
JOURNAL     Patent: US 6596490-A 15 22-JUL-2003;
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Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AR360427      Sequence 15 from patent US 6596490.
AR360427      0.4%; Score 18.4; DB 1; Length 20;
AR360427      Best Local Similarity 95.0%; Pred. No. 79;
AR360427      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2580  AAAAAAAATTGGAGAAAAA 2599
Db      1  AAAAAAAATTGGAGAAAAA 20

RESULT 51
AX441511
LOCUS      AX441511              20 bp      DNA      linear      PAT 02-JUL-2002
DEFINITION Sequence 15 from Patent WO0206531.
ACCESSION  AX441511
VERSION     AX441511.1  GI:21690472
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Dattagupta, N.
TITLE       Nucleic acid hairpin probes and uses thereof
JOURNAL     Patent: WO 0206531-A 15 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AX441511      Sequence 15 from Patent WO0206531.
AX441511      0.4%; Score 18.4; DB 1; Length 20;
AX441511      Best Local Similarity 95.0%; Pred. No. 79;
AX441511      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2580  AAAAAAAATTGGAGAAAAA 2599
Db      1  AAAAAAAATTGGAGAAAAA 20

RESULT 51
AX441511
LOCUS      AX441511              20 bp      DNA      linear      PAT 02-JUL-2002
DEFINITION Sequence 15 from Patent WO0206531.
ACCESSION  AX441511
VERSION     AX441511.1  GI:21690472
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Dattagupta, N.
TITLE       Nucleic acid hairpin probes and uses thereof
JOURNAL     Patent: WO 0206531-A 15 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligo AGT02022"

Query Match      0.4%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AX441511      Sequence 15 from Patent WO0206531.
AX441511      0.4%; Score 18.4; DB 1; Length 20;
AX441511      Best Local Similarity 95.0%; Pred. No. 79;
AX441511      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2580  AAAAAAAATTGGAGAAAAA 2599
Db      1  AAAAAAAATTGGAGAAAAA 20
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| Best Local Similarity 90.9%; Pred. No. 83;                  |      |                           |  |  |  |  |  |  |  |
| Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |      |                           |  |  |  |  |  |  |  |
| Qy  | 2200 | GGGATCTTGATGGAATGGAT 2221 |  |  |  |  |  |  |  |
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| RESULT 45   |      |                           |  |  |  |  |  |  |  |
| AX030592  |      |                           |  |  |  |  |  |  |  |
| LOCUS 22 bp DNA linear PAT 20-SEP-2000                      |      |                           |  |  |  |  |  |  |  |
| DEFINITION Sequence 19 from Patent EP1013284.               |      |                           |  |  |  |  |  |  |  |
| ACCESSION AX030592  |      |                           |  |  |  |  |  |  |  |
| VERSION AX030592.1 GI:10278118                              |      |                           |  |  |  |  |  |  |  |
| KEYWORDS  |      |                           |  |  |  |  |  |  |  |
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| REFERENCE 1   |      |                           |  |  |  |  |  |  |  |
| AUTHORS Frenz, J., Shire, S. and Sliwowski, M.B.            |      |                           |  |  |  |  |  |  |  |
| TITLE Purified forms of dnase                               |      |                           |  |  |  |  |  |  |  |
| JOURNAL Patent: EP 1013284-A 19 28-JUN-2000;                |      |                           |  |  |  |  |  |  |  |
| GENENTECH INC (US)  |      |                           |  |  |  |  |  |  |  |
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| Query Match 0.4%; Score 18.8; DB 1; Length 22;              |      |                           |  |  |  |  |  |  |  |
| Best Local Similarity 90.9%; Pred. No. 83;                  |      |                           |  |  |  |  |  |  |  |
| Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |      |                           |  |  |  |  |  |  |  |
| Qy  | 615  | GCGCGCGCGCAGCAGCGCGC 636  |  |  |  |  |  |  |  |
| Db  | 1    | GCGCGCGCGCGCGCGCGC 22     |  |  |  |  |  |  |  |
| RESULT 46   |      |                           |  |  |  |  |  |  |  |
| AX030592/c  |      |                           |  |  |  |  |  |  |  |
| LOCUS 22 bp DNA linear PAT 20-SEP-2000                      |      |                           |  |  |  |  |  |  |  |
| DEFINITION Sequence 19 from Patent EP1013284.               |      |                           |  |  |  |  |  |  |  |
| ACCESSION AX030592  |      |                           |  |  |  |  |  |  |  |
| VERSION AX030592.1 GI:10278118                              |      |                           |  |  |  |  |  |  |  |
| KEYWORDS  |      |                           |  |  |  |  |  |  |  |
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| ORGANISM  |      |                           |  |  |  |  |  |  |  |
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| unclassified.   |      |                           |  |  |  |  |  |  |  |
| REFERENCE 1   |      |                           |  |  |  |  |  |  |  |
| AUTHORS Frenz, J., Shire, S. and Sliwowski, M.B.            |      |                           |  |  |  |  |  |  |  |
| TITLE Purified forms of dnase                               |      |                           |  |  |  |  |  |  |  |
| JOURNAL Patent: EP 1013284-A 19 28-JUN-2000;                |      |                           |  |  |  |  |  |  |  |
| GENENTECH INC (US)  |      |                           |  |  |  |  |  |  |  |
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| /db_xref="taxon:32644"                                      |      |                           |  |  |  |  |  |  |  |
| Query Match 0.4%; Score 18.8; DB 1; Length 22;              |      |                           |  |  |  |  |  |  |  |
| Best Local Similarity 90.9%; Pred. No. 83;                  |      |                           |  |  |  |  |  |  |  |
| Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |      |                           |  |  |  |  |  |  |  |
| Qy  | 615  | GCGCGCGCGCAGCAGCGCGC 636  |  |  |  |  |  |  |  |
| Db  | 22   | GCGCGCGCGCGCGCGCGC 1      |  |  |  |  |  |  |  |
| RESULT 47   |      |                           |  |  |  |  |  |  |  |
| A88388/c  |      |                           |  |  |  |  |  |  |  |

ORGANISM unidentified  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 200151000-A 545 07-AUG-2001;  
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
OS Unknown  
PN JP 2001511000-A/545  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
Location/Qualifiers  
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FT Location/Qualifiers  
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Query Match 0.4%; Score 19; DB 1; Length 19;  
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QY 2149 GAAATGTCAGGATAATTG 2167  
Db 19 GAAATGTCAGGATAATTG 1  
RESULT 38  
AR019469  
LOCUS AR019469 22 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 18 from patent US 5783433.  
ACCESSION AR019469  
VERSION AR019469.1 GI:3974583  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Frenz,J. and Sliwowski,M.B.  
TITLE Purified forms of DNase  
JOURNAL Patent: US 5783433-A 18 21-JUL-1998;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
Query Match 0.4%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 83;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 615 GCGCGCGCGCGCGCGCGC 636  
Db 1 GCGCGCGCGCGCGCGCGCGC 22  
RESULT 39  
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LOCUS AR019469 22 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 18 from patent US 5783433.  
ACCESSION AR019469  
VERSION AR019469.1 GI:3974583  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Frenz,J. and Sliwowski,M.B.

TITLE Purified forms of DNase  
JOURNAL Patent: US 5783433-A 18 21-JUL-1998;  
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Best Local Similarity 90.9%; Pred. No. 83;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 615 GCGCGCGCGCGCGCGCGC 636  
Db 22 GCGCGCGCGCGCGCGCGCGC 1  
RESULT 40  
AR038951  
LOCUS AR038951 22 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 34 from patent US 5807713.  
ACCESSION AR038951  
VERSION AR038951.1 GI:5958314  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.  
TITLE DNA encoding growth/differentiation factor  
JOURNAL Patent: US 5807713-A 34 15-SEP-1998;  
FEATURES Location/Qualifiers  
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Query Match 0.4%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 83;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2200 GGGATCTTGGATGGAATGGAT 2221  
Db 1 GGGATCTAGGTGGAAATGGAT 22  
RESULT 41  
AR091306  
LOCUS AR091306 22 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 25 from patent US 5994094.  
ACCESSION AR091306  
VERSION AR091306.1 GI:10018061  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Hotten,G., Neidhardt,H. and Paulista,M.  
TITLE Growth/differentiation factor of the TGF-.beta. family  
JOURNAL Patent: US 5994094-A 25 30-NOV-1999;  
FEATURES Location/Qualifiers  
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Query Match 0.4%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 83;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2200 GGGATCTTGGATGGAATGGAT 2221  
Db 1 GGGATCTAGGTGGAAATGGAT 22  
RESULT 42

|                       |            |                         |  |       |             |        |                 |  |
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| RESULT 33             | A88397/c   | LOCUS                   | Sequence 545 from Patent WO9833904.                              | 19 bp | DNA         | linear | PAT 22-JAN-2000 |  |
| DEFINITION            | A88397     | ACCESSION               | A88397   | 1     | GI:6736967  |        |                 |  |
| VERSION               |            | KEYWORDS                | unidentified   |       |             |        |                 |  |
| SOURCE                |            | ORGANISM                | unidentified   |       |             |        |                 |  |
| REFERENCE             |            |                         | 1 (bases 1 to 19)  |       |             |        |                 |  |
| AUTHORS               |            |                         | Brysch,W. and Schlingensiepen,K.                                 |       |             |        |                 |  |
| TITLE                 |            |                         | AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD                  |       |             |        |                 |  |
| JOURNAL               |            |                         | Patent: WO 9833904-A 545 06-AUG-1998;                            |       |             |        |                 |  |
| FEATURES              |            |                         | BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)                        |       |             |        |                 |  |
| source                |            |                         | 1..19  |       |             |        |                 |  |
|                       |            |                         | /organism="unidentified"   |       |             |        |                 |  |
|                       |            |                         | /mol_type="unassigned DNA"                                       |       |             |        |                 |  |
|                       |            |                         | /db_xref="taxon:32644"   |       |             |        |                 |  |
| Query Match           |            |                         | 0.4%; Score 19; DB 1; Length 19;                                 |       |             |        |                 |  |
| Best Local Similarity |            |                         | 100.0%; Pred. No. 53;  |       |             |        |                 |  |
| Matches               |            |                         | 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |       |             |        |                 |  |
| Qy                    | 2149       | GAATGTGCAGGATAATTG 2167 |  |       |             |        |                 |  |
| Db                    | 19         | GAATGTGCAGGATAATTG 1    |  |       |             |        |                 |  |
| RESULT 34             | A90364/c   | LOCUS                   | Sequence 545 from Patent EP0856579.                              | 19 bp | DNA         | linear | PAT 22-JAN-2000 |  |
| DEFINITION            | A90364     | ACCESSION               | A90364   | 1     | GI:6738878  |        |                 |  |
| VERSION               |            | KEYWORDS                | unidentified   |       |             |        |                 |  |
| SOURCE                |            | ORGANISM                | unclassified.  |       |             |        |                 |  |
| REFERENCE             |            |                         | 1 (bases 1 to 19)  |       |             |        |                 |  |
| AUTHORS               |            |                         | Brysch,W.D. and Schlingensiepen,K.D.                             |       |             |        |                 |  |
| TITLE                 |            |                         | An antisense oligonucleotide preparation method                  |       |             |        |                 |  |
| JOURNAL               |            |                         | Patent: EP 0856579-A 545 05-AUG-1998;                            |       |             |        |                 |  |
| FEATURES              |            |                         | BIOGNOSTIK GES (DE)  |       |             |        |                 |  |
| source                |            |                         | 1..19  |       |             |        |                 |  |
|                       |            |                         | /organism="unidentified"   |       |             |        |                 |  |
|                       |            |                         | /mol_type="unassigned DNA"                                       |       |             |        |                 |  |
|                       |            |                         | /db_xref="taxon:32644"   |       |             |        |                 |  |
| Query Match           |            |                         | 0.4%; Score 19; DB 1; Length 19;                                 |       |             |        |                 |  |
| Best Local Similarity |            |                         | 100.0%; Pred. No. 53;  |       |             |        |                 |  |
| Matches               |            |                         | 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |       |             |        |                 |  |
| Qy                    | 2149       | GAATGTGCAGGATAATTG 2167 |  |       |             |        |                 |  |
| Db                    | 19         | GAATGTGCAGGATAATTG 1    |  |       |             |        |                 |  |
| RESULT 35             | BD234915/c | LOCUS                   | Sequence 545 from Patent WO9833904.                              | 19 bp | DNA         | linear | PAT 17-JUL-2003 |  |
| DEFINITION            | BD234915   | ACCESSION               | BD234915   | 1     | GI:33044685 |        |                 |  |
| VERSION               |            | KEYWORDS                | unidentified   |       |             |        |                 |  |
| SOURCE                |            | ORGANISM                | unclassified.  |       |             |        |                 |  |
| REFERENCE             |            |                         | 1 (bases 1 to 19)  |       |             |        |                 |  |
| AUTHORS               |            |                         | Brysch,W. and Schlingensiepen,K.                                 |       |             |        |                 |  |
| TITLE                 |            |                         | AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD                  |       |             |        |                 |  |
| JOURNAL               |            |                         | Patent: WO 9833904-A 545 06-AUG-1998;                            |       |             |        |                 |  |
| FEATURES              |            |                         | BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)                        |       |             |        |                 |  |
| source                |            |                         | 1..19  |       |             |        |                 |  |
|                       |            |                         | /organism="unidentified"   |       |             |        |                 |  |
|                       |            |                         | /mol_type="unassigned DNA"                                       |       |             |        |                 |  |
|                       |            |                         | /db_xref="taxon:32644"   |       |             |        |                 |  |
| Query Match           |            |                         | 0.4%; Score 19; DB 1; Length 19;                                 |       |             |        |                 |  |
| Best Local Similarity |            |                         | 100.0%; Pred. No. 53;  |       |             |        |                 |  |
| Matches               |            |                         | 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |       |             |        |                 |  |
| Qy                    | 2149       | GAATGTGCAGGATAATTG 2167 |  |       |             |        |                 |  |
| Db                    | 19         | GAATGTGCAGGATAATTG 1    |  |       |             |        |                 |  |
| RESULT 36             | AX008986/c | LOCUS                   | Sequence 19 from Patent WO9963975.                               | 19 bp | DNA         | linear | PAT 06-SEP-2000 |  |
| DEFINITION            | AX008986   | ACCESSION               | AX008986   | 1     | GI:9996360  |        |                 |  |
| VERSION               |            | KEYWORDS                | Homo sapiens (human)   |       |             |        |                 |  |
| SOURCE                |            | ORGANISM                | Homo sapiens   |       |             |        |                 |  |
| REFERENCE             |            |                         | 1 (bases 1 to 19)  |       |             |        |                 |  |
| AUTHORS               |            |                         | Brysch,W. and Schlingensiepen,K.H. and Schlingensiepen,R.        |       |             |        |                 |  |
| TITLE                 |            |                         | A method for stimulating the immune system                       |       |             |        |                 |  |
| JOURNAL               |            |                         | Patent: WO 9963975-A 19 16-DEC-1999;                             |       |             |        |                 |  |
| FEATURES              |            |                         | BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSTIEPEN KARL |       |             |        |                 |  |
| source                |            |                         | 1..19  |       |             |        |                 |  |
|                       |            |                         | /organism="Homo sapiens"   |       |             |        |                 |  |
|                       |            |                         | /mol_type="unassigned DNA"                                       |       |             |        |                 |  |
|                       |            |                         | /db_xref="taxon:9606"  |       |             |        |                 |  |
| Query Match           |            |                         | 0.4%; Score 19; DB 1; Length 19;                                 |       |             |        |                 |  |
| Best Local Similarity |            |                         | 100.0%; Pred. No. 53;  |       |             |        |                 |  |
| Matches               |            |                         | 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |       |             |        |                 |  |
| Qy                    | 2149       | GAATGTGCAGGATAATTG 2167 |  |       |             |        |                 |  |
| Db                    | 19         | GAATGTGCAGGATAATTG 1    |  |       |             |        |                 |  |
| RESULT 37             | BD065910/c | LOCUS                   | An antisense oligonucleotide preparation method.                 | 19 bp | DNA         | linear | PAT 27-AUG-2002 |  |
| DEFINITION            | BD065910   | ACCESSION               | BD065910   | 1     | GI:22611513 |        |                 |  |
| VERSION               |            | KEYWORDS                | unidentified   |       |             |        |                 |  |
| SOURCE                |            | ORGANISM                | unclassified.  |       |             |        |                 |  |
| REFERENCE             |            |                         | 1 (bases 1 to 19)  |       |             |        |                 |  |
| AUTHORS               |            |                         | Brysch,W. and Schlingensiepen,K.H. and Schlingensiepen,R.        |       |             |        |                 |  |
| TITLE                 |            |                         | A method for stimulating the immune system                       |       |             |        |                 |  |
| JOURNAL               |            |                         | Patent: WO 9963975-A 19 16-DEC-1999;                             |       |             |        |                 |  |
| FEATURES              |            |                         | BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSTIEPEN KARL |       |             |        |                 |  |
| source                |            |                         | 1..19  |       |             |        |                 |  |
|                       |            |                         | /organism="Homo sapiens"   |       |             |        |                 |  |
|                       |            |                         | /mol_type="unassigned DNA"                                       |       |             |        |                 |  |
|                       |            |                         | /db_xref="taxon:9606"  |       |             |        |                 |  |
| Query Match           |            |                         | 0.4%; Score 19; DB 1; Length 19;                                 |       |             |        |                 |  |
| Best Local Similarity |            |                         | 100.0%; Pred. No. 53;  |       |             |        |                 |  |
| Matches               |            |                         | 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |       |             |        |                 |  |
| Qy                    | 2149       | GAATGTGCAGGATAATTG 2167 |  |       |             |        |                 |  |
| Db                    | 19         | GAATGTGCAGGATAATTG 1    |  |       |             |        |                 |  |
| RESULT 38             | BD065910/c | LOCUS                   | An antisense oligonucleotide preparation method.                 | 19 bp | DNA         | linear | PAT 27-AUG-2002 |  |
| DEFINITION            | BD065910   | ACCESSION               | BD065910   | 1     | GI:22611513 |        |                 |  |
| VERSION               |            | KEYWORDS                | unidentified   |       |             |        |                 |  |
| SOURCE                |            | ORGANISM                | unclassified.  |       |             |        |                 |  |
| REFERENCE             |            |                         | 1 (bases 1 to 19)  |       |             |        |                 |  |
| AUTHORS               |            |                         | Brysch,W. and Schlingensiepen,K.H. and Schlingensiepen,R.        |       |             |        |                 |  |
| TITLE                 |            |                         | A method for stimulating the immune system                       |       |             |        |                 |  |
| JOURNAL               |            |                         | Patent: WO 9963975-A 19 16-DEC-1999;                             |       |             |        |                 |  |
| FEATURES              |            |                         | BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSTIEPEN KARL |       |             |        |                 |  |
| source                |            |                         | 1..19  |       |             |        |                 |  |
|                       |            |                         | /organism="Homo sapiens"   |       |             |        |                 |  |
|                       |            |                         | /mol_type="unassigned DNA"                                       |       |             |        |                 |  |
|                       |            |                         | /db_xref="taxon:9606"  |       |             |        |                 |  |
| Query Match           |            |                         | 0.4%; Score 19; DB 1; Length 19;                                 |       |             |        |                 |  |
| Best Local Similarity |            |                         | 100.0%; Pred. No. 53;  |       |             |        |                 |  |
| Matches               |            |                         | 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |       |             |        |                 |  |
| Qy                    | 2149       | GAATGTGCAGGATAATTG 2167 |  |       |             |        |                 |  |
| Db                    | 19         | GAATGTGCAGGATAATTG 1    |  |       |             |        |                 |  |

RESULT 28  
LOCUS 143133 24 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 13 from patent US 5631135.  
ACCESSION I43133  
VERSION I43133.1 GI:2468377  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.  
TITLE Oligonucleotide N3'.fwdarw.P5' phosphoramidates: hybridization and nuclease resistance properties  
JOURNAL Patent: US 5631135-A 13 20-MAY-1997;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2731 AAAAAGAAACATCTTTT 2754  
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Db 1 AAAAAAAACCCCTTTT 24

RESULT 29  
LOCUS 192011 24 bp DNA linear PAT 01-DEC-1998  
DEFINITION Sequence 13 from patent US 5726297.  
ACCESSION 192011  
VERSION 192011.1 GI:3936481  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.  
TITLE Oligodeoxyribonucleotide N3' P5' phosphoramidates  
JOURNAL Patent: US 5726297-A 13 10-MAR-1998;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2731 AAAAAGAAACATCTTTT 2754  
|||||  
Db 1 AAAAAAAACCCCTTTT 24

RESULT 30  
LOCUS AR306126 24 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 67 from patent US 6548251.  
ACCESSION AR306126  
VERSION AR306126.1 GI:31695813  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Kozayvkin,S.A., Malykh,A.G., Polouchine,N.N. and Slesarev,A.I.  
TITLE Inhibition of molecular and biological processes using modified oligonucleotides

JOURNAL Patent: US 6548251-A 67 15-APR-2003;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2730 CAAAAGAAACATCTTTT 2753  
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Db 1 CAAAAGAAACATCTTTT 24

RESULT 31  
LOCUS AR473409 24 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 22 from patent US 6686516.  
ACCESSION AR473409  
VERSION AR473409.1 GI:42708866  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Lebel,E.G., Heifetz,P.B. and Goff,S.A.  
TITLE Expression of trehalose 6-phosphate synthase in plant plastids  
JOURNAL Patent: US 6686516-A 22 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 968 AGATTCCCGCCCGCCCGCCCA 991  
|||||  
Db 1 AGCTTCCCGCCCGCCCGCCCA 24

RESULT 32  
LOCUS AX278211 24 bp DNA linear PAT 01-NOV-2001  
DEFINITION Sequence 22 from Patent WO0177353.  
ACCESSION AX278211  
VERSION AX278211.1 GI:16605262  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Heifetz,P.B., Goff,S.A., Tuttle,A.B. and Griot-Wenk,M.E.  
TITLE Expression of pollen allergens in plastids  
JOURNAL Patent: WO 0177353-A 22 18-OCT-2001;  
Syngenta Participations AG (CH)  
FEATURES Location/Qualifiers  
source 1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="oligonucleotide"

Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 968 AGATTCCCGCCCGCCCGCCCA 991  
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Db 1 AGCTTCCCGCCCGCCCGCCCA 24

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VERSION BD188897.1 GI:32998636
KEYWORDS JP 2003012688-A/13.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound hybridization and nuclease tolerant characteristics
JOURNAL Patent: JP 2003012688-A 13 15-JAN-2003; LYNX THERAPEUTICS INC
COMMENT OS Unidentified
PN JP 2003012688-A/13
PD 15-JAN-2003
PF 12-JUN-2002 JP 2002171743
PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 P1
SERGEI M GRVAZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02.C12Q1/68
CC Strandedness: Both;
CC Topology: Linear;
CC Oligonucleotide N3', to P5' phosphoramidate: synthesis and CC compound;
CC hybridization and nuclease tolerant characteristics FH Key Location/Qualifiers
FT source
FT 1. .24
/organism='Unidentified'.
FEATURES
source
Location/Qualifiers
1. .24
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT TTTT 2754
||||| ||||| ||||| |||||
DB 1 AAAA AAAAACCCTTTT TTTT 24

RESULT 25
BD237693 24 bp DNA linear PAT 17-JUL-2003
LOCUS Therapeutically active proteins in plants.
DEFINITION BD237693
ACCESSION BD237693
VERSION BD237693.1 GI:33047463
KEYWORDS JP 2002526116-A/22.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Heifetz,P.B., Goff,S.A., Tuttle,A.B. and Wenk,M.E.G.
TITLE Therapeutically active proteins in plants
JOURNAL Patent: JP 2002526116-A 22 20-AUG-2002; SYNGENTA PARTICIPATIONS AG
COMMENT OS Artificial Sequence
PN JP 2002526116-A/22
PD 20-AUG-2002
PF 05-OCT-1999 JP 2000574707
PR 07-OCT-1998 US 09/167362,07-OCT-1998 US 09/168231 P1
PETER BERNARD HEIFETZ,STEPHEN ARTHUR GOFF,ANNMARIE BLOOM PI TUTTLE,
PI MONIKA ELSE GRIOT WENK
PC A01H5/00,A23L1/30,A23L1/30,A61K38/00,A61K38/16,A61K38/22, PC A61K38/28,
PC A61K38/43,A61K39/00,A61K39/35,A61P29/00,A61P37/00,A61P37/06, PC A61P37/08,
PC C12N5/10.C12N15/09// (C12N5/10,C12R1:91),C12N15/00,C12N5/00, PC A61K37/02,
PC A61K37/26,A61K37/48,A61K37/04,A61K37/24, (C12N5/00,C12R1:91) CC Description of Artificial Sequence: oligonucleotide FH Key Location/Qualifiers

FEATURES
source
Location/Qualifiers
1. .24
/organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1. .24
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 AGATTCCCGCCCGCCCGCCCA 991
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DB 1 AGCTTCCCGCCCGCCCGCCCA 24

RESULT 26
I33258 24 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 13 from patent US 5591607.
DEFINITION I33258
ACCESSION I33258
VERSION I33258.1 GI:1824049
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3.fwdarw.P5' phosphoramidates: triplex DNA formation
JOURNAL Patent: US 5591607-A 13 07-JAN-1997;
FEATURES
source
Location/Qualifiers
1. .24
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT TTTT 2754
||||| ||||| ||||| |||||
DB 1 AAAA AAAAACCCTTTT TTTT 24

RESULT 27
I35523 24 bp DNA linear PAT 13-MAY-1997
LOCUS Sequence 13 from patent US 5599922.
DEFINITION I35523
ACCESSION I35523
VERSION I35523.1 GI:2088491
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-P5' phosphoramidates: hybridization and nuclease resistance properties
JOURNAL Patent: US 5599922-A 13 04-FEB-1997;
FEATURES
source
Location/Qualifiers
1. .24
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 86;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAGAAAACATCTTTT TTTT 2754
||||| ||||| ||||| |||||
DB 1 AAAA AAAAACCCTTTT TTTT 24

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DEFINITION Sequence 13 from patent US 5965720.  
ACCESSION AR079586  
VERSION AR079586.1 GI:10006330  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.  
TITLE Oligonucleotide N3'.fwdarw.p5' phosphoramidates  
JOURNAL Patent: US 5965720-A 13 12-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred.No.86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2731 AAAAGAGAAACATCTTTTITTTT 2754  
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Db 1 AAAAAAAAAACCCCTTTTITTTT 24  
RESULT 21  
BD138045  
LOCUS AR123295 24 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 13 from patent US 6169170.  
ACCESSION AR123295  
VERSION AR123295.1 GI:14108261  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.  
TITLE Oligonucleotide N3'.fwdarw.N5'Phosphoramidate Duplexes  
JOURNAL Patent: US 6169170-A 13 02-JAN-2001;  
FEATURES Location/Qualifiers  
source 1..24  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred.No.86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2731 AAAAGAGAAACATCTTTTITTTT 2754  
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Db 1 AAAAAAAAAACCCCTTTTITTTT 24  
RESULT 22  
BD138045  
LOCUS AR138045 24 bp DNA linear PAT 18-SEP-2002  
DEFINITION Expression of trehalose biosynthetic genes in plants.  
ACCESSION BD138045  
VERSION BD138045.1 GI:23232990  
KEYWORDS JP 2002505875-A/22.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Lebel,E.G., Heifetz,P.B. and Goff,S.A.  
TITLE Expression of trehalose biosynthetic genes in plants  
JOURNAL Patent: JP 2002505875-A 22 26-FEB-2002;  
COMMENT NOVARTIS AG  
OS Artificial Sequence  
PN JP 2002505875-A/22  
PD 26-FEB-2002  
PF 09-MAR-1999 JP 2000535737  
PR 11-MAR-1998 US 60/077665

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PI GOFF  
PC A01H5/00,C12N5/10,C12N9/10,C12N15/09,C12P19/12,C12N5/  
PC 00,C12N15/00  
CC Description of Artificial Sequence:oligonucleotide FH Key  
Location/Qualifiers  
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FT /organism='Artificial Sequence'.  
FEATURES  
source 1..24  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred.No.86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 968 AGATTCCCCCCCCACCCGCCCA 991  
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Db 1 AGCTTCCCCCCCCCCCCCCCCCA 24  
RESULT 23  
BD175807  
LOCUS BD175807 24 bp DNA linear PAT 18-MAR-2003  
DEFINITION 2'-4'-BNA oligonucleotide having N3'-p5' binding.  
ACCESSION BD175807  
VERSION BD175807.1 GI:29121509  
KEYWORDS JP 2002255990-A/10.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Imanishi,T. and Kohiga,S.  
TITLE 2'-4'-BNA oligonucleotide having N3'-p5' binding  
JOURNAL Patent: JP 2002255990-A 10 11-SEP-2002;  
COMMENT SANKYO CO LTD  
OS Artificial Sequence  
PN JP 2002255990-A/10  
PD 11-SEP-2002  
PF 19-NOV-2001 JP 2001352543  
PI TAKESHI IMANISHI,SATOSHI KOHIGA  
PC C07H19/06,A61K31/712,A61K48/00,A61P31/18,C07H19/16,C07H21/00,  
PC C12N15/09,  
PC C12N15/00  
CC Description of Artificial Sequence: Synthesized and hairpin-  
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CC oligonucleotide  
FT Key Location/Qualifiers  
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FT /organism='Artificial Sequence'.  
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Best Local Similarity 87.5%; Pred.No.86;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2731 AAAAGAGAAACATCTTTTITTTT 2754  
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Db 1 AAAAAAAAAACCCCTTTTITTTT 24  
RESULT 24  
BD188897  
LOCUS BD188897 24 bp DNA linear PAT 17-JUL-2003  
DEFINITION Oligonucleotide N3' to p5' phosphoramidate: synthesis and compound;  
ACCESSION hybridization and nuclease tolerant characteristics.  
BD188897



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VERSION AX043186.1 GI:11341794
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 005088-A 752 02-NOV-2000;
Amer sham Pharmacia Biotech AB (SE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPB1 Heterozygote Primer Sequence"
Query Match
Best Local Similarity 0.5%; Score 20.2; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 918 TCCTTCCAGGAGAAAAAACA 942
Db 25 TCCTTCCAGGAGAAAAAACA 1
RESULT 16
LOCUS AR367879 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 8 from patent US 6376199.
ACCESSION AR367879
VERSION AR367879.1 GI:34601335
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Caniggia,I., Post,M. and Lye,S.
TITLE Methods to diagnose a required regulation of trophoblast invasion
JOURNAL Patent: US 6376199-A 8 23-APR-2002;
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 0.5%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1254 CATCTGTCCTCCGTGGCGCT 1273
Db 1 CATCTGTCCTCCGTGGCGCT 20
RESULT 17
LOCUS A23914 21 bp DNA linear PAT 25-JAN-1995
DEFINITION TGF-beta hybrid PCR primer.
ACCESSION A23914
VERSION A23914.1 GI:833308
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 20 19-MAY-1993;
CIBA-GEIGY AG
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/db_xref="taxon:32630"
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Best Local Similarity 0.5%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2234 AGGTACAAATGCTAACTTCTG 2254
Db 1 AGGTACAAATGCCAACTTCTG 21
RESULT 18
LOCUS A23915/c 21 bp DNA linear PAT 25-JAN-1995
DEFINITION TGF-beta hybrid PCR primer.
ACCESSION A23915
VERSION A23915.1 GI:833309
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 21 19-MAY-1993;
CIBA-GEIGY AG
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2234 AGGTACAAATGCTAACTTCTG 2254
Db 21 AGGTACAAATGCCAACTTCTG 1
RESULT 19
LOCUS AR058881 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5837835.
ACCESSION AR058881
VERSION AR058881.1 GI:5984458
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 13 17-NOV-1998;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match
Best Local Similarity 0.4%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2731 AAAAGAAAACATCTTTTITTTT 2754
Db 1 AAAAGAAAACCCCTTTTITTTT 24
RESULT 20
LOCUS AR079586 24 bp DNA linear PAT 31-AUG-2000
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| /note="SYNTHETIC OLIGONUCLEOTIDE" |   |
| Query Match                       | 0.5%; Score 22.2; DB 1; Length 27;  |
| Best Local Similarity             | 88.9%; Pred. No. 29;  |
| Matches                           | 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;                               |
| QY                                | 1520 GGAGGTTTATAAATCGACATGCGTC 1546<br>   |
| Db                                | 27 GGAGGTTTACAAAATAGACATGCGCC 1<br>   |
| RESULT 11                         |   |
| CQ778291/c                        |   |
| LOCUS                             | CQ778291 22 bp DNA linear PAT 11-MAR-2004   |
| DEFINITION                        | Sequence 1977 from Patent EP1394274.  |
| ACCESSION                         | CQ778291  |
| VERSION                           | CQ778291.1 GI:45381009  |
| KEYWORDS                          | synthetic construct   |
| SOURCE                            | synthetic construct   |
| ORGANISM                          | other sequences; artificial sequences.  |
| REFERENCE                         | 1   |
| AUTHORS                           | Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhashi, K.          |
| TITLE                             | Methods of testing for bronchial asthma or chronic obstructive pulmonary disease  |
| JOURNAL                           | Patent: EP 1394274-A 1977 03-MAR-2004;  |
| Genex Research, Inc. (JP)         |   |
| FEATURES                          | Location/Qualifiers   |
| source                            | 1..22   |
|                                   | /organism="synthetic construct"   |
|                                   | /mol_type="unassigned DNA"  |
|                                   | /db_xref="taxon:32630"  |
|                                   | /note="an artificially synthesized primer sequence"                               |
| Query Match                       | 0.5%; Score 22; DB 1; Length 22;  |
| Best Local Similarity             | 100.0%; Pred. No. 19;   |
| Matches                           | 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                               |
| QY                                | 317 TGTGTTCACAGGGGTTAAGG 338<br>  |
| Db                                | 22 TGTGTTCACAGGGGTTAAGG 1<br>   |
| RESULT 12                         |   |
| AR409919                          |   |
| LOCUS                             | AR409919 22 bp RNA linear PAT 18-DEC-2003   |
| DEFINITION                        | Sequence 32 from patent US 6635422.   |
| ACCESSION                         | AR409919  |
| VERSION                           | AR409919.1 GI:40161054  |
| KEYWORDS                          | Unknown.  |
| SOURCE                            | Unknown.  |
| ORGANISM                          | Unclassified.   |
| REFERENCE                         | 1 (bases 1 to 22)   |
| AUTHORS                           | Keene, J.D., Tenenbaum, S.A. and Carson, C.C.                                     |
| TITLE                             | Methods for isolating and characterizing endogenous mRNA-protein (mRNP) complexes |
| JOURNAL                           | Patent: US 6635422-A 32 21-OCT-2003;  |
| Genex Research, Inc. (JP)         |   |
| FEATURES                          | Location/Qualifiers   |
| source                            | 1..22   |
|                                   | /organism="unknown"   |
|                                   | /mol_type="unassigned RNA"  |
| Query Match                       | 0.5%; Score 22; DB 1; Length 22;  |
| Best Local Similarity             | 100.0%; Pred. No. 19;   |
| Matches                           | 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                               |
| QY                                | 4078 TTTTCTTTAATGTTTTTT 4099<br>  |
| Db                                | 1 TTTTCTTTAATGTTTTTT 22<br>   |
| RESULT 13                         |   |
| AX043186                          |   |
| LOCUS                             | AX043186 25 bp DNA linear PAT 23-NOV-2000   |
| DEFINITION                        | Sequence 752 from Patent WO0065089.   |
| ACCESSION                         | AX043186  |

|   |   |
|---|---|
| CQ778188  |   |
| LOCUS   | CQ778188 25 bp DNA linear PAT 12-MAR-2004   |
| DEFINITION  | Sequence 1874 from Patent EP1394274.  |
| ACCESSION   | CQ778188  |
| VERSION   | CQ778188.1 GI:45380906  |
| KEYWORDS  | synthetic construct   |
| SOURCE  | synthetic construct   |
| ORGANISM  | other sequences; artificial sequences.  |
| REFERENCE   | 1   |
| AUTHORS   | Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuhashi, K.                      |
| TITLE   | Methods of testing for bronchial asthma or chronic obstructive pulmonary disease              |
| JOURNAL   | Patent: EP 1394274-A 1874 03-MAR-2004;  |
| Genex Research, Inc. (JP)                               |   |
| FEATURES  | Location/Qualifiers   |
| source  | 1..25   |
|   | /organism="synthetic construct"   |
|   | /mol_type="unassigned DNA"  |
|   | /db_xref="taxon:32630"  |
|   | /note="an artificially synthesized TagMan probe sequence"                                     |
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| misc_feature  | 25  |
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|   | TAMRA(6-carboxy-N,N,N#-tetramethylrhodamine)"   |
| Query Match   | 0.5%; Score 21.8; DB 1; Length 25;  |
| Best Local Similarity                                   | 92.0%; Pred. No. 28;  |
| Matches   | 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;   |
| QY  | 1759 CCCAGCGCTACATCGATAGCAAGGT 1783<br>   |
| Db  | 1 CCCAGCGCTACATCGACAGCAAGT 25<br>   |
| RESULT 14   |   |
| AX113804  |   |
| LOCUS   | AX113804 24 bp DNA linear PAT 01-MAY-2001   |
| DEFINITION  | Sequence 50 from Patent WO0127256.  |
| ACCESSION   | AX113804  |
| VERSION   | AX113804.1 GI:13939970  |
| KEYWORDS  | synthetic construct   |
| SOURCE  | synthetic construct   |
| ORGANISM  | other sequences; artificial sequences.  |
| REFERENCE   | 1   |
| AUTHORS   | Wu, L., Carey, M.F. and Belleggrun, A.S.  |
| TITLE   | Chimeric transcriptional regulatory element and methods for prostate-targeted gene expression |
| JOURNAL   | Patent: WO 0127256-A 50 19-APR-2001;  |
| The Regents of the University of California System (US) |   |
| FEATURES  | Location/Qualifiers   |
| source  | 1..24   |
|   | /organism="synthetic construct"   |
|   | /mol_type="unassigned DNA"  |
|   | /db_xref="taxon:32630"  |
|   | /note="SYNTHETIC OLIGONUCLEOTIDE"   |
| Query Match   | 0.5%; Score 21.4; DB 1; Length 24;  |
| Best Local Similarity                                   | 95.7%; Pred. No. 31;  |
| Matches   | 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   |
| QY  | 1278 CTGCTACCTGCAGCACCTCGA 1300<br>   |
| Db  | 2 CTGCTACCTGCAGCACCTCGA 24<br>  |
| RESULT 15   |   |
| AX043186/c  |   |
| LOCUS   | AX043186 25 bp DNA linear PAT 23-NOV-2000   |
| DEFINITION  | Sequence 752 from Patent WO0065089.   |
| ACCESSION   | AX043186  |

Db 1 TTTTTCCTTCCCTTTAAATGTGAATGGTTCTTT 33  
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RESULT 6  
AR409918  
LOCUS AR409918 25 bp RNA linear PAT 18-DEC-2003  
DEFINITION Sequence 31 from patent US 6635422.  
ACCESSION AR409918  
VERSION AR409918.1 GI:40161053  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Keene,J.D., Tenenbaum,S.A. and Carson,C.C.  
TITLE Methods for isolating and characterizing endogenous mRNA-protein  
(mRNP) complexes  
JOURNAL Patent: US 6635422-A 31 21-OCT-2003;  
FEATURES Location/Qualifiers  
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Query Match 0.6%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3693 TTCAATTTTTTTTATATACTATCTT 3717  
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Db 1 TTCAATTTTTTTTATATACTATCTT 25  
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RESULT 7  
CQ778289  
LOCUS CQ778289 23 bp DNA linear PAT 11-MAR-2004  
DEFINITION Sequence 1975 from Patent EP1394274.  
ACCESSION CQ778289  
VERSION CQ778289.1 GI:45381007  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuohara,K.  
TITLE Methods of testing for bronchial asthma or chronic obstructive  
pulmonary disease  
JOURNAL Patent: EP 1394274-A 1975 03-MAR-2004;  
Genox Research, Inc. (JP)  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 13;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 217 TTACCCTAAGCGAGAAAGTGCAA 239  
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Db 1 TTACCCTAAGCGAGAAAGTGCAA 23  
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RESULT 8  
A23924  
LOCUS A23924 26 bp DNA linear PAT 25-JAN-1995  
DEFINITION TGF-beta hybrid PCR primer.  
ACCESSION A23924  
VERSION A23924.1 GI:833318  
KEYWORDS .  
SOURCE synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Wu,L., Carey,M.F. and Belldegrun,A.S.  
TITLE Chimeric transcriptional regulatory element and methods for  
prostate-targeted gene expression  
JOURNAL Patent: WO 0127256-A 51 19-APR-2001;  
The Regents of the University of California System (US)  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.  
TITLE Novel hybrid transforming growth factors  
JOURNAL Patent: EP 0542679-A 30 19-MAY-1993;  
CIBA-GEIGY AG  
FEATURES Location/Qualifiers  
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Best Local Similarity 92.3%; Pred. No. 20;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2265 TGCCCATATCTATGAGTTCAGACAC 2290  
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Db 1 TGCCCGTATTATGAGTTCAGACAC 26  
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RESULT 9  
A23925/c  
LOCUS A23925 26 bp DNA linear PAT 25-JAN-1995  
DEFINITION TGF-beta hybrid PCR primer.  
ACCESSION A23925  
VERSION A23925.1 GI:833319  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.  
TITLE Novel hybrid transforming growth factors  
JOURNAL Patent: EP 0542679-A 31 19-MAY-1993;  
CIBA-GEIGY AG  
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Query Match 0.5%; Score 22.8; DB 1; Length 26;  
Best Local Similarity 92.3%; Pred. No. 20;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2265 TGCCCATATCTATGAGTTCAGACAC 2290  
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Db 26 TGCCCGTATTATGAGTTCAGACAC 1  
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RESULT 10  
AX113805/c  
LOCUS AX113805 27 bp DNA linear PAT 01-MAY-2001  
DEFINITION Sequence 51 from Patent WO0127256.  
ACCESSION AX113805  
VERSION AX113805.1 GI:13939971  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Wu,L., Carey,M.F. and Belldegrun,A.S.  
TITLE Chimeric transcriptional regulatory element and methods for  
prostate-targeted gene expression  
JOURNAL Patent: WO 0127256-A 51 19-APR-2001;  
The Regents of the University of California System (US)  
FEATURES Location/Qualifiers  
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RESULT 1
A18285
LOCUS           A18285           39 bp    DNA          linear    PAT 17-MAY-1994
DEFINITION     oligonucleotide.
ACCESSION      A18285
VERSION        A18285.1  GI:513245
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 39)
AUTHORS        Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE          Process for the production of biologically active protein (e.g.
               TGF)
JOURNAL        Patent: EP 0433225-A 12 19-JUN-1991;
               CIBA-GEIGY AG
FEATURES       Location/Qualifiers
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Query Match    0.8%; Score 35.8; DB 1; Length 39;
Best Local Similarity 94.9%; Pred. No. 0.12;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2124  GCTTTGGATGCTGCTACTGCTTTAGAAATGTGCAGGAT 2162
Db  1  GCTTTGGATGCGGCCATTGCTTTAGAAATGTGCAGGAT 39

RESULT 2
I56859
LOCUS           I56859           39 bp    DNA          linear    PAT 07-OCT-1997
DEFINITION     Sequence 6 from patent US 5650494.
ACCESSION      I56859
VERSION        I56859.1  GI:2477272
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 39)
AUTHORS        Cerletti,N., McMaster,G.Kent., Cox,D., Schmitz,A. and Meyhack,B.
TITLE          Process for refolding recombinantly produced TGF-.beta.-like
               proteins
JOURNAL        Patent: US 5650494-A 6 22-JUL-1997;
               Location/Qualifiers
               source
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               /mol_type="unassigned DNA"

Query Match    0.8%; Score 35.8; DB 1; Length 39;
Best Local Similarity 94.9%; Pred. No. 0.12;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2124  GCTTTGGATGCTGCTACTGCTTTAGAAATGTGCAGGAT 2162
Db  1  GCTTTGGATGCGGCCATTGCTTTAGAAATGTGCAGGAT 39

RESULT 3
A18286/c
LOCUS           A18286           39 bp    DNA          linear    PAT 17-MAY-1994
DEFINITION     oligonucleotide.
ACCESSION      A18286
VERSION        A18286.1  GI:513246
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 39)
AUTHORS        Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
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TITLE          Process for the production of biologically active protein (e.g.
               TGF)
JOURNAL        Patent: EP 0433225-A 13 19-JUN-1991;
               CIBA-GEIGY AG
FEATURES       Location/Qualifiers
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               /db_xref="taxon:32630"

Query Match    0.8%; Score 34.2; DB 1; Length 39;
Best Local Similarity 92.3%; Pred. No. 0.25;
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2424  CTTTCCAATATGATTGTCAAGTCTTGTAATGCAGCTAA 2462
Db  39  CTTTCAATATGATTGTAAAGTCTTGCAATGCAGCTAA 1

RESULT 4
I56860/c
LOCUS           I56860           39 bp    DNA          linear    PAT 07-OCT-1997
DEFINITION     Sequence 7 from patent US 5650494.
ACCESSION      I56860
VERSION        I56860.1  GI:2477273
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 39)
AUTHORS        Cerletti,N., McMaster,G.Kent., Cox,D., Schmitz,A. and Meyhack,B.
TITLE          Process for refolding recombinantly produced TGF-.beta.-like
               proteins
JOURNAL        Patent: US 5650494-A 7 22-JUL-1997;
               Location/Qualifiers
               source
               1..39
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match    0.8%; Score 34.2; DB 1; Length 39;
Best Local Similarity 92.3%; Pred. No. 0.25;
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2424  CTTTCCAATATGATTGTCAAGTCTTGTAATGCAGCTAA 2462
Db  39  CTTTCAATATGATTGTAAAGTCTTGCAATGCAGCTAA 1

RESULT 5
AR409916
LOCUS           AR409916         33 bp    RNA          linear    PAT 18-DEC-2003
DEFINITION     Sequence 29 from patent US 6635422.
ACCESSION      AR409916
VERSION        AR409916.1  GI:40161051
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 33)
AUTHORS        Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
TITLE          Methods for isolating and characterizing endogenous mRNA-protein
               (mRNP) complexes
JOURNAL        Patent: US 6635422-A 29 21-OCT-2003;
               Location/Qualifiers
               source
               1..33
               /organism="unknown"
               /mol_type="unassigned RNA"

Query Match    0.8%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3264  TTTTTCCTTTTAAATTGTAATGGTTCTTT 3296
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| 693   | 13.8 | 0.3 | 17 | 1 | AR229837  | ACCESSION:AR229837  | c 766 | 13.8 | 0.3 | 17 | 1 | AX648557 | ACCESSION:AX648557 |
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| c 751 | 13.8 | 0.3 | 17 | 1 | AX265059  | ACCESSION:AX265059  | c 819 | 13.8 | 0.3 | 17 | 1 | BD091751 | ACCESSION:BD091751 |
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ALIGNMENTS

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| C 546 | 14 | 0.3 | 14 | 1 | AX030174 | ACCESSION:AX030174 | 619   | 14   | 0.3 | 17 | 1 | AX730621 | ACCESSION:AX730621 |
| C 547 | 14 | 0.3 | 14 | 1 | AX316416 | ACCESSION:AX316416 | C 620 | 14   | 0.3 | 17 | 1 | AX735813 | ACCESSION:AX735813 |
| C 548 | 14 | 0.3 | 14 | 1 | AX316422 | ACCESSION:AX316422 | 621   | 14   | 0.3 | 17 | 1 | AX737087 | ACCESSION:AX737087 |
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| C 551 | 14 | 0.3 | 14 | 1 | AX316434 | ACCESSION:AX316434 | C 624 | 14   | 0.3 | 17 | 1 | BD011730 | ACCESSION:BD011730 |
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| C 555 | 14 | 0.3 | 14 | 1 | AX316465 | ACCESSION:AX316465 | C 628 | 14   | 0.3 | 17 | 1 | BD097334 | ACCESSION:BD097334 |
| C 556 | 14 | 0.3 | 14 | 1 | AX316481 | ACCESSION:AX316481 | C 629 | 13.8 | 0.3 | 17 | 1 | AR266625 | ACCESSION:AR266625 |
| C 557 | 14 | 0.3 | 14 | 1 | AX316495 | ACCESSION:AX316495 | 630   | 13.8 | 0.3 | 17 | 1 | AR8312   | ACCESSION:AR8312   |
| C 558 | 14 | 0.3 | 14 | 1 | BD065884 | ACCESSION:BD065884 | 631   | 13.8 | 0.3 | 17 | 1 | A90279   | ACCESSION:A90279   |
| C 559 | 14 | 0.3 | 14 | 1 | BD065912 | ACCESSION:BD065912 | 632   | 13.8 | 0.3 | 17 | 1 | AR040485 | ACCESSION:AR040485 |
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| C 561 | 14 | 0.3 | 14 | 1 | BD066560 | ACCESSION:BD066560 | 634   | 13.8 | 0.3 | 17 | 1 | AR065045 | ACCESSION:AR065045 |
| C 562 | 14 | 0.3 | 14 | 1 | BD066566 | ACCESSION:BD066566 | 635   | 13.8 | 0.3 | 17 | 1 | AR164696 | ACCESSION:AR164696 |
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| C 570 | 14 | 0.3 | 14 | 1 | BD066636 | ACCESSION:BD066636 | 643   | 13.8 | 0.3 | 17 | 1 | BD201512 | ACCESSION:BD201512 |
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| C 582 | 14 | 0.3 | 15 | 1 | AR113355 | ACCESSION:AR113355 | C 655 | 13.8 | 0.3 | 17 | 1 | BD258338 | ACCESSION:BD258338 |
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| C 584 | 14 | 0.3 | 15 | 1 | AR113913 | ACCESSION:AR113913 | 657   | 13.8 | 0.3 | 17 | 1 | BD258484 | ACCESSION:BD258484 |
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| C 588 | 14 | 0.3 | 15 | 1 | BD207266 | ACCESSION:BD207266 | 661   | 13.8 | 0.3 | 17 | 1 | BD258575 | ACCESSION:BD258575 |
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| C 594 | 14 | 0.3 | 15 | 1 | AX633203 | ACCESSION:AX633203 | 667   | 13.8 | 0.3 | 17 | 1 | CQ624486 | ACCESSION:CQ624486 |
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| C 597 | 14 | 0.3 | 15 | 1 | BD065951 | ACCESSION:BD065951 | C 670 | 13.8 | 0.3 | 17 | 1 | CQ868213 | ACCESSION:CQ868213 |
| C 598 | 14 | 0.3 | 16 | 1 | I28577   | ACCESSION:I28577   | C 671 | 13.8 | 0.3 | 17 | 1 | E34259   | ACCESSION:E34259   |
| C 599 | 14 | 0.3 | 16 | 1 | I58739   | ACCESSION:I58739   | 672   | 13.8 | 0.3 | 17 | 1 | I32590   | ACCESSION:I32590   |
| C 600 | 14 | 0.3 | 17 | 1 | AX676082 | ACCESSION:AX676082 | C 673 | 13.8 | 0.3 | 17 | 1 | AR186202 | ACCESSION:AR186202 |
| 601   | 14 | 0.3 | 17 | 1 | AX738493 | ACCESSION:AX738493 | C 674 | 13.8 | 0.3 | 17 | 1 | AR186698 | ACCESSION:AR186698 |
| 602   | 14 | 0.3 | 17 | 1 | AX757892 | ACCESSION:AX757892 | C 675 | 13.8 | 0.3 | 17 | 1 | AR186827 | ACCESSION:AR186827 |
| C 603 | 14 | 0.3 | 17 | 1 | BD142808 | ACCESSION:BD142808 | C 676 | 13.8 | 0.3 | 17 | 1 | AR187056 | ACCESSION:AR187056 |
| C 604 | 14 | 0.3 | 17 | 1 | BD143834 | ACCESSION:BD143834 | C 677 | 13.8 | 0.3 | 17 | 1 | AR187057 | ACCESSION:AR187057 |
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| C 607 | 14 | 0.3 | 17 | 1 | BD168111 | ACCESSION:BD168111 | C 680 | 13.8 | 0.3 | 17 | 1 | AR187063 | ACCESSION:AR187063 |
| C 608 | 14 | 0.3 | 17 | 1 | BD171177 | ACCESSION:BD171177 | C 681 | 13.8 | 0.3 | 17 | 1 | AR187064 | ACCESSION:AR187064 |
| C 609 | 14 | 0.3 | 17 | 1 | E02988   | ACCESSION:E02988   | C 682 | 13.8 | 0.3 | 17 | 1 | AR187068 | ACCESSION:AR187068 |
| C 610 | 14 | 0.3 | 17 | 1 | E34258   | ACCESSION:E34258   | 683   | 13.8 | 0.3 | 17 | 1 | AR187239 | ACCESSION:AR187239 |
| C 611 | 14 | 0.3 | 17 | 1 | AR266625 | ACCESSION:AR266625 | 684   | 13.8 | 0.3 | 17 | 1 | AR188517 | ACCESSION:AR188517 |
| C 612 | 14 | 0.3 | 17 | 1 | AX215415 | ACCESSION:AX215415 | C 685 | 13.8 | 0.3 | 17 | 1 | AR188526 | ACCESSION:AR188526 |
| C 613 | 14 | 0.3 | 17 | 1 | AX216957 | ACCESSION:AX216957 | 686   | 13.8 | 0.3 | 17 | 1 | AR188812 | ACCESSION:AR188812 |
| C 614 | 14 | 0.3 | 17 | 1 | AX216958 | ACCESSION:AX216958 | 687   | 13.8 | 0.3 | 17 | 1 | AR190075 | ACCESSION:AR190075 |
| C 615 | 14 | 0.3 | 17 | 1 | AX532502 | ACCESSION:AX532502 | 688   | 13.8 | 0.3 | 17 | 1 | AR190475 | ACCESSION:AR190475 |
| C 616 | 14 | 0.3 | 17 | 1 | AX532503 | ACCESSION:AX532503 | C 689 | 13.8 | 0.3 | 17 | 1 | AR192138 | ACCESSION:AR192138 |
| C 617 | 14 | 0.3 | 17 | 1 | AX532504 | ACCESSION:AX532504 | C 690 | 13.8 | 0.3 | 17 | 1 | AR196413 | ACCESSION:AR196413 |

|     |      |     |    |   |          |                    |       |      |     |    |   |          |                    |
|-----|------|-----|----|---|----------|--------------------|-------|------|-----|----|---|----------|--------------------|
| 399 | 14.4 | 0.3 | 17 | 1 | I54412   | ACCSSION:I54412    | C 472 | 14.4 | 0.3 | 18 | 1 | BD107507 | ACCESSION:BD107507 |
| 400 | 14.4 | 0.3 | 17 | 1 | I54418   | ACCESSION:I54418   | C 473 | 14.2 | 0.3 | 16 | 1 | ES2143   | ACCESSION:ES2143   |
| 401 | 14.4 | 0.3 | 17 | 1 | I54420   | ACCESSION:I54420   | C 474 | 14.2 | 0.3 | 16 | 1 | ES3842   | ACCESSION:ES3842   |
| 402 | 14.4 | 0.3 | 17 | 1 | I94415   | ACCESSION:I94415   | C 475 | 14.2 | 0.3 | 17 | 1 | AX406535 | ACCESSION:AX406535 |
| 403 | 14.4 | 0.3 | 17 | 1 | I94418   | ACCESSION:I94418   | C 476 | 14.2 | 0.3 | 17 | 1 | AX721791 | ACCESSION:AX721791 |
| 404 | 14.4 | 0.3 | 17 | 1 | AR188518 | ACCESSION:AR188518 | C 477 | 14   | 0.3 | 14 | 1 | A40172   | ACCESSION:A40172   |
| 405 | 14.4 | 0.3 | 17 | 1 | AR192340 | ACCESSION:AR192340 | C 478 | 14   | 0.3 | 14 | 1 | A40520   | ACCESSION:A40520   |
| 406 | 14.4 | 0.3 | 17 | 1 | AR324371 | ACCESSION:AR324371 | C 479 | 14   | 0.3 | 14 | 1 | A40526   | ACCESSION:A40526   |
| 407 | 14.4 | 0.3 | 17 | 1 | AR326210 | ACCESSION:AR326210 | C 480 | 14   | 0.3 | 14 | 1 | A40534   | ACCESSION:A40534   |
| 408 | 14.4 | 0.3 | 17 | 1 | AR329023 | ACCESSION:AR329023 | C 481 | 14   | 0.3 | 14 | 1 | A40537   | ACCESSION:A40537   |
| 409 | 14.4 | 0.3 | 17 | 1 | AX214791 | ACCESSION:AX214791 | C 482 | 14   | 0.3 | 14 | 1 | A40538   | ACCESSION:A40538   |
| 410 | 14.4 | 0.3 | 17 | 1 | AX227570 | ACCESSION:AX227570 | C 483 | 14   | 0.3 | 14 | 1 | A40554   | ACCESSION:A40554   |
| 411 | 14.4 | 0.3 | 17 | 1 | AX671893 | ACCESSION:AX671893 | C 484 | 14   | 0.3 | 14 | 1 | A40564   | ACCESSION:A40564   |
| 412 | 14.4 | 0.3 | 17 | 1 | AX673880 | ACCESSION:AX673880 | C 485 | 14   | 0.3 | 14 | 1 | A40566   | ACCESSION:A40566   |
| 413 | 14.4 | 0.3 | 17 | 1 | AX674166 | ACCESSION:AX674166 | C 486 | 14   | 0.3 | 14 | 1 | A40569   | ACCESSION:A40569   |
| 414 | 14.4 | 0.3 | 17 | 1 | AX676082 | ACCESSION:AX676082 | C 487 | 14   | 0.3 | 14 | 1 | A40585   | ACCESSION:A40585   |
| 415 | 14.4 | 0.3 | 17 | 1 | AX724450 | ACCESSION:AX724450 | C 488 | 14   | 0.3 | 14 | 1 | A40599   | ACCESSION:A40599   |
| 416 | 14.4 | 0.3 | 17 | 1 | AX726113 | ACCESSION:AX726113 | C 489 | 14   | 0.3 | 14 | 1 | A88371   | ACCESSION:A88371   |
| 417 | 14.4 | 0.3 | 17 | 1 | AX726611 | ACCESSION:AX726611 | C 490 | 14   | 0.3 | 14 | 1 | A88399   | ACCESSION:A88399   |
| 418 | 14.4 | 0.3 | 17 | 1 | AX733221 | ACCESSION:AX733221 | C 491 | 14   | 0.3 | 14 | 1 | A88439   | ACCESSION:A88439   |
| 419 | 14.4 | 0.3 | 17 | 1 | AX735212 | ACCESSION:AX735212 | C 492 | 14   | 0.3 | 14 | 1 | A89047   | ACCESSION:A89047   |
| 420 | 14.4 | 0.3 | 17 | 1 | AX736066 | ACCESSION:AX736066 | C 493 | 14   | 0.3 | 14 | 1 | A89053   | ACCESSION:A89053   |
| 421 | 14.4 | 0.3 | 17 | 1 | AX736332 | ACCESSION:AX736332 | C 494 | 14   | 0.3 | 14 | 1 | A89060   | ACCESSION:A89060   |
| 422 | 14.4 | 0.3 | 17 | 1 | AX737597 | ACCESSION:AX737597 | C 495 | 14   | 0.3 | 14 | 1 | A89062   | ACCESSION:A89062   |
| 423 | 14.4 | 0.3 | 17 | 1 | AX738493 | ACCESSION:AX738493 | C 496 | 14   | 0.3 | 14 | 1 | A89063   | ACCESSION:A89063   |
| 424 | 14.4 | 0.3 | 17 | 1 | AX739553 | ACCESSION:AX739553 | C 497 | 14   | 0.3 | 14 | 1 | A89079   | ACCESSION:A89079   |
| 425 | 14.4 | 0.3 | 17 | 1 | AX739596 | ACCESSION:AX739596 | C 498 | 14   | 0.3 | 14 | 1 | A89089   | ACCESSION:A89089   |
| 426 | 14.4 | 0.3 | 17 | 1 | AX757067 | ACCESSION:AX757067 | C 499 | 14   | 0.3 | 14 | 1 | A89091   | ACCESSION:A89091   |
| 427 | 14.4 | 0.3 | 17 | 1 | AX757780 | ACCESSION:AX757780 | C 500 | 14   | 0.3 | 14 | 1 | A89109   | ACCESSION:A89109   |
| 428 | 14.4 | 0.3 | 17 | 1 | AX757892 | ACCESSION:AX757892 | C 501 | 14   | 0.3 | 14 | 1 | A89123   | ACCESSION:A89123   |
| 429 | 14.4 | 0.3 | 17 | 1 | AX759064 | ACCESSION:AX759064 | C 502 | 14   | 0.3 | 14 | 1 | A90338   | ACCESSION:A90338   |
| 430 | 14.4 | 0.3 | 17 | 1 | AX759785 | ACCESSION:AX759785 | C 503 | 14   | 0.3 | 14 | 1 | A90366   | ACCESSION:A90366   |
| 431 | 14.4 | 0.3 | 17 | 1 | AX761129 | ACCESSION:AX761129 | C 504 | 14   | 0.3 | 14 | 1 | A90406   | ACCESSION:A90406   |
| 432 | 14.4 | 0.3 | 17 | 1 | AX761716 | ACCESSION:AX761716 | C 505 | 14   | 0.3 | 14 | 1 | AR174027 | ACCESSION:AR174027 |
| 433 | 14.4 | 0.3 | 17 | 1 | AX761717 | ACCESSION:AX761717 | C 506 | 14   | 0.3 | 14 | 1 | AR174031 | ACCESSION:AR174031 |
| 434 | 14.4 | 0.3 | 18 | 1 | AR078640 | ACCESSION:AR078640 | 507   | 14   | 0.3 | 14 | 1 | BD176798 | ACCESSION:BD176798 |
| 435 | 14.4 | 0.3 | 18 | 1 | BD145035 | ACCESSION:BD145035 | 508   | 14   | 0.3 | 14 | 1 | BD176799 | ACCESSION:BD176799 |
| 436 | 14.4 | 0.3 | 18 | 1 | BD145036 | ACCESSION:BD145036 | C 509 | 14   | 0.3 | 14 | 1 | BD176801 | ACCESSION:BD176801 |
| 437 | 14.4 | 0.3 | 18 | 1 | BD145037 | ACCESSION:BD145037 | C 510 | 14   | 0.3 | 14 | 1 | BD234897 | ACCESSION:BD234897 |
| 438 | 14.4 | 0.3 | 18 | 1 | BD145039 | ACCESSION:BD145039 | C 511 | 14   | 0.3 | 14 | 1 | BD234898 | ACCESSION:BD234898 |
| 439 | 14.4 | 0.3 | 18 | 1 | BD166035 | ACCESSION:BD166035 | C 512 | 14   | 0.3 | 14 | 1 | BD234901 | ACCESSION:BD234901 |
| 440 | 14.4 | 0.3 | 18 | 1 | BD166036 | ACCESSION:BD166036 | C 513 | 14   | 0.3 | 14 | 1 | BD234907 | ACCESSION:BD234907 |
| 441 | 14.4 | 0.3 | 18 | 1 | BD166037 | ACCESSION:BD166037 | C 514 | 14   | 0.3 | 14 | 1 | BD234955 | ACCESSION:BD234955 |
| 442 | 14.4 | 0.3 | 18 | 1 | BD166039 | ACCESSION:BD166039 | C 515 | 14   | 0.3 | 14 | 1 | BD234960 | ACCESSION:BD234960 |
| 443 | 14.4 | 0.3 | 18 | 1 | CQ807628 | ACCESSION:CQ807628 | C 516 | 14   | 0.3 | 14 | 1 | BD234986 | ACCESSION:BD234986 |
| 444 | 14.4 | 0.3 | 18 | 1 | CQ814895 | ACCESSION:CQ814895 | C 517 | 14   | 0.3 | 14 | 1 | AR232800 | ACCESSION:AR232800 |
| 445 | 14.4 | 0.3 | 18 | 1 | AR196692 | ACCESSION:AR196692 | C 518 | 14   | 0.3 | 14 | 1 | AR232806 | ACCESSION:AR232806 |
| 446 | 14.4 | 0.3 | 18 | 1 | AR208427 | ACCESSION:AR208427 | C 519 | 14   | 0.3 | 14 | 1 | AR232814 | ACCESSION:AR232814 |
| 447 | 14.4 | 0.3 | 18 | 1 | AR264931 | ACCESSION:AR264931 | C 520 | 14   | 0.3 | 14 | 1 | AR232817 | ACCESSION:AR232817 |
| 448 | 14.4 | 0.3 | 18 | 1 | AR264932 | ACCESSION:AR264932 | C 521 | 14   | 0.3 | 14 | 1 | AR232818 | ACCESSION:AR232818 |
| 449 | 14.4 | 0.3 | 18 | 1 | AR264933 | ACCESSION:AR264933 | C 522 | 14   | 0.3 | 14 | 1 | AR232834 | ACCESSION:AR232834 |
| 450 | 14.4 | 0.3 | 18 | 1 | AR264935 | ACCESSION:AR264935 | C 523 | 14   | 0.3 | 14 | 1 | AR232844 | ACCESSION:AR232844 |
| 451 | 14.4 | 0.3 | 18 | 1 | AR371952 | ACCESSION:AR371952 | C 524 | 14   | 0.3 | 14 | 1 | AR232846 | ACCESSION:AR232846 |
| 452 | 14.4 | 0.3 | 18 | 1 | AR478212 | ACCESSION:AR478212 | C 525 | 14   | 0.3 | 14 | 1 | AR232849 | ACCESSION:AR232849 |
| 453 | 14.4 | 0.3 | 18 | 1 | AR478213 | ACCESSION:AR478213 | C 526 | 14   | 0.3 | 14 | 1 | AR232865 | ACCESSION:AR232865 |
| 454 | 14.4 | 0.3 | 18 | 1 | AR478214 | ACCESSION:AR478214 | C 527 | 14   | 0.3 | 14 | 1 | AR232879 | ACCESSION:AR232879 |
| 455 | 14.4 | 0.3 | 18 | 1 | AR478216 | ACCESSION:AR478216 | 528   | 14   | 0.3 | 14 | 1 | AR242022 | ACCESSION:AR242022 |
| 456 | 14.4 | 0.3 | 18 | 1 | AX085253 | ACCESSION:AX085253 | C 529 | 14   | 0.3 | 14 | 1 | AX008968 | ACCESSION:AX008968 |
| 457 | 14.4 | 0.3 | 18 | 1 | AX599312 | ACCESSION:AX599312 | C 530 | 14   | 0.3 | 14 | 1 | AX008969 | ACCESSION:AX008969 |
| 458 | 14.4 | 0.3 | 18 | 1 | AX599726 | ACCESSION:AX599726 | C 531 | 14   | 0.3 | 14 | 1 | AX008972 | ACCESSION:AX008972 |
| 459 | 14.4 | 0.3 | 18 | 1 | AX767728 | ACCESSION:AX767728 | C 532 | 14   | 0.3 | 14 | 1 | AX008978 | ACCESSION:AX008978 |
| 460 | 14.4 | 0.3 | 18 | 1 | AX796166 | ACCESSION:AX796166 | C 533 | 14   | 0.3 | 14 | 1 | AX009026 | ACCESSION:AX009026 |
| 461 | 14.4 | 0.3 | 18 | 1 | AX822692 | ACCESSION:AX822692 | C 534 | 14   | 0.3 | 14 | 1 | AX009031 | ACCESSION:AX009031 |
| 462 | 14.4 | 0.3 | 18 | 1 | AX823114 | ACCESSION:AX823114 | C 535 | 14   | 0.3 | 14 | 1 | AX009057 | ACCESSION:AX009057 |
| 463 | 14.4 | 0.3 | 18 | 1 | AX826332 | ACCESSION:AX826332 | C 536 | 14   | 0.3 | 14 | 1 | AX030095 | ACCESSION:AX030095 |
| 464 | 14.4 | 0.3 | 18 | 1 | AX826754 | ACCESSION:AX826754 | C 537 | 14   | 0.3 | 14 | 1 | AX030101 | ACCESSION:AX030101 |
| 465 | 14.4 | 0.3 | 18 | 1 | BD072876 | ACCESSION:BD072876 | C 538 | 14   | 0.3 | 14 | 1 | AX030109 | ACCESSION:AX030109 |
| 466 | 14.4 | 0.3 | 18 | 1 | BD072877 | ACCESSION:BD072877 | C 539 | 14   | 0.3 | 14 | 1 | AX030112 | ACCESSION:AX030112 |
| 467 | 14.4 | 0.3 | 18 | 1 | BD072878 | ACCESSION:BD072878 | C 540 | 14   | 0.3 | 14 | 1 | AX030113 | ACCESSION:AX030113 |
| 468 | 14.4 | 0.3 | 18 | 1 | BD072880 | ACCESSION:BD072880 | C 541 | 14   | 0.3 | 14 | 1 | AX030129 | ACCESSION:AX030129 |
| 469 | 14.4 | 0.3 | 18 | 1 | BD107503 | ACCESSION:BD107503 | C 542 | 14   | 0.3 | 14 | 1 | AX030139 | ACCESSION:AX030139 |
| 470 | 14.4 | 0.3 | 18 | 1 | BD107504 | ACCESSION:BD107504 | C 543 | 14   | 0.3 | 14 | 1 | AX030141 | ACCESSION:AX030141 |
| 471 | 14.4 | 0.3 | 18 | 1 | BD107505 | ACCESSION:BD107505 | C 544 | 14   | 0.3 | 14 | 1 | AX030144 | ACCESSION:AX030144 |

|       |      |     |    |   |          |                    |       |      |     |    |   |           |                    |
|-------|------|-----|----|---|----------|--------------------|-------|------|-----|----|---|-----------|--------------------|
| C 253 | 15.4 | 0.4 | 19 | 1 | BD211727 | ACCESSION:BD211727 | 326   | 14.8 | 0.3 | 18 | 1 | AR262417  | ACCESSION:AR262417 |
| C 254 | 15.4 | 0.4 | 19 | 1 | CQ808384 | ACCESSION:CQ808384 | 327   | 14.8 | 0.3 | 18 | 1 | AR262418  | ACCESSION:AR262418 |
| C 255 | 15.4 | 0.4 | 19 | 1 | CQ829560 | ACCESSION:CQ829560 | C 328 | 14.8 | 0.3 | 18 | 1 | AR264936  | ACCESSION:AR264936 |
| C 256 | 15.4 | 0.4 | 19 | 1 | AR241645 | ACCESSION:AR241645 | C 329 | 14.8 | 0.3 | 18 | 1 | AR410329  | ACCESSION:AR410329 |
| C 257 | 15.4 | 0.4 | 19 | 1 | AR292884 | ACCESSION:AR292884 | C 330 | 14.8 | 0.3 | 18 | 1 | AR478217  | ACCESSION:AR478217 |
| C 258 | 15.4 | 0.4 | 19 | 1 | AR473599 | ACCESSION:AR473599 | C 331 | 14.8 | 0.3 | 18 | 1 | AX008976  | ACCESSION:AX008976 |
| C 259 | 15.4 | 0.4 | 19 | 1 | AR478107 | ACCESSION:AR478107 | C 332 | 14.8 | 0.3 | 18 | 1 | AX008980  | ACCESSION:AX008980 |
| C 260 | 15.4 | 0.4 | 19 | 1 | AX132308 | ACCESSION:AX132308 | C 333 | 14.8 | 0.3 | 18 | 1 | AX008983  | ACCESSION:AX008983 |
| C 261 | 15.4 | 0.4 | 19 | 1 | AX132311 | ACCESSION:AX132311 | C 334 | 14.8 | 0.3 | 18 | 1 | AX009032  | ACCESSION:AX009032 |
| C 262 | 15.4 | 0.4 | 20 | 1 | AR488890 | ACCESSION:AR488890 | C 335 | 14.8 | 0.3 | 18 | 1 | AX030110  | ACCESSION:AX030110 |
| C 263 | 15   | 0.4 | 15 | 1 | A88391   | ACCESSION:A88391   | C 336 | 14.8 | 0.3 | 18 | 1 | AX030117  | ACCESSION:AX030117 |
| C 264 | 15   | 0.4 | 15 | 1 | A88392   | ACCESSION:A88392   | C 337 | 14.8 | 0.3 | 18 | 1 | AX030123  | ACCESSION:AX030123 |
| C 265 | 15   | 0.4 | 15 | 1 | A88440   | ACCESSION:A88440   | C 338 | 14.8 | 0.3 | 18 | 1 | AX030134  | ACCESSION:AX030134 |
| C 266 | 15   | 0.4 | 15 | 1 | A90358   | ACCESSION:A90358   | C 339 | 14.8 | 0.3 | 18 | 1 | AX030153  | ACCESSION:AX030153 |
| C 267 | 15   | 0.4 | 15 | 1 | A90359   | ACCESSION:A90359   | C 340 | 14.8 | 0.3 | 18 | 1 | AX030166  | ACCESSION:AX030166 |
| C 268 | 15   | 0.4 | 15 | 1 | A90407   | ACCESSION:A90407   | C 341 | 14.8 | 0.3 | 18 | 1 | AX030169  | ACCESSION:AX030169 |
| C 269 | 15   | 0.4 | 15 | 1 | AR002256 | ACCESSION:AR002256 | C 342 | 14.8 | 0.3 | 18 | 1 | AX047272  | ACCESSION:AX047272 |
| C 270 | 15   | 0.4 | 15 | 1 | AR045206 | ACCESSION:AR045206 | C 343 | 14.8 | 0.3 | 18 | 1 | AX047274  | ACCESSION:AX047274 |
| C 271 | 15   | 0.4 | 15 | 1 | AR051237 | ACCESSION:AR051237 | C 344 | 14.8 | 0.3 | 18 | 1 | AX191970  | ACCESSION:AX191970 |
| C 272 | 15   | 0.4 | 15 | 1 | AR084519 | ACCESSION:AR084519 | C 345 | 14.8 | 0.3 | 18 | 1 | AX252494  | ACCESSION:AX252494 |
| C 273 | 15   | 0.4 | 15 | 1 | AR127784 | ACCESSION:AR127784 | C 346 | 14.8 | 0.3 | 18 | 1 | AX316431  | ACCESSION:AX316431 |
| C 274 | 15   | 0.4 | 15 | 1 | I16031   | ACCESSION:I16031   | C 347 | 14.8 | 0.3 | 18 | 1 | AX316438  | ACCESSION:AX316438 |
| C 275 | 15   | 0.4 | 15 | 1 | I28366   | ACCESSION:I28366   | C 348 | 14.8 | 0.3 | 18 | 1 | AX316444  | ACCESSION:AX316444 |
| C 276 | 15   | 0.4 | 15 | 1 | BD065904 | ACCESSION:BD065904 | C 349 | 14.8 | 0.3 | 18 | 1 | AX316455  | ACCESSION:AX316455 |
| C 277 | 15   | 0.4 | 15 | 1 | BD065905 | ACCESSION:BD065905 | C 350 | 14.8 | 0.3 | 18 | 1 | AX316474  | ACCESSION:AX316474 |
| C 278 | 15   | 0.4 | 15 | 1 | BD065953 | ACCESSION:BD065953 | C 351 | 14.8 | 0.3 | 18 | 1 | AX316487  | ACCESSION:AX316487 |
| C 279 | 15   | 0.4 | 17 | 1 | AX729109 | ACCESSION:AX729109 | C 352 | 14.8 | 0.3 | 18 | 1 | AX316491  | ACCESSION:AX316491 |
| C 280 | 15   | 0.4 | 18 | 1 | E32456   | ACCESSION:E32456   | C 353 | 14.8 | 0.3 | 18 | 1 | AX822988  | ACCESSION:AX822988 |
| C 281 | 14.8 | 0.3 | 18 | 1 | A28690   | ACCESSION:A28690   | C 354 | 14.8 | 0.3 | 18 | 1 | AX826628  | ACCESSION:AX826628 |
| C 282 | 14.8 | 0.3 | 18 | 1 | A28695   | ACCESSION:A28695   | C 355 | 14.8 | 0.3 | 18 | 1 | BD064848  | ACCESSION:BD064848 |
| C 283 | 14.8 | 0.3 | 18 | 1 | A36755   | ACCESSION:A36755   | C 356 | 14.8 | 0.3 | 18 | 1 | BD066574  | ACCESSION:BD066574 |
| C 284 | 14.8 | 0.3 | 18 | 1 | A40535   | ACCESSION:A40535   | C 357 | 14.8 | 0.3 | 18 | 1 | BD066580  | ACCESSION:BD066580 |
| C 285 | 14.8 | 0.3 | 18 | 1 | A40542   | ACCESSION:A40542   | C 358 | 14.8 | 0.3 | 18 | 1 | BD066586  | ACCESSION:BD066586 |
| C 286 | 14.8 | 0.3 | 18 | 1 | A40548   | ACCESSION:A40548   | C 359 | 14.8 | 0.3 | 18 | 1 | BD066597  | ACCESSION:BD066597 |
| C 287 | 14.8 | 0.3 | 18 | 1 | A40559   | ACCESSION:A40559   | C 360 | 14.8 | 0.3 | 18 | 1 | BD066615  | ACCESSION:BD066615 |
| C 288 | 14.8 | 0.3 | 18 | 1 | A40578   | ACCESSION:A40578   | C 361 | 14.8 | 0.3 | 18 | 1 | BD066628  | ACCESSION:BD066628 |
| C 289 | 14.8 | 0.3 | 18 | 1 | A40591   | ACCESSION:A40591   | C 362 | 14.8 | 0.3 | 18 | 1 | BD066632  | ACCESSION:BD066632 |
| C 290 | 14.8 | 0.3 | 18 | 1 | A40595   | ACCESSION:A40595   | C 363 | 14.8 | 0.3 | 18 | 1 | BD072881  | ACCESSION:BD072881 |
| C 291 | 14.8 | 0.3 | 18 | 1 | A89061   | ACCESSION:A89061   | C 364 | 14.8 | 0.3 | 18 | 1 | BD104178  | ACCESSION:BD104178 |
| C 292 | 14.8 | 0.3 | 18 | 1 | A89067   | ACCESSION:A89067   | C 365 | 14.8 | 0.3 | 18 | 1 | BD107508  | ACCESSION:BD107508 |
| C 293 | 14.8 | 0.3 | 18 | 1 | A89073   | ACCESSION:A89073   | C 366 | 14.8 | 0.3 | 18 | 1 | ASE250931 | ACCESSION:AJ250931 |
| C 294 | 14.8 | 0.3 | 18 | 1 | A89084   | ACCESSION:A89084   | C 367 | 14.4 | 0.3 | 16 | 1 | A40557    | ACCESSION:A40557   |
| C 295 | 14.8 | 0.3 | 18 | 1 | A89102   | ACCESSION:A89102   | C 368 | 14.4 | 0.3 | 16 | 1 | A40570    | ACCESSION:A40570   |
| C 296 | 14.8 | 0.3 | 18 | 1 | A89115   | ACCESSION:A89115   | C 369 | 14.4 | 0.3 | 16 | 1 | A88395    | ACCESSION:A88395   |
| C 297 | 14.8 | 0.3 | 18 | 1 | A89119   | ACCESSION:A89119   | C 370 | 14.4 | 0.3 | 16 | 1 | A88402    | ACCESSION:A88402   |
| C 298 | 14.8 | 0.3 | 18 | 1 | AR034902 | ACCESSION:AR034902 | C 371 | 14.4 | 0.3 | 16 | 1 | A89082    | ACCESSION:A89082   |
| C 299 | 14.8 | 0.3 | 18 | 1 | AR066298 | ACCESSION:AR066298 | C 372 | 14.4 | 0.3 | 16 | 1 | A89094    | ACCESSION:A89094   |
| C 300 | 14.8 | 0.3 | 18 | 1 | AR084526 | ACCESSION:AR084526 | C 373 | 14.4 | 0.3 | 16 | 1 | A90362    | ACCESSION:A90362   |
| C 301 | 14.8 | 0.3 | 18 | 1 | AR084527 | ACCESSION:AR084527 | C 374 | 14.4 | 0.3 | 16 | 1 | A90369    | ACCESSION:A90369   |
| C 302 | 14.8 | 0.3 | 18 | 1 | AR144877 | ACCESSION:AR144877 | C 375 | 14.4 | 0.3 | 16 | 1 | AR232837  | ACCESSION:AR232837 |
| C 303 | 14.8 | 0.3 | 18 | 1 | AR168816 | ACCESSION:AR168816 | C 376 | 14.4 | 0.3 | 16 | 1 | AR232850  | ACCESSION:AR232850 |
| C 304 | 14.8 | 0.3 | 18 | 1 | AR168817 | ACCESSION:AR168817 | C 377 | 14.4 | 0.3 | 16 | 1 | AX030132  | ACCESSION:AX030132 |
| C 305 | 14.8 | 0.3 | 18 | 1 | BD145040 | ACCESSION:BD145040 | C 378 | 14.4 | 0.3 | 16 | 1 | AX030145  | ACCESSION:AX030145 |
| C 306 | 14.8 | 0.3 | 18 | 1 | BD166040 | ACCESSION:BD166040 | C 379 | 14.4 | 0.3 | 16 | 1 | AX316453  | ACCESSION:AX316453 |
| C 307 | 14.8 | 0.3 | 18 | 1 | BD234905 | ACCESSION:BD234905 | C 380 | 14.4 | 0.3 | 16 | 1 | AX316466  | ACCESSION:AX316466 |
| C 308 | 14.8 | 0.3 | 18 | 1 | BD234909 | ACCESSION:BD234909 | C 381 | 14.4 | 0.3 | 16 | 1 | AX419943  | ACCESSION:AX419943 |
| C 309 | 14.8 | 0.3 | 18 | 1 | BD234912 | ACCESSION:BD234912 | C 382 | 14.4 | 0.3 | 16 | 1 | BD065908  | ACCESSION:BD065908 |
| C 310 | 14.8 | 0.3 | 18 | 1 | BD234912 | ACCESSION:BD234912 | C 383 | 14.4 | 0.3 | 16 | 1 | BD065915  | ACCESSION:BD065915 |
| C 311 | 14.8 | 0.3 | 18 | 1 | CQ080832 | ACCESSION:CQ080832 | C 384 | 14.4 | 0.3 | 16 | 1 | BD066595  | ACCESSION:BD066595 |
| C 312 | 14.8 | 0.3 | 18 | 1 | E32455   | ACCESSION:E32455   | C 385 | 14.4 | 0.3 | 16 | 1 | BD066607  | ACCESSION:BD066607 |
| C 313 | 14.8 | 0.3 | 18 | 1 | E32458   | ACCESSION:E32458   | C 386 | 14.4 | 0.3 | 17 | 1 | AR029903  | ACCESSION:AR029903 |
| C 314 | 14.8 | 0.3 | 18 | 1 | I27810   | ACCESSION:I27810   | C 387 | 14.4 | 0.3 | 17 | 1 | AR029906  | ACCESSION:AR029906 |
| C 315 | 14.8 | 0.3 | 18 | 1 | I27811   | ACCESSION:I27811   | C 388 | 14.4 | 0.3 | 17 | 1 | AR047360  | ACCESSION:AR047360 |
| C 316 | 14.8 | 0.3 | 18 | 1 | I33107   | ACCESSION:I33107   | C 389 | 14.4 | 0.3 | 17 | 1 | AR047366  | ACCESSION:AR047366 |
| C 317 | 14.8 | 0.3 | 18 | 1 | AR200285 | ACCESSION:AR200285 | C 390 | 14.4 | 0.3 | 17 | 1 | AR047368  | ACCESSION:AR047368 |
| C 318 | 14.8 | 0.3 | 18 | 1 | AR200286 | ACCESSION:AR200286 | C 391 | 14.4 | 0.3 | 17 | 1 | BD255269  | ACCESSION:BD255269 |
| C 319 | 14.8 | 0.3 | 18 | 1 | AR232815 | ACCESSION:AR232815 | C 392 | 14.4 | 0.3 | 17 | 1 | BD255585  | ACCESSION:BD255585 |
| C 320 | 14.8 | 0.3 | 18 | 1 | AR232822 | ACCESSION:AR232822 | C 393 | 14.4 | 0.3 | 17 | 1 | BD257465  | ACCESSION:BD257465 |
| C 321 | 14.8 | 0.3 | 18 | 1 | AR232828 | ACCESSION:AR232828 | C 394 | 14.4 | 0.3 | 17 | 1 | BD258537  | ACCESSION:BD258537 |
| C 322 | 14.8 | 0.3 | 18 | 1 | AR232839 | ACCESSION:AR232839 | C 395 | 14.4 | 0.3 | 17 | 1 | BD258538  | ACCESSION:BD258538 |
| C 323 | 14.8 | 0.3 | 18 | 1 | AR232856 | ACCESSION:AR232856 | C 396 | 14.4 | 0.3 | 17 | 1 | I27983    | ACCESSION:I27983   |
| C 324 | 14.8 | 0.3 | 18 | 1 | AR232871 | ACCESSION:AR232871 | C 397 | 14.4 | 0.3 | 17 | 1 | I37565    | ACCESSION:I37565   |
| C 325 | 14.8 | 0.3 | 18 | 1 | AR232875 | ACCESSION:AR232875 | C 398 | 14.4 | 0.3 | 17 | 1 | I37568    | ACCESSION:I37568   |



|       |      |     |    |   |           |                    |       |      |     |    |   |          |                    |
|-------|------|-----|----|---|-----------|--------------------|-------|------|-----|----|---|----------|--------------------|
| C 107 | 16.8 | 0.4 | 20 | 1 | AR364958  | ACCESSION:AR264958 | C 180 | 16   | 0.4 | 16 | 1 | AX316464 | ACCESSION:AX316464 |
| C 108 | 16.8 | 0.4 | 20 | 1 | AR360398  | ACCESSION:AR360398 | C 181 | 16   | 0.4 | 16 | 1 | AX316472 | ACCESSION:AX316472 |
| C 109 | 16.8 | 0.4 | 20 | 1 | AR360399  | ACCESSION:AR360399 | C 182 | 16   | 0.4 | 16 | 1 | BD065911 | ACCESSION:BD065911 |
| C 110 | 16.8 | 0.4 | 20 | 1 | AR360425  | ACCESSION:AR360425 | C 183 | 16   | 0.4 | 16 | 1 | BD066606 | ACCESSION:BD066606 |
| C 111 | 16.8 | 0.4 | 20 | 1 | AR360426  | ACCESSION:AR360426 | C 184 | 16   | 0.4 | 16 | 1 | BD066613 | ACCESSION:BD066613 |
| C 112 | 16.8 | 0.4 | 20 | 1 | AR363652  | ACCESSION:AR363652 | C 185 | 16   | 0.4 | 17 | 1 | BD234956 | ACCESSION:BD234956 |
| C 113 | 16.8 | 0.4 | 20 | 1 | AR378239  | ACCESSION:AR478239 | C 186 | 16   | 0.4 | 17 | 1 | AR337667 | ACCESSION:AR337667 |
| C 114 | 16.8 | 0.4 | 20 | 1 | AX008975  | ACCESSION:AX008975 | C 187 | 16   | 0.4 | 17 | 1 | AX009027 | ACCESSION:AX009027 |
| C 115 | 16.8 | 0.4 | 20 | 1 | AX030137  | ACCESSION:AX030137 | C 188 | 16   | 0.4 | 17 | 1 | BD131940 | ACCESSION:BD131940 |
| C 116 | 16.8 | 0.4 | 20 | 1 | AX104328  | ACCESSION:AX104328 | C 189 | 16   | 0.4 | 18 | 1 | I73187   | ACCESSION:I73187   |
| C 117 | 16.8 | 0.4 | 20 | 1 | AX104328  | ACCESSION:AX104328 | C 190 | 16   | 0.4 | 19 | 1 | BD137911 | ACCESSION:BD137911 |
| C 118 | 16.8 | 0.4 | 20 | 1 | AX104577  | ACCESSION:AX104577 | C 191 | 16   | 0.4 | 19 | 1 | AR200636 | ACCESSION:AR200636 |
| C 119 | 16.8 | 0.4 | 20 | 1 | AX104577  | ACCESSION:AX104577 | C 192 | 16   | 0.4 | 20 | 1 | AR116591 | ACCESSION:AR116591 |
| C 120 | 16.8 | 0.4 | 20 | 1 | AX316458  | ACCESSION:AX316458 | C 193 | 16   | 0.4 | 20 | 1 | AR275849 | ACCESSION:AR275849 |
| C 121 | 16.8 | 0.4 | 20 | 1 | AX355164  | ACCESSION:AX355164 | C 194 | 16   | 0.4 | 20 | 1 | AX048440 | ACCESSION:AX048440 |
| C 122 | 16.8 | 0.4 | 20 | 1 | AX355164  | ACCESSION:AX355164 | C 195 | 16   | 0.4 | 20 | 1 | AX048441 | ACCESSION:AX048441 |
| C 123 | 16.8 | 0.4 | 20 | 1 | AX355165  | ACCESSION:AX355165 | C 196 | 16   | 0.4 | 20 | 1 | AX048442 | ACCESSION:AX048442 |
| C 124 | 16.8 | 0.4 | 20 | 1 | AX355165  | ACCESSION:AX355165 | C 197 | 16   | 0.4 | 20 | 1 | AX048443 | ACCESSION:AX048443 |
| C 125 | 16.8 | 0.4 | 20 | 1 | AX441509  | ACCESSION:AX441509 | C 198 | 16   | 0.4 | 24 | 1 | AR058881 | ACCESSION:AR058881 |
| C 126 | 16.8 | 0.4 | 20 | 1 | AX441510  | ACCESSION:AX441510 | C 199 | 16   | 0.4 | 24 | 1 | AR079586 | ACCESSION:AR079586 |
| C 127 | 16.8 | 0.4 | 20 | 1 | AX547381  | ACCESSION:AX547381 | C 200 | 16   | 0.4 | 24 | 1 | AR123295 | ACCESSION:AR123295 |
| C 128 | 16.8 | 0.4 | 20 | 1 | AX547381  | ACCESSION:AX547381 | C 201 | 16   | 0.4 | 24 | 1 | BD175807 | ACCESSION:BD175807 |
| C 129 | 16.8 | 0.4 | 20 | 1 | AX547630  | ACCESSION:AX547630 | C 202 | 16   | 0.4 | 24 | 1 | BD188897 | ACCESSION:BD188897 |
| C 130 | 16.8 | 0.4 | 20 | 1 | AX547630  | ACCESSION:AX547630 | C 203 | 16   | 0.4 | 24 | 1 | I33258   | ACCESSION:I33258   |
| C 131 | 16.8 | 0.4 | 20 | 1 | BD065894  | ACCESSION:BD065894 | C 204 | 16   | 0.4 | 24 | 1 | I35523   | ACCESSION:I35523   |
| C 132 | 16.8 | 0.4 | 20 | 1 | BD066600  | ACCESSION:BD066600 | C 205 | 16   | 0.4 | 24 | 1 | I43133   | ACCESSION:I43133   |
| C 133 | 16.8 | 0.4 | 20 | 1 | BD069970  | ACCESSION:BD069970 | C 206 | 16   | 0.4 | 24 | 1 | I92011   | ACCESSION:I92011   |
| C 134 | 16.8 | 0.4 | 20 | 1 | BD069970  | ACCESSION:BD069970 | C 207 | 15.8 | 0.4 | 19 | 1 | A05202   | ACCESSION:A05202   |
| C 135 | 16.8 | 0.4 | 21 | 1 | E08187    | ACCESSION:E08187   | C 208 | 15.8 | 0.4 | 19 | 1 | A88380   | ACCESSION:A88380   |
| C 136 | 16.8 | 0.4 | 21 | 1 | ATH523738 | ACCESSION:AJ523738 | C 209 | 15.8 | 0.4 | 19 | 1 | A88400   | ACCESSION:A88400   |
| C 137 | 16.6 | 0.4 | 24 | 1 | AR306126  | ACCESSION:AR306126 | C 210 | 15.8 | 0.4 | 19 | 1 | A90347   | ACCESSION:A90347   |
| C 138 | 16.4 | 0.4 | 18 | 1 | A40539    | ACCESSION:A40539   | C 211 | 15.8 | 0.4 | 19 | 1 | A90367   | ACCESSION:A90367   |
| C 139 | 16.4 | 0.4 | 18 | 1 | A40596    | ACCESSION:A40596   | C 212 | 15.8 | 0.4 | 19 | 1 | BD234903 | ACCESSION:BD234903 |
| C 140 | 16.4 | 0.4 | 18 | 1 | A89064    | ACCESSION:A89064   | C 213 | 15.8 | 0.4 | 19 | 1 | AX008974 | ACCESSION:AX008974 |
| C 141 | 16.4 | 0.4 | 18 | 1 | A89120    | ACCESSION:A89120   | C 214 | 15.8 | 0.4 | 19 | 1 | AX103946 | ACCESSION:AX103946 |
| C 142 | 16.4 | 0.4 | 18 | 1 | BD234908  | ACCESSION:BD234908 | C 215 | 15.8 | 0.4 | 19 | 1 | AX103946 | ACCESSION:AX103946 |
| C 143 | 16.4 | 0.4 | 18 | 1 | BD234922  | ACCESSION:BD234922 | C 216 | 15.8 | 0.4 | 19 | 1 | AX132849 | ACCESSION:AX132849 |
| C 144 | 16.4 | 0.4 | 18 | 1 | BD234966  | ACCESSION:BD234966 | C 217 | 15.8 | 0.4 | 19 | 1 | AX355314 | ACCESSION:AX355314 |
| C 145 | 16.4 | 0.4 | 18 | 1 | AR232819  | ACCESSION:AR232819 | C 218 | 15.8 | 0.4 | 19 | 1 | AX355314 | ACCESSION:AX355314 |
| C 146 | 16.4 | 0.4 | 18 | 1 | AR232876  | ACCESSION:AR232876 | C 219 | 15.8 | 0.4 | 19 | 1 | AX546999 | ACCESSION:AX546999 |
| C 147 | 16.4 | 0.4 | 18 | 1 | AX008979  | ACCESSION:AX008979 | C 220 | 15.8 | 0.4 | 19 | 1 | AX546999 | ACCESSION:AX546999 |
| C 148 | 16.4 | 0.4 | 18 | 1 | AX008993  | ACCESSION:AX008993 | C 221 | 15.8 | 0.4 | 19 | 1 | AX785856 | ACCESSION:AX785856 |
| C 149 | 16.4 | 0.4 | 18 | 1 | AX009037  | ACCESSION:AX009037 | C 222 | 15.8 | 0.4 | 19 | 1 | BD065893 | ACCESSION:BD065893 |
| C 150 | 16.4 | 0.4 | 18 | 1 | AX030114  | ACCESSION:AX030114 | C 223 | 15.8 | 0.4 | 19 | 1 | BD065913 | ACCESSION:BD065913 |
| C 151 | 16.4 | 0.4 | 18 | 1 | AX030171  | ACCESSION:AX030171 | C 224 | 15.6 | 0.4 | 22 | 1 | AR409919 | ACCESSION:AR409919 |
| C 152 | 16.4 | 0.4 | 18 | 1 | AX316435  | ACCESSION:AX316435 | C 225 | 15.6 | 0.4 | 22 | 1 | AX404674 | ACCESSION:AX404674 |
| C 153 | 16.4 | 0.4 | 18 | 1 | AX316492  | ACCESSION:AX316492 | C 226 | 15.4 | 0.4 | 17 | 1 | AR047362 | ACCESSION:AR047362 |
| C 154 | 16.4 | 0.4 | 18 | 1 | BD066577  | ACCESSION:BD066577 | C 227 | 15.4 | 0.4 | 17 | 1 | AR047364 | ACCESSION:AR047364 |
| C 155 | 16.4 | 0.4 | 18 | 1 | BD066633  | ACCESSION:BD066633 | C 228 | 15.4 | 0.4 | 17 | 1 | BD234968 | ACCESSION:BD234968 |
| C 156 | 16.4 | 0.4 | 19 | 1 | CQ808226  | ACCESSION:CQ808226 | C 229 | 15.4 | 0.4 | 17 | 1 | I37566   | ACCESSION:I37566   |
| C 157 | 16.4 | 0.4 | 19 | 1 | AX132309  | ACCESSION:AX132309 | C 230 | 15.4 | 0.4 | 17 | 1 | I37567   | ACCESSION:I37567   |
| C 158 | 16.4 | 0.4 | 19 | 1 | AX132310  | ACCESSION:AX132310 | C 231 | 15.4 | 0.4 | 17 | 1 | I54414   | ACCESSION:I54414   |
| C 159 | 16.4 | 0.4 | 20 | 1 | AR207116  | ACCESSION:AR207116 | C 232 | 15.4 | 0.4 | 17 | 1 | I54416   | ACCESSION:I54416   |
| C 160 | 16.4 | 0.4 | 20 | 1 | AR312091  | ACCESSION:AR312091 | C 233 | 15.4 | 0.4 | 17 | 1 | I94416   | ACCESSION:I94416   |
| C 161 | 16.4 | 0.4 | 20 | 1 | AX613450  | ACCESSION:AX613450 | C 234 | 15.4 | 0.4 | 17 | 1 | I94417   | ACCESSION:I94417   |
| C 162 | 16   | 0.4 | 16 | 1 | A40568    | ACCESSION:A40568   | C 235 | 15.4 | 0.4 | 17 | 1 | AX009039 | ACCESSION:AX009039 |
| C 163 | 16   | 0.4 | 16 | 1 | A40576    | ACCESSION:A40576   | C 236 | 15.4 | 0.4 | 17 | 1 | AX736539 | ACCESSION:AX736539 |
| C 164 | 16   | 0.4 | 16 | 1 | A88398    | ACCESSION:A88398   | C 237 | 15.4 | 0.4 | 18 | 1 | A40575   | ACCESSION:A40575   |
| C 165 | 16   | 0.4 | 16 | 1 | A89093    | ACCESSION:A89093   | C 238 | 15.4 | 0.4 | 18 | 1 | A89099   | ACCESSION:A89099   |
| C 166 | 16   | 0.4 | 16 | 1 | A89100    | ACCESSION:A89100   | C 239 | 15.4 | 0.4 | 18 | 1 | BD145038 | ACCESSION:BD145038 |
| C 167 | 16   | 0.4 | 16 | 1 | A90365    | ACCESSION:A90365   | C 240 | 15.4 | 0.4 | 18 | 1 | BD166038 | ACCESSION:BD166038 |
| C 168 | 16   | 0.4 | 16 | 1 | BD234914  | ACCESSION:BD234914 | C 241 | 15.4 | 0.4 | 18 | 1 | AR232855 | ACCESSION:AR232855 |
| C 169 | 16   | 0.4 | 16 | 1 | BD234916  | ACCESSION:BD234916 | C 242 | 15.4 | 0.4 | 18 | 1 | AR237465 | ACCESSION:AR237465 |
| C 170 | 16   | 0.4 | 16 | 1 | BD234917  | ACCESSION:BD234917 | C 243 | 15.4 | 0.4 | 18 | 1 | AR237467 | ACCESSION:AR237467 |
| C 171 | 16   | 0.4 | 16 | 1 | AR232848  | ACCESSION:AR232848 | C 244 | 15.4 | 0.4 | 18 | 1 | AR264934 | ACCESSION:AR264934 |
| C 172 | 16   | 0.4 | 16 | 1 | AR232856  | ACCESSION:AR232856 | C 245 | 15.4 | 0.4 | 18 | 1 | AR478215 | ACCESSION:AR478215 |
| C 173 | 16   | 0.4 | 16 | 1 | AR367887  | ACCESSION:AR367887 | C 246 | 15.4 | 0.4 | 18 | 1 | AX030150 | ACCESSION:AX030150 |
| C 174 | 16   | 0.4 | 16 | 1 | AR367888  | ACCESSION:AR367888 | C 247 | 15.4 | 0.4 | 18 | 1 | AX316471 | ACCESSION:AX316471 |
| C 175 | 16   | 0.4 | 16 | 1 | AX008985  | ACCESSION:AX008985 | C 248 | 15.4 | 0.4 | 18 | 1 | AX599662 | ACCESSION:AX599662 |
| C 176 | 16   | 0.4 | 16 | 1 | AX008987  | ACCESSION:AX008987 | C 249 | 15.4 | 0.4 | 18 | 1 | BD066612 | ACCESSION:BD066612 |
| C 177 | 16   | 0.4 | 16 | 1 | AX008988  | ACCESSION:AX008988 | C 250 | 15.4 | 0.4 | 18 | 1 | BD072879 | ACCESSION:BD072879 |
| C 178 | 16   | 0.4 | 16 | 1 | AX030143  | ACCESSION:AX030143 | C 251 | 15.4 | 0.4 | 18 | 1 | BD107506 | ACCESSION:BD107506 |
| C 179 | 16   | 0.4 | 16 | 1 | AX030151  | ACCESSION:AX030151 | C 252 | 15.4 | 0.4 | 19 | 1 | AR167910 | ACCESSION:AR167910 |

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 25, 2005, 09:41:44 ; Search time 32 Seconds  
(without alignments)  
3.676 Million cell updates/sec

Title: US-10-633-163-47

Perfect score: 4267

Sequence: 1 ggtatctgtgcagcagg.....tgcagggtgattaaaaaa 4267

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 790 seqs, 13783 residues

Total number of hits satisfying chosen parameters: 1580

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 832 summaries

Database : fetchrge47.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description        |
|------------|-------|---------------|--------|----|--------------------|
| 1          | 35.8  | 0.8           | 39     | 1  | ACCESSION:A18285   |
| 2          | 35.8  | 0.8           | 39     | 1  | ACCESSION:I56859   |
| C 3        | 34.2  | 0.8           | 39     | 1  | ACCESSION:A18286   |
| C 4        | 34.2  | 0.8           | 39     | 1  | ACCESSION:I56860   |
| 5          | 33    | 0.8           | 33     | 1  | ACCESSION:AR409916 |
| 6          | 25    | 0.6           | 25     | 1  | ACCESSION:AR409918 |
| 7          | 23    | 0.5           | 23     | 1  | ACCESSION:CQ778289 |
| 8          | 22.8  | 0.5           | 26     | 1  | ACCESSION:A23924   |
| C 9        | 22.8  | 0.5           | 26     | 1  | ACCESSION:A23925   |
| C 10       | 22.2  | 0.5           | 27     | 1  | ACCESSION:AX113805 |
| C 11       | 22    | 0.5           | 22     | 1  | ACCESSION:CQ778291 |
| 12         | 22    | 0.5           | 22     | 1  | ACCESSION:AR409919 |
| 13         | 21.8  | 0.5           | 25     | 1  | ACCESSION:CQ778188 |
| 14         | 21.4  | 0.5           | 24     | 1  | ACCESSION:AX113804 |
| C 15       | 20.2  | 0.5           | 25     | 1  | ACCESSION:AX043186 |
| 16         | 20    | 0.5           | 20     | 1  | ACCESSION:AR367879 |
| C 17       | 19.4  | 0.5           | 21     | 1  | ACCESSION:A23914   |
| C 18       | 19.4  | 0.5           | 21     | 1  | ACCESSION:A23915   |
| 19         | 19.2  | 0.4           | 24     | 1  | ACCESSION:AR058881 |
| 20         | 19.2  | 0.4           | 24     | 1  | ACCESSION:AR079586 |
| 21         | 19.2  | 0.4           | 24     | 1  | ACCESSION:AR123295 |
| 22         | 19.2  | 0.4           | 24     | 1  | BD138045           |
| 23         | 19.2  | 0.4           | 24     | 1  | BD175807           |
| 24         | 19.2  | 0.4           | 24     | 1  | BD188897           |
| 25         | 19.2  | 0.4           | 24     | 1  | BD237693           |
| 26         | 19.2  | 0.4           | 24     | 1  | I33258             |
| 27         | 19.2  | 0.4           | 24     | 1  | I35523             |
| 28         | 19.2  | 0.4           | 24     | 1  | I43133             |
| 29         | 19.2  | 0.4           | 24     | 1  | I92011             |
| 30         | 19.2  | 0.4           | 24     | 1  | ACCESSION:AR306126 |
| 31         | 19.2  | 0.4           | 24     | 1  | AR473409           |
| 32         | 19.2  | 0.4           | 24     | 1  | ACCESSION:AX278211 |
| C 33       | 19    | 0.4           | 19     | 1  | ACCESSION:A88397   |

|       |      |     |    |   |          |
|-------|------|-----|----|---|----------|
| C 34  | 19   | 0.4 | 19 | 1 | A90364   |
| C 35  | 19   | 0.4 | 19 | 1 | BD234915 |
| C 36  | 19   | 0.4 | 19 | 1 | AX008986 |
| C 37  | 19   | 0.4 | 19 | 1 | BD065910 |
| C 38  | 18.8 | 0.4 | 22 | 1 | AR019469 |
| C 39  | 18.8 | 0.4 | 22 | 1 | AR019469 |
| 40    | 18.8 | 0.4 | 22 | 1 | AR038951 |
| 41    | 18.8 | 0.4 | 22 | 1 | AR091306 |
| 42    | 18.8 | 0.4 | 22 | 1 | AR123404 |
| 43    | 18.8 | 0.4 | 22 | 1 | AR137687 |
| 44    | 18.8 | 0.4 | 22 | 1 | AR564998 |
| 45    | 18.8 | 0.4 | 22 | 1 | AX030592 |
| C 46  | 18.8 | 0.4 | 22 | 1 | AX030592 |
| C 47  | 18.4 | 0.4 | 20 | 1 | A88388   |
| C 48  | 18.4 | 0.4 | 20 | 1 | A90355   |
| 49    | 18.4 | 0.4 | 20 | 1 | AR360400 |
| 50    | 18.4 | 0.4 | 20 | 1 | AR360427 |
| 51    | 18.4 | 0.4 | 20 | 1 | AX441511 |
| C 52  | 18.4 | 0.4 | 20 | 1 | BD065901 |
| C 53  | 18.4 | 0.4 | 23 | 1 | A87861   |
| C 54  | 18.4 | 0.4 | 23 | 1 | A89828   |
| C 55  | 18.4 | 0.4 | 23 | 1 | BD065374 |
| C 56  | 18   | 0.4 | 18 | 1 | A40530   |
| C 57  | 18   | 0.4 | 18 | 1 | A40567   |
| C 58  | 18   | 0.4 | 18 | 1 | A88394   |
| C 59  | 18   | 0.4 | 18 | 1 | A89056   |
| C 60  | 18   | 0.4 | 18 | 1 | A89092   |
| C 61  | 18   | 0.4 | 18 | 1 | A90361   |
| C 62  | 18   | 0.4 | 18 | 1 | BD234913 |
| C 63  | 18   | 0.4 | 18 | 1 | AR232810 |
| C 64  | 18   | 0.4 | 18 | 1 | AR232847 |
| C 65  | 18   | 0.4 | 18 | 1 | AR367880 |
| C 66  | 18   | 0.4 | 18 | 1 | AX008984 |
| C 67  | 18   | 0.4 | 18 | 1 | AX030105 |
| C 68  | 18   | 0.4 | 18 | 1 | AX030142 |
| C 69  | 18   | 0.4 | 18 | 1 | AX316426 |
| C 70  | 18   | 0.4 | 18 | 1 | AX316463 |
| C 71  | 18   | 0.4 | 18 | 1 | BD065907 |
| C 72  | 18   | 0.4 | 18 | 1 | BD066569 |
| C 73  | 18   | 0.4 | 18 | 1 | BD066605 |
| 74    | 17.8 | 0.4 | 22 | 1 | AX404674 |
| 75    | 17.4 | 0.4 | 19 | 1 | A88386   |
| C 76  | 17.4 | 0.4 | 19 | 1 | A88407   |
| C 77  | 17.4 | 0.4 | 19 | 1 | A90353   |
| C 78  | 17.4 | 0.4 | 19 | 1 | A90374   |
| C 79  | 17.4 | 0.4 | 19 | 1 | BD065899 |
| C 80  | 17.4 | 0.4 | 19 | 1 | BD065920 |
| C 81  | 17.4 | 0.4 | 21 | 1 | AR103576 |
| C 82  | 17.4 | 0.4 | 21 | 1 | AR530745 |
| C 83  | 17.4 | 0.4 | 21 | 1 | AX096770 |
| 84    | 17.4 | 0.4 | 21 | 1 | BD129806 |
| C 85  | 17   | 0.4 | 17 | 1 | A88374   |
| C 86  | 17   | 0.4 | 17 | 1 | A90341   |
| C 87  | 17   | 0.4 | 17 | 1 | BD234899 |
| C 88  | 17   | 0.4 | 17 | 1 | BD234964 |
| C 89  | 17   | 0.4 | 17 | 1 | CQ778290 |
| C 90  | 17   | 0.4 | 17 | 1 | AX008970 |
| C 91  | 17   | 0.4 | 17 | 1 | AX009035 |
| C 92  | 17   | 0.4 | 17 | 1 | BD065887 |
| C 93  | 17   | 0.4 | 20 | 1 | AR488890 |
| C 94  | 16.8 | 0.4 | 20 | 1 | A40562   |
| C 95  | 16.8 | 0.4 | 20 | 1 | A88381   |
| C 96  | 16.8 | 0.4 | 20 | 1 | A90807   |
| C 97  | 16.8 | 0.4 | 20 | 1 | A90348   |
| 98    | 16.8 | 0.4 | 20 | 1 | AR30495  |
| 99    | 16.8 | 0.4 | 20 | 1 | AR084562 |
| C 100 | 16.8 | 0.4 | 20 | 1 | AR084562 |
| C 101 | 16.8 | 0.4 | 20 | 1 | BD234904 |
| 102   | 16.8 | 0.4 | 20 | 1 | AR182850 |
| C 103 | 16.8 | 0.4 | 20 | 1 | AR182850 |
| 104   | 16.8 | 0.4 | 20 | 1 | AR182904 |
| C 105 | 16.8 | 0.4 | 20 | 1 | AR182904 |
| C 106 | 16.8 | 0.4 | 20 | 1 | AR232842 |

|                    |
|--------------------|
| ACCESSION:A90364   |
| ACCESSION:BD234915 |
| ACCESSION:AX008986 |
| ACCESSION:BD065910 |
| ACCESSION:AR019469 |
| ACCESSION:AR019469 |
| ACCESSION:AR038951 |
| ACCESSION:AR091306 |
| ACCESSION:AR123404 |
| ACCESSION:AR137687 |
| ACCESSION:AR564998 |
| ACCESSION:AX030592 |
| ACCESSION:AX030592 |
| ACCESSION:A88388   |
| ACCESSION:A90355   |
| ACCESSION:AR360400 |
| ACCESSION:AR360427 |
| ACCESSION:AX441511 |
| ACCESSION:BD065901 |
| ACCESSION:A87861   |
| ACCESSION:A89828   |
| ACCESSION:BD065374 |
| ACCESSION:A40530   |
| ACCESSION:A40567   |
| ACCESSION:A88394   |
| ACCESSION:A89056   |
| ACCESSION:A89092   |
| ACCESSION:A90361   |
| ACCESSION:BD234913 |
| ACCESSION:AR232810 |
| ACCESSION:AR232847 |
| ACCESSION:AR367880 |
| ACCESSION:AX008984 |
| ACCESSION:AX030105 |
| ACCESSION:AX030142 |
| ACCESSION:AX316426 |
| ACCESSION:AX316463 |
| ACCESSION:BD065907 |
| ACCESSION:BD066569 |
| ACCESSION:BD066605 |
| ACCESSION:AX404674 |
| ACCESSION:A88386   |
| ACCESSION:A88407   |
| ACCESSION:A90353   |
| ACCESSION:A90374   |
| ACCESSION:BD065899 |
| ACCESSION:BD065920 |
| ACCESSION:AR103576 |
| ACCESSION:AR530745 |
| ACCESSION:AX096770 |
| ACCESSION:BD129806 |
| ACCESSION:A88374   |
| ACCESSION:A90341   |
| ACCESSION:BD234899 |
| ACCESSION:BD234964 |
| ACCESSION:CQ778290 |
| ACCESSION:AX008970 |
| ACCESSION:AX009035 |
| ACCESSION:BD065887 |
| ACCESSION:AR488890 |
| ACCESSION:A40562   |
| ACCESSION:A88381   |
| ACCESSION:A90807   |
| ACCESSION:A90348   |
| ACCESSION:AR030495 |
| ACCESSION:AR084562 |
| ACCESSION:BD234904 |
| ACCESSION:AR182850 |
| ACCESSION:AR182850 |
| ACCESSION:AR182904 |
| ACCESSION:AR182904 |
| ACCESSION:AR232842 |

Db 14 CCCACTTTCTACAG 1

RESULT 483  
A40554/c  
LOCUS 14 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 91 from Patent WO9425578.  
ACCESSION A40554  
VERSION A40554.1 GI:2296589  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE  
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))  
BIOGNOSTIK GES (DE)  
PATENT: WO 9425578-A 91 10-NOV-1994;  
FEATURES Location/Qualifiers  
source 1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1807 AATGGCTCTCCTTC 1820  
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Db 14 AATGGCTCTCCTTC 1

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 484  
A40564/c  
LOCUS 14 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 101 from Patent WO9425578.  
ACCESSION A40564  
VERSION A40564.1 GI:2296599  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE  
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))  
BIOGNOSTIK GES (DE)  
PATENT: WO 9425578-A 101 10-NOV-1994;  
FEATURES Location/Qualifiers  
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/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1971 GGTATTGATGGCAC 1984  
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Db 14 GGTATTGATGGCAC 1

RESULT 485  
A40566/c  
LOCUS 14 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 103 from Patent WO9425578.  
ACCESSION A40566  
VERSION A40566.1 GI:2296601  
KEYWORDS  
SOURCE unidentified

ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE  
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))  
BIOGNOSTIK GES (DE)  
PATENT: WO 9425578-A 103 10-NOV-1994;  
FEATURES Location/Qualifiers  
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/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1997 CAGTGGTGATCAGA 2010  
|||||  
Db 14 CAGTGGTGATCAGA 1

RESULT 486  
A40569/c  
LOCUS 14 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 106 from Patent WO9425578.  
ACCESSION A40569  
VERSION A40569.1 GI:2296604  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE  
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))  
BIOGNOSTIK GES (DE)  
PATENT: WO 9425578-A 106 10-NOV-1994;  
FEATURES Location/Qualifiers  
source 1..14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2046 AAGACCCCATCTCT 2059  
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Db 14 AAGACCCCATCTCT 1

RESULT 487  
A40585/c  
LOCUS 14 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 122 from Patent WO9425578.  
ACCESSION A40585  
VERSION A40585.1 GI:2296620  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS  
TITLE ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE  
JOURNAL EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))  
BIOGNOSTIK GES (DE)  
PATENT: WO 9425578-A 122 10-NOV-1994;  
FEATURES Location/Qualifiers  
source 1..14  
/organism="unidentified"

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RESULT 490
A88399/c
LOCUS           A88399           14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 547 from Patent WO9833904.
ACCESSION       A88399
VERSION         A88399.1  GI:6736969
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 547 06-AUG-1998;
               BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES       Location/Qualifiers
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               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
               Query Match          0.3%; Score 14; DB 1; Length 14;
               Best Local Similarity 100.0%; Pred. No. 2.4e+02;
               Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2159  GGATAATTGCTGCC 2172
Db      14  GGATAATTGCTGCC 1

RESULT 491
A88439/c
LOCUS           A88439           14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 587 from Patent WO9833904.
ACCESSION       A88439
VERSION         A88439.1  GI:6737009
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 587 06-AUG-1998;
               BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES       Location/Qualifiers
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               /db_xref="taxon:32644"
               Query Match          0.3%; Score 14; DB 1; Length 14;
               Best Local Similarity 100.0%; Pred. No. 2.4e+02;
               Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1919  TAATAATTACATCA 1932
Db      14  TAATAATTACATCA 1

RESULT 492
A89047/c
LOCUS           A89047           14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 1195 from Patent WO9833904.
ACCESSION       A89047
VERSION         A89047.1  GI:6737617
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match          0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1222  ACTACTGTGTGCTG 1235
Db      14  ACTACTGTGTGCTG 1

RESULT 489
A88371/c
LOCUS           A88371           14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 519 from Patent WO9833904.
ACCESSION       A88371
VERSION         A88371.1  GI:6736941
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 519 06-AUG-1998;
               BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES       Location/Qualifiers
               source
               1..14
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
               Query Match          0.3%; Score 14; DB 1; Length 14;
               Best Local Similarity 100.0%; Pred. No. 2.4e+02;
               Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1220  GCACACTGTGTGC 1233
Db      14  GCACACTGTGTGC 1
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RESULT 490
A88399/c
LOCUS           A88399           14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 547 from Patent WO9833904.
ACCESSION       A88399
VERSION         A88399.1  GI:6736969
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 547 06-AUG-1998;
               BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES       Location/Qualifiers
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               /db_xref="taxon:32644"
               Query Match          0.3%; Score 14; DB 1; Length 14;
               Best Local Similarity 100.0%; Pred. No. 2.4e+02;
               Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2159  GGATAATTGCTGCC 2172
Db      14  GGATAATTGCTGCC 1

RESULT 491
A88439/c
LOCUS           A88439           14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 587 from Patent WO9833904.
ACCESSION       A88439
VERSION         A88439.1  GI:6737009
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 587 06-AUG-1998;
               BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES       Location/Qualifiers
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
               Query Match          0.3%; Score 14; DB 1; Length 14;
               Best Local Similarity 100.0%; Pred. No. 2.4e+02;
               Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1919  TAATAATTACATCA 1932
Db      14  TAATAATTACATCA 1

RESULT 492
A89047/c
LOCUS           A89047           14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 1195 from Patent WO9833904.
ACCESSION       A89047
VERSION         A89047.1  GI:6737617
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match          0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1222  ACTACTGTGTGCTG 1235
Db      14  ACTACTGTGTGCTG 1

RESULT 489
A88371/c
LOCUS           A88371           14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION      Sequence 519 from Patent WO9833904.
ACCESSION       A88371
VERSION         A88371.1  GI:6736941
KEYWORDS        .
SOURCE          unidentified
ORGANISM        unclassified.
REFERENCE       1 (bases 1 to 14)
AUTHORS        Brysch,W. and Schlingensiepen,K.
TITLE          AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL        Patent: WO 9833904-A 519 06-AUG-1998;
               BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES       Location/Qualifiers
               source
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               Query Match          0.3%; Score 14; DB 1; Length 14;
               Best Local Similarity 100.0%; Pred. No. 2.4e+02;
               Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1220  GCACACTGTGTGC 1233
Db      14  GCACACTGTGTGC 1
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JOURNAL Patent: WO 9833904-A 1195 06-AUG-1998;  
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES  
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Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACCTACTGTGTG 1232  
|||||  
Db 14 TGCACCTACTGTGTG 1

RESULT 493  
A89053/c  
LOCUS 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1201 from Patent WO9833904.  
ACCESSION A89053  
VERSION A89053.1 GI:6737623  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch, W. and Schlingensiepen, K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1201 06-AUG-1998;  
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES  
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/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAA 1357  
|||||  
Db 14 CAGATCCTGAGCAA 1

RESULT 494  
A89060/c  
LOCUS 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1208 from Patent WO9833904.  
ACCESSION A89060  
VERSION A89060.1 GI:6737630  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch, W. and Schlingensiepen, K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1208 06-AUG-1998;  
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES  
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/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAG 1520  
|||||  
Db 14 AGTACTACGCCAAG 1

RESULT 495  
A89062/c  
LOCUS 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1210 from Patent WO9833904.  
ACCESSION A89062  
VERSION A89062.1 GI:6737632  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch, W. and Schlingensiepen, K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1210 06-AUG-1998;  
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES  
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/organism="unidentified"  
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/db\_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 AAAATGCCATCCCG 1574  
|||||  
Db 14 AAAATGCCATCCCG 1

RESULT 496  
A89063/c  
LOCUS 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1211 from Patent WO9833904.  
ACCESSION A89063  
VERSION A89063.1 GI:6737633  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Brysch, W. and Schlingensiepen, K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 1211 06-AUG-1998;  
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES  
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/db\_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCCACTTTCTACAG 1588  
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Db 14 CCCACTTTCTACAG 1

RESULT 497  
A89079/c  
LOCUS 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1227 from Patent WO9833904.  
ACCESSION A89079  
VERSION A89079.1 GI:6737649  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

[illegible]

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VERSION A90338.1 GI:6738852
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 519 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GCACTACTGTGTC 1233
Db 14 GCACTACTGTGTC 1

RESULT 503
A90366/c
LOCUS A90366 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 547 from Patent EP0856579.
ACCESSION A90366
VERSION A90366.1 GI:6738880
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 547 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
source
1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2159 GGATAATTGCTGCC 2172
Db 14 GGATAATTGCTGCC 1

RESULT 504
A90406/c
LOCUS A90406 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 587 from Patent EP0856579.
ACCESSION A90406
VERSION A90406.1 GI:6738920
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 587 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
source
1..14
/organism="unidentified"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAATTCATCA 2587
Db 14 TTAATAATTCATCA 1

RESULT 505
ARI174027/c
LOCUS ARI174027 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6306624.
ACCESSION ARI174027
VERSION ARI174027.1 GI:17914347
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 17 23-OCT-2001;
LOCATION/Qualifiers
FEATURES
source
1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAATTCATCA 2814
Db 14 TGAATAATTCATCA 1

RESULT 507
BD176798
LOCUS BD176798 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
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ACCESSION B0176798
VERSION B0176798.1 GI:29122510
KEYWORDS WO 02074951-A/45
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
JOURNAL Patent: WO 02074951-A 45 26-SEP-2002;
COMMENT KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
OS Artificial Sequence
PN WO 02074951-A/45
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Artificial Sequence'.
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/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2576 AAAAAAAAAAAAT 2589
|||||
DB 1 AAAAAAAAAAAAT 14
RESULT 508
LOCUS B0176799
DEFINITION 14 bp DNA linear PAT 18-MAR-2003
METHOD of constructing cDNA tag for identifying expressed gene and
METHOD of analyzing gene expression.
ACCESSION B0176799
VERSION B0176799.1 GI:29122511
KEYWORDS WO 02074951-A/46.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
JOURNAL Patent: WO 02074951-A 46 26-SEP-2002;
COMMENT KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
OS Artificial Sequence
PN WO 02074951-A/46
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
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FH Key Location/Qualifiers
FT source 1..14
FT /organism='Artificial Sequence'.
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/db_xref='taxon:32630'
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2803 AAAAAAAAAACA 2816
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DB 1 AAAAAAAAAACA 14
RESULT 509
LOCUS B0176801/c
DEFINITION 14 bp DNA linear PAT 18-MAR-2003
METHOD of constructing cDNA tag for identifying expressed gene and
METHOD of analyzing gene expression.
ACCESSION B0176801
VERSION B0176801.1 GI:29122513
KEYWORDS WO 02074951-A/48.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
JOURNAL Patent: WO 02074951-A 48 26-SEP-2002;
COMMENT KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
OS Artificial Sequence
PN WO 02074951-A/48
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2575 TAAAAAAAAA 2588
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DB 14 TAAAAAAAAA 1
RESULT 510
LOCUS B0234897/c
DEFINITION 14 bp DNA linear PAT 17-JUL-2003
METHOD for stimulating the immune system.
ACCESSION B0234897
VERSION B0234897.1 GI:33044667
KEYWORDS JP 2002517434-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 14)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
JOURNAL A method for stimulating the immune system
PATENT: JP 2002517434-A 1 18-JUN-2002;
COMMENT BIOGOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/1
PD 18-JUN-2002
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PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
FT source 1..14
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACACTGTGTG 1232
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Db 14 TGCACACTGTGTG 1

RESULT 511
BD234898/c
LOCUS BD234898 14 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234898
VERSION BD234898.1 GI:33044668
KEYWORDS JP 2002517434-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 2 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/2
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
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FH Key Location/Qualifiers
FT source 1..14
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GCACACTGTGTGC 1233
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Db 14 GCACACTGTGTGC 1

RESULT 512
BD234901/c
LOCUS BD234901 14 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234901
VERSION BD234901.1 GI:33044671
KEYWORDS JP 2002517434-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 5 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/5
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
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PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
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method for stimulating the immune system
FH Key Location/Qualifiers
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Query Match 0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1507 AGTACTACGCCAAG 1520
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Db 14 AGTACTACGCCAAG 1

RESULT 513
BD234907/c
LOCUS BD234907 14 bp DNA linear PAT 17-JUL-2003
DEFINITION A method for stimulating the immune system.
ACCESSION BD234907
VERSION BD234907.1 GI:33044677
KEYWORDS JP 2002517434-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14)
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.
A method for stimulating the immune system
Patent: JP 2002517434-A 11 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
OS Homo sapiens (human)
PN JP 2002517434-A/11
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI
BRYSCH
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/
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PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
method for stimulating the immune system
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1575 CCCACTTCTACAG 1588  
14 CCCACTTCTACAG 1

RESULT 514  
BD234955/c

LOCUS BD234955 14 bp DNA linear PAT 17-JUL-2003

DEFINITION A method for stimulating the immune system.

ACCESSION BD234955

VERSION BD234955.1 GI:33044725

KEYWORDS JP 2002517434-A/59.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 14)  
Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.

AUTHORS A method for stimulating the immune system

TITLE Patent: JP 2002517434-A 59 18-JUN-2002;

JOURNAL BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Homo sapiens (human)  
PN JP 2002517434-A/59  
PD 18-JUN-2002  
PF 10-JUN-1999 JP 2000553044  
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI  
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI  
BRYSCH  
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/00,A61P35/00.  
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A  
method for stimulating the immune system  
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Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1478 CGCCTCGGAGCGC 1491  
14 CGCCTCGGAGCGC 1

RESULT 516  
BD234986/c

LOCUS BD234986 14 bp DNA linear PAT 17-JUL-2003

DEFINITION A method for stimulating the immune system.

ACCESSION BD234986

VERSION BD234986.1 GI:33044756

KEYWORDS JP 2002517434-A/90.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 14)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.

TITLE A method for stimulating the immune system

JOURNAL BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH

COMMENT OS Homo sapiens (human)  
PN JP 2002517434-A/90  
PD 18-JUN-2002  
PF 10-JUN-1999 JP 2000553044  
PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI  
KARL HERMANN SCHLINGENSIEPEN,REIMAR SCHLINGENSIEPEN,WOLFGANG PI  
BRYSCH  
PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395,A61P31/00,A61P35/00.  
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A  
method for stimulating the immune system  
FH Key Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2109 CGCGGAGAGCGC 2122  
14 CGCGGAGAGCGC 1

RESULT 515  
BD234960/c

LOCUS BD234960 14 bp DNA linear PAT 17-JUL-2003

DEFINITION A method for stimulating the immune system.

ACCESSION BD234960

VERSION BD234960.1 GI:33044730

KEYWORDS JP 2002517434-A/64.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 14)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Schlingensiepen,K.H., Schlingensiepen,R. and Brysch,W.

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Db      14  CGAGGCCATCCGCG 1
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RESULT 517
AR232800/c
LOCUS      AR232800      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 57 from patent US 6455689.
ACCESSION AR232800
VERSION    AR232800.1 GI:27275138
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL    Patent: US 6455689-A 57 24-SEP-2002;
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1219  TGCACACTACTGTG 1232
Db      14  TGCACACTACTGTG 1
|||||
RESULT 518
AR232806/c
LOCUS      AR232806      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 63 from patent US 6455689.
ACCESSION AR232806
VERSION    AR232806.1 GI:27275144
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL    Patent: US 6455689-A 63 24-SEP-2002;
FEATURES   Location/Qualifiers
            source          1..14
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1344  CAGATCCTGAGCAA 1357
Db      14  CAGATCCTGAGCAA 1
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RESULT 519
AR232814/c
LOCUS      AR232814      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 71 from patent US 6455689.
ACCESSION AR232814
VERSION    AR232814.1 GI:27275152
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1507  AGTACTACGCCAAG 1520
Db      14  AGTACTACGCCAAG 1
|||||
RESULT 520
AR232817/c
LOCUS      AR232817      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 74 from patent US 6455689.
ACCESSION AR232817
VERSION    AR232817.1 GI:27275155
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL    Patent: US 6455689-A 74 24-SEP-2002;
FEATURES   Location/Qualifiers
            source          1..14
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1561  AAAATGCCATCCCG 1574
Db      14  AAAATGCCATCCCG 1
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RESULT 521
AR232818/c
LOCUS      AR232818      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 75 from patent US 6455689.
ACCESSION AR232818
VERSION    AR232818.1 GI:27275156
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL    Patent: US 6455689-A 75 24-SEP-2002;
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1561  AAAATGCCATCCCG 1574
Db      14  AAAATGCCATCCCG 1
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Unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL    Patent: US 6455689-A 71 24-SEP-2002;
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1507  AGTACTACGCCAAG 1520
Db      14  AGTACTACGCCAAG 1
|||||
RESULT 520
AR232817/c
LOCUS      AR232817      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 74 from patent US 6455689.
ACCESSION AR232817
VERSION    AR232817.1 GI:27275155
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL    Patent: US 6455689-A 74 24-SEP-2002;
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1561  AAAATGCCATCCCG 1574
Db      14  AAAATGCCATCCCG 1
|||||
RESULT 521
AR232818/c
LOCUS      AR232818      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 75 from patent US 6455689.
ACCESSION AR232818
VERSION    AR232818.1 GI:27275156
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE      Antisense-oligonucleotides for transforming growth factor-.beta.
(JGF-.beta.)
JOURNAL    Patent: US 6455689-A 75 24-SEP-2002;
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1561  AAAATGCCATCCCG 1574
Db      14  AAAATGCCATCCCG 1
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CCACATTTCTACAG 1588  
Db 14 CCACATTTCTACAG 1

RESULT 522  
AR232834/c  
LOCUS AR232834 14 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 91 from patent US 6455689.  
ACCESSION AR232834  
VERSION AR232834.1 GI:27275172  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
JOURNAL Patent: US 6455689-A 91 24-SEP-2002;  
FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1807 AATGGCTCTCCTTC 1820  
Db 14 AATGGCTCTCCTTC 1

RESULT 523  
AR232844/c  
LOCUS AR232844 14 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 101 from patent US 6455689.  
ACCESSION AR232844  
VERSION AR232844.1 GI:27275182  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
JOURNAL Patent: US 6455689-A 101 24-SEP-2002;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTATTGATGGCAC 1984  
Db 14 GGTATTGATGGCAC 1

RESULT 524  
AR232846/c  
LOCUS AR232846 14 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 103 from patent US 6455689.  
ACCESSION AR232846

VERSION AR232846.1 GI:27275184  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
JOURNAL Patent: US 6455689-A 103 24-SEP-2002;  
FEATURES Location/Qualifiers  
source 1. .14  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 CAGTGGTGATCAGA 2010  
Db 14 CAGTGGTGATCAGA 1

RESULT 525  
AR232849/c  
LOCUS AR232849 14 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 106 from patent US 6455689.  
ACCESSION AR232849  
VERSION AR232849.1 GI:27275187  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
JOURNAL Patent: US 6455689-A 106 24-SEP-2002;  
FEATURES Location/Qualifiers  
source 1. .14  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AAGACCCACATCT 2059  
Db 14 AAGACCCACATCT 1

RESULT 526  
AR232865/c  
LOCUS AR232865 14 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 122 from patent US 6455689.  
ACCESSION AR232865  
VERSION AR232865.1 GI:27275203  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for transforming growth factor-.beta.  
(TGF-.beta.)  
JOURNAL Patent: US 6455689-A 122 24-SEP-2002;  
FEATURES Location/Qualifiers  
source 1. .14

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/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACACT 2291
Db 14 GGAGTTCAGACACT 1

RESULT 527
AR232879/c
LOCUS
DEFINITION      Sequence 136 from patent US 6455689.
ACCESSION      AR232879
VERSION        AR232879.1 GI:27275217
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE
Antisense-oligonucleotides for transforming growth factor-.beta.
(JTF-.beta.)
JOURNAL
Patent: US 6455689-A 136 24-SEP-2002;
FEATURES
source
1..14
Location/Qualifiers
/mol_type="genomic DNA"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
Db 14 ACTACTGTGTGCTG 1

RESULT 528
AR242022
LOCUS
DEFINITION      Sequence 310 from patent US 6472154.
ACCESSION      AR242022
VERSION        AR242022.1 GI:27287834
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE
Polymorphic repeats in human genes
JOURNAL
Patent: US 6472154-A 310 29-OCT-2002;
FEATURES
source
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Location/Qualifiers
/mol_type="genomic DNA"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACAAA 944
Db 1 AAAAAAAAAACAAA 14

RESULT 529
AX008968/c
LOCUS
DEFINITION      Sequence 1 from Patent WO9963975.
ACCESSION      AX008968
VERSION        AX008968.1 GI:9996342
KEYWORDS
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
A method for stimulating the immune system
Patent: WO 9963975-A 1 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
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Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1219 TGCACACTGTGTG 1232
Db 14 TGCACACTGTGTG 1

RESULT 530
AX008969/c
LOCUS
DEFINITION      Sequence 2 from Patent WO9963975.
ACCESSION      AX008969
VERSION        AX008969.1 GI:9996343
KEYWORDS
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
A method for stimulating the immune system
Patent: WO 9963975-A 2 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
source
1..14
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GCACTACTGTGTGC 1233
Db 14 GCACTACTGTGTGC 1

RESULT 531
AX008972/c
LOCUS
DEFINITION      Sequence 5 from Patent WO9963975.
ACCESSION      AX008972
VERSION        AX008972.1 GI:9996346
KEYWORDS
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
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AUTHORS      Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE        A method for stimulating the immune system
JOURNAL      PATENT: WO 963975-A 5 16-DEC-1999;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
              HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1507 AGTACTACGCCAAG 1520
Db      14 AGTACTACGCCAAG 1

RESULT 532
AX008978/c
LOCUS      AX008978      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 11 from Patent WO963975.
ACCESSION  AX008978
VERSION     AX008978.1 GI:9996352
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     PATENT: WO 963975-A 11 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1575 CCCACTTCTACAG 1588
Db      14 CCCACTTCTACAG 1

RESULT 533
AX009026/c
LOCUS      AX009026      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 59 from Patent WO963975.
ACCESSION  AX009026
VERSION     AX009026.1 GI:9996400
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     PATENT: WO 963975-A 59 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1575 CCCACTTCTACAG 1588
Db      14 CCCACTTCTACAG 1

RESULT 533
AX009026/c
LOCUS      AX009026      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 59 from Patent WO963975.
ACCESSION  AX009026
VERSION     AX009026.1 GI:9996400
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     PATENT: WO 963975-A 59 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1478 CGCCTGCGAGCGCG 1491
Db      14 CGCCTGCGAGCGCG 1

RESULT 535
AX009057/c
LOCUS      AX009057      14 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 90 from Patent WO963975.
ACCESSION  AX009057
VERSION     AX009057.1 GI:9996431
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     PATENT: WO 963975-A 90 16-DEC-1999;
             BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
             HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
              /organism="Homo sapiens"
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1328 CGAGGCCATCCGCG 1341
Db      14 CGAGGCCATCCGCG 1

AUTHORS      Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE        A method for stimulating the immune system
JOURNAL      PATENT: WO 963975-A 5 16-DEC-1999;
              BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
              HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES     Location/Qualifiers
source       1..14
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1328 CGAGGCCATCCGCG 1341
Db      14 CGAGGCCATCCGCG 1
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[illegible]

AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2(tgf-b2)  
JOURNAL Patent: EP 1008649-A 75 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
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Qy 1575 CCCACTTCTACAG 1588  
Db 14 CCCACTTCTACAG 1  
RESULT 541  
AX030129/c  
LOCUS AX030129 14 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 91 from Patent EP1008649.  
ACCESSION AX030129  
VERSION AX030129.1 GI:10190346  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2(tgf-b2)  
JOURNAL Patent: EP 1008649-A 91 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1807 AATGGCTCTCCTTC 1820  
Db 14 AATGGCTCTCCTTC 1  
RESULT 542  
AX030139/c  
LOCUS AX030139 14 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 101 from Patent EP1008649.  
ACCESSION AX030139  
VERSION AX030139.1 GI:10190356  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2(tgf-b2)  
JOURNAL Patent: EP 1008649-A 101 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers

source 1..14  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1971 GGTATTGATGGCAC 1984  
Db 14 GGTATTGATGGCAC 1  
RESULT 543  
AX030141/c  
LOCUS AX030141 14 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 103 from Patent EP1008649.  
ACCESSION AX030141  
VERSION AX030141.1 GI:10190358  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2(tgf-b2)  
JOURNAL Patent: EP 1008649-A 103 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"  
Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1997 CAGTGGTGATCAGA 2010  
Db 14 CAGTGGTGATCAGA 1  
RESULT 544  
AX030144/c  
LOCUS AX030144 14 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 106 from Patent EP1008649.  
ACCESSION AX030144  
VERSION AX030144.1 GI:10190361  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2(tgf-b2)  
JOURNAL Patent: EP 1008649-A 106 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
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Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1997 CAGTGGTGATCAGA 2010  
Db 14 CAGTGGTGATCAGA 1  
RESULT 544  
AX030144/c  
LOCUS AX030144 14 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 106 from Patent EP1008649.  
ACCESSION AX030144  
VERSION AX030144.1 GI:10190361  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2(tgf-b2)  
JOURNAL Patent: EP 1008649-A 106 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2046 AAGACCCCATCT 2059  
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Db 14 AAGACCCCATCT 1

RESULT 545  
AX030160/c  
LOCUS  
DEFINITION Sequence 122 from Patent EP1008649.  
ACCESSION AX030160  
VERSION AX030160.1 GI:10190377  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2 (tgf-b2)  
JOURNAL Patent: EP 1008649-A 122 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers  
source  
1. .14  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2278 GGAGTTCAGACACT 2291  
|||||  
Db 14 GGAGTTCAGACACT 1

RESULT 546  
AX030174/c  
LOCUS  
DEFINITION Sequence 136 from Patent EP1008649.  
ACCESSION AX030174  
VERSION AX030174.1 GI:10190391  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Bogdahn,U., Brysch,W., Schlingensiepen,G.F., Schlingensiepen,K.H.  
and Schlingensiepen,R.  
TITLE Antisense-oligonucleotides for the treatment of immuno-suppressive  
effects of transforming growth factor-b2 (tgf-b2)  
JOURNAL Patent: EP 1008649-A 136 14-JUN-2000;  
BIOGNOSTIK GES (DE)  
FEATURES Location/Qualifiers  
source  
1. .14  
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/mol\_type="unassigned DNA"  
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Query Match 0.3%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1222 ACTACTGTGTGCTG 1235  
|||||  
Db 14 ACTACTGTGTGCTG 1

RESULT 547  
AX316416/c  
LOCUS  
DEFINITION Sequence 57 from Patent EP1160319.  
ACCESSION AX316416  
VERSION AX316416.1 GI:117899589  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 57 05-DEC-2001;  
BIOGNOSTIK GESLLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1219 TGCACACTGTGTG 1232  
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Db 14 TGCACACTGTGTG 1

RESULT 548  
AX316422/c  
LOCUS  
DEFINITION Sequence 63 from Patent EP1160319.  
ACCESSION AX316422  
VERSION AX316422.1 GI:117899595  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 63 05-DEC-2001;  
BIOGNOSTIK GESLLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1344 CAGATCCTGAGCAA 1357  
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Db 14 CAGATCCTGAGCAA 1

RESULT 549  
AX316430/c  
LOCUS  
DEFINITION Sequence 71 from Patent EP1160319.  
ACCESSION AX316430  
VERSION AX316430.1 GI:117899603  
KEYWORDS

SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 71 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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QY 1507 AGTACTACGCCAAG 1520  
Db 14 AGTACTACGCCAAG 1

RESULT 550  
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LOCUS AX316433 14 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 74 from Patent EP1160319.  
ACCESSION AX316433  
VERSION AX316433.1 GI:17899606  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 74 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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QY 1561 AAAATGCCATCCCG 1574  
Db 14 AAAATGCCATCCCG 1

RESULT 551  
AX316434/c  
LOCUS AX316434 14 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 75 from Patent EP1160319.  
ACCESSION AX316434  
VERSION AX316434.1 GI:17899607  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive

JOURNAL effects of transforming growth factor-beta (tgf-beta)  
Patent: EP 1160319-A 75 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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Db 14 CCCACTTCTACAG 1

RESULT 552  
AX316450/c  
LOCUS AX316450 14 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 91 from Patent EP1160319.  
ACCESSION AX316450  
VERSION AX316450.1 GI:17899623  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 91 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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RESULT 553  
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DEFINITION Sequence 101 from Patent EP1160319.  
ACCESSION AX316460  
VERSION AX316460.1 GI:17899633  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,  
Schlingensiepen,R. and Bogdahn,U.  
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive  
effects of transforming growth factor-beta (tgf-beta)  
JOURNAL Patent: EP 1160319-A 101 05-DEC-2001;  
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)  
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QY 1971 GGTATTGATGGCAC 1984
Db 14 GGTATTGATGGCAC 1

RESULT 554
AX316462/c
LOCUS AX316462 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 103 from Patent EP1160319.
ACCESSION AX316462
VERSION AX316462.1 GI:17899635
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 103 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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QY 1997 CAGTGTGATCACA 2010
Db 14 CAGTGTGATCACA 1

RESULT 555
AX316465/c
LOCUS AX316465 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 106 from Patent EP1160319.
ACCESSION AX316465
VERSION AX316465.1 GI:17899638
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 106 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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Db 14 ACTACTGTGTGCTG 1

RESULT 558
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Db 14 AAGACCCCATCT 1

RESULT 556
AX316481/c
LOCUS AX316481 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 122 from Patent EP1160319.
ACCESSION AX316481
VERSION AX316481.1 GI:17899654
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 122 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACT 2291
Db 14 GGAGTTCAGACT 1

RESULT 557
AX316495/c
LOCUS AX316495 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 136 from Patent EP1160319.
ACCESSION AX316495
VERSION AX316495.1 GI:17899668
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 136 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
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LOCUS BD065884 14 bp DNA linear PAT 27-AUG-2002  
 DEFINITION An antisense oligonucleotide preparation method.  
 ACCESSION BD065884  
 VERSION JP 2001511000-A/519.  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Schlengersiepen,K.H. and Brysch,W.  
 TITLE An antisense oligonucleotide preparation method  
 JOURNAL Patent: JP 2001511000-A 519 07-AUG-2001;  
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
 COMMENT OS Unknown  
 PN JP 2001511000-A/519  
 PD 07-AUG-2001  
 PF 30-JAN-1998 JP 1998532533  
 PR 31-JAN-1997 EP 97101531.8  
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
 PC C12N15/11,C07H21/04,A61K31/70  
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 Db 14 GCATACTGTGTC 1  
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 LOCUS  
 DEFINITION An antisense oligonucleotide preparation method.  
 ACCESSION BD065912  
 VERSION JP 2001511000-A/547.  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Schlengersiepen,K.H. and Brysch,W.  
 TITLE An antisense oligonucleotide preparation method  
 JOURNAL Patent: JP 2001511000-A 547 07-AUG-2001;  
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
 COMMENT OS Unknown  
 PN JP 2001511000-A/547  
 PD 07-AUG-2001  
 PF 30-JAN-1998 JP 1998532533  
 PR 31-JAN-1997 EP 97101531.8  
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
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 Db 14 GCATACTGTGTC 1  
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 LOCUS  
 DEFINITION An antisense oligonucleotide preparation method.  
 ACCESSION BD065912  
 VERSION JP 2001511000-A/547.  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Schlengersiepen,K.H. and Brysch,W.  
 TITLE An antisense oligonucleotide preparation method  
 JOURNAL Patent: JP 2001511000-A 547 07-AUG-2001;  
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
 COMMENT OS Unknown  
 PN JP 2001511000-A/547  
 PD 07-AUG-2001  
 PF 30-JAN-1998 JP 1998532533  
 PR 31-JAN-1997 EP 97101531.8  
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
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LOCUS BD065952 14 bp DNA linear PAT 27-AUG-2002  
 DEFINITION An antisense oligonucleotide preparation method.  
 ACCESSION BD065952  
 VERSION JP 2001511000-A/587.  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Schlengersiepen,K.H. and Brysch,W.  
 TITLE An antisense oligonucleotide preparation method  
 JOURNAL Patent: JP 2001511000-A 587 07-AUG-2001;  
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
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 PN JP 2001511000-A/587  
 PD 07-AUG-2001  
 PF 30-JAN-1998 JP 1998532533  
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 QY 1919 TAATAATTACATCA 1932  
 Db 14 TAATAATTACATCA 1  
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 BD066560/c  
 LOCUS  
 DEFINITION An antisense oligonucleotide preparation method.  
 ACCESSION BD066560  
 VERSION JP 2001511000-A/1195.  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Schlengersiepen,K.H. and Brysch,W.  
 TITLE An antisense oligonucleotide preparation method  
 JOURNAL Patent: JP 2001511000-A 1195 07-AUG-2001;  
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
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 PN JP 2001511000-A/1195  
 PD 07-AUG-2001  
 PF 30-JAN-1998 JP 1998532533  
 PR 31-JAN-1997 EP 97101531.8  
 PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
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QY 1219 TGCACACTGTGTG 1232
Db 14 TGCACACTGTGTG 1

RESULT 562
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LOCUS
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  ACCESSION BD066566
  VERSION BD066566.1 GI:22612169
  KEYWORDS JP 2001511000-A/1201.
  SOURCE unidentified
  ORGANISM unidentified
  REFERENCE 1 (bases 1 to 14)
  AUTHORS Schlingensiepen,K.H. and Brysch,W.
  TITLE An antisense oligonucleotide preparation method
  JOURNAL Patent: JP 2001511000-A 1201 07-AUG-2001;
  COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
  PN JP 2001511000-A/1201
  PD 07-AUG-2001
  PF 30-JAN-1998 JP 1998532533
  PR 31-JAN-1997 EP 97101531.8
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QY 1507 AGTACTACGCCAAG 1520
Db 14 AGTACTACGCCAAG 1

RESULT 564
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LOCUS
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  VERSION BD066575.1 GI:22612178
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  SOURCE unidentified
  ORGANISM unidentified
  REFERENCE 1 (bases 1 to 14)
  AUTHORS Schlingensiepen,K.H. and Brysch,W.
  TITLE An antisense oligonucleotide preparation method
  JOURNAL Patent: JP 2001511000-A 1210 07-AUG-2001;
  COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
  PN JP 2001511000-A/1210
  PD 07-AUG-2001
  PF 30-JAN-1998 JP 1998532533
  PR 31-JAN-1997 EP 97101531.8
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Db 14 CAGATCTGAGCAA 1

RESULT 563
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LOCUS
  DEFINITION An antisense oligonucleotide preparation method.
  ACCESSION BD066573
  VERSION BD066573.1 GI:22612176
  KEYWORDS JP 2001511000-A/1208.
  SOURCE unidentified
  ORGANISM unidentified
  REFERENCE 1 (bases 1 to 14)
  AUTHORS Schlingensiepen,K.H. and Brysch,W.
  TITLE An antisense oligonucleotide preparation method
  JOURNAL Patent: JP 2001511000-A 1208 07-AUG-2001;
  COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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QY 1561 AAAATGCCATCCCG 1574
Db 14 AAAATGCCATCCCG 1

RESULT 565
BD066576/c
LOCUS
  DEFINITION An antisense oligonucleotide preparation method.
  ACCESSION BD066576
  VERSION BD066576.1 GI:22612179
  KEYWORDS JP 2001511000-A/1211.
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SOURCE unidentified  
ORGANISM unclassified  
1 (bases 1 to 14)  
REFERENCE Schlingensiepen,K.H. and Brysch,W.  
AUTHORS An antisense oligonucleotide preparation method  
TITLE Patent: JP 2001511000-A 1211 07-AUG-2001;  
JOURNAL BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Unknown  
PN JP 2001511000-A/1211  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
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QY 1575 CCCACTTTCTACAG 1588  
Db 14 CCCACTTTCTACAG 1  
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RESULT 566  
BD066592/c  
LOCUS 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066592  
VERSION BD066592.1 GI:22612195  
KEYWORDS JP 2001511000-A/1227.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Unknown  
PN JP 2001511000-A/1227  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1807 AATGGCTCTCCTTC 1820  
Db 14 AATGGCTCTCCTTC 1  
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RESULT 567  
BD066602/c  
LOCUS 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066602  
VERSION BD066602.1 GI:22612205  
KEYWORDS JP 2001511000-A/1237.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Unknown  
PN JP 2001511000-A/1237  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH  
PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1971 GGTATTGATGGCAC 1984  
Db 14 GGTATTGATGGCAC 1  
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RESULT 568  
BD066604/c  
LOCUS 14 bp DNA linear PAT 27-AUG-2002  
DEFINITION An antisense oligonucleotide preparation method.  
ACCESSION BD066604  
VERSION BD066604.1 GI:22612207  
KEYWORDS JP 2001511000-A/1239.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,K.H. and Brysch,W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Unknown  
PN JP 2001511000-A/1239  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 1998532533  
PR 31-JAN-1997 EP 97101531.8  
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PC C12N15/11,C07H21/04,A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 CAGTGTGATCAGA 2010
Db 14 CAGTGTGATCAGA 1

RESULT 569
BD066622/c
LOCUS          14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    An antisense oligonucleotide preparation method.
ACCESSION     BD066622
VERSION       BD066622.1 GI:22612225
KEYWORDS      JP 2001511000-A/1257.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 14)
AUTHORS      Schlingensiepen,K.H. and Brysch,W.
TITLE        An antisense oligonucleotide preparation method
JOURNAL      Patent: JP 2001511000-A 1257 07-AUG-2001;
COMMENT      BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS           Unknown
PN           JP 2001511000-A/1257
PD           07-AUG-2001
PF           30-JAN-1998 JP 1998532533
PR           31-JAN-1997 EP 97101531.8
PI           KARL HERMANN SCHLINGENSTIEPEN,WOLFGANG BRYSCH
PC           C12N15/11,C07H21/04,A61K31/70
CC           An antisense oligonucleotide preparation method FH Key
LOCUS/Qualifiers
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1222 ACTACTGTGTGCTG 1235
Db 14 ACTACTGTGTGCTG 1

RESULT 571
BD073880/c
LOCUS          14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Isolation of novel aging factor gene P23.
ACCESSION     BD073880
VERSION       BD073880.1 GI:22619483
KEYWORDS      JP 2001512698-A/5.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 14)
AUTHORS      Suishelm,K., Hosier,S. and Kubbies,M.
TITLE        Isolation of novel aging factor gene P23
JOURNAL      Patent: JP 2001512698-A 5 28-AUG-2001;
COMMENT      UNIVERSITY OF WASHINGTON
OS           Unidentified
PN           JP 2001512698-A/5
PD           28-AUG-2001
PF           05-AUG-1998 JP 2000506375
PR           08-AUG-1997 US 08/908873
PI           KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
PC           C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N15/09, PC
C12P21/02,
PC           C12P21/08,C12N15/00
CC           Strandedness: Single;
CC           Topology: Linear;
CC           Isolation of novel aging factor gene P23
FH Key        Location/Qualifiers
FT source     1. .14
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Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2587
Db 14 TTAATAAAAAAAAAA 1

RESULT 572
BD073882/c
LOCUS          14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Isolation of novel aging factor gene P23.
ACCESSION     BD073882
VERSION       BD073882.1 GI:22619485
KEYWORDS      JP 2001512698-A/7.
SOURCE        unidentified

Query Match      0.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 GGAGTTCAGACACT 2291
Db 14 GGAGTTCAGACACT 1

RESULT 570
BD066636/c
LOCUS          14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    An antisense oligonucleotide preparation method.
ACCESSION     BD066636
VERSION       BD066636.1 GI:22612239
KEYWORDS      JP 2001511000-A/1271.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 14)
AUTHORS      Schlingensiepen,K.H. and Brysch,W.
TITLE        An antisense oligonucleotide preparation method
JOURNAL      Patent: JP 2001511000-A 1271 07-AUG-2001;
COMMENT      BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS           Unknown
PN           JP 2001511000-A/1271
PD           07-AUG-2001
PF           30-JAN-1998 JP 1998532533
PR           31-JAN-1997 EP 97101531.8
PI           KARL HERMANN SCHLINGENSTIEPEN,WOLFGANG BRYSCH
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ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.  
TITLE Isolation of novel aging factor gene P23  
JOURNAL Patent: JP 2001512698-A 7 28-AUG-2001;  
UNIVERSITY OF WASHINGTON  
COMMENT OS Unidentified  
PN JP 2001512698-A/7  
PD 28-AUG-2001  
PF 05-AUG-1998 JP 2000506375  
PR 08-AUG-1997 US 08/908873  
PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC  
C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC  
C12P21/02.  
PC C12P21/08,C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
CC Isolation of novel aging factor gene P23  
FH Key Location/Qualifiers  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2801 TGAATAATTAATACAT 2814  
Db 14 TGAATAATTAATACAT 1  
RESULT 573  
A88438/c  
LOCUS A88438 15 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 586 from Patent WO9833904.  
ACCESSION A88438  
VERSION A88438.1 GI:6737008  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W. and Schlingensiepen,K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 586 06-AUG-1998;  
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)  
FEATURES Location/Qualifiers  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1917 TCTAATAATTACAT 1930  
Db 14 TCTAATAATTACAT 1  
RESULT 574  
A90405/c  
LOCUS A90405 15 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 586 from Patent EP0856579.  
ACCESSION A90405  
VERSION A90405.1 GI:6738919

KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: EP 0856579-A 586 05-AUG-1998;  
BIOGOSTIK GES (DE)  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1917 TCTAATAATTACAT 1930  
Db 14 TCTAATAATTACAT 1  
RESULT 575  
AR033533/c  
LOCUS AR033533 15 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 299 from patent US 5869253.  
ACCESSION AR033533  
VERSION AR033533.1 GI:5949138  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 5869253-A 299 09-FEB-1999;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3210 TGCCCGAAGGCCT 3223  
Db 15 TGCCCGAAGGCCT 2  
RESULT 576  
AR033534/c  
LOCUS AR033534 15 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 300 from patent US 5869253.  
ACCESSION AR033534  
VERSION AR033534.1 GI:5949139  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 5869253-A 300 09-FEB-1999;  
FEATURES Location/Qualifiers  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCAGAGGCT 3223  
 Db 14 TGCCAGAGGCT 1

RESULT 577  
 AR056155/c  
 LOCUS 15 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 359 from patent US 5837542.  
 ACCESSION AR056155  
 VERSION AR056155.1 GI:5981732  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 359 17-NOV-1998;  
 FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
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QY 2576 AAAAAAAAAAAAT 2589  
 Db 15 AAAAAAAAAAAAT 2

RESULT 578  
 AR056156/c  
 LOCUS 15 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 360 from patent US 5837542.  
 ACCESSION AR056156  
 VERSION AR056156.1 GI:5981733  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 360 17-NOV-1998;  
 FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAAT 2589  
 Db 14 AAAAAAAAAAAAT 1

RESULT 579  
 AR056160/c  
 LOCUS 15 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 364 from patent US 5837542.  
 ACCESSION AR056160  
 VERSION AR056160.1 GI:5981737  
 KEYWORDS .  
 SOURCE Unknown.

ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 364 17-NOV-1998;  
 FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAA 2814  
 Db 15 TGAATAAAAAAAAA 2

RESULT 580  
 AR056161/c  
 LOCUS 15 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 365 from patent US 5837542.  
 ACCESSION AR056161  
 VERSION AR056161.1 GI:5981738  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 365 17-NOV-1998;  
 FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAA 2814  
 Db 14 TGAATAAAAAAAAA 1

RESULT 581  
 AR076566/c  
 LOCUS 15 bp DNA linear PAT 30-AUG-2000  
 DEFINITION Sequence 1 from patent US 5959090.  
 ACCESSION AR076566  
 VERSION AR076566.1 GI:10003312  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Guzaev,A., Azhaye,A. and Lonnberg,H.  
 TITLE Chemical phosphorylation of oligonucleotides and reactants used therefor  
 JOURNAL Patent: US 5959090-A 1 28-SEP-1999;  
 FEATURES Location/Qualifiers  
 source 1..15

Query Match 0.3%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
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QY 2524 ACCACCATGATGTT 2537  
Db 15 ACCACCATGATGTT 2

RESULT 582  
AR113355/c  
LOCUS AR113355 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 299 from patent US 6132966.  
ACCESSION AR113355  
VERSION AR113355.1 GI:14093677  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 6132966-A 299 17-OCT-2000;  
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Query Match 0.3%; Score 14; DB 1; Length 15;  
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QY 3210 TGCCCGAGAGGCCT 3223  
Db 15 TGCCCGAGAGGCCT 2

RESULT 583  
AR113356/c  
LOCUS AR113356 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 300 from patent US 6132966.  
ACCESSION AR113356  
VERSION AR113356.1 GI:14093678  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Draper,K.G.  
TITLE Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 6132966-A 300 17-OCT-2000;  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCGAGAGGCCT 3223  
Db 14 TGCCCGAGAGGCCT 1

RESULT 584  
AR113913/c  
LOCUS AR113913 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 359 from patent US 6132967.  
ACCESSION AR113913  
VERSION AR113913.1 GI:14094235  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 359 17-OCT-2000;  
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Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAT 2589  
Db 15 AAAAAAAAAAAT 2

RESULT 585  
AR113914/c  
LOCUS AR113914 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 360 from patent US 6132967.  
ACCESSION AR113914  
VERSION AR113914.1 GI:14094236  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 360 17-OCT-2000;  
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QY 2576 AAAAAAAAAAAT 2589  
Db 14 AAAAAAAAAAAT 1

RESULT 586  
AR113918/c  
LOCUS AR113918 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 364 from patent US 6132967.  
ACCESSION AR113918  
VERSION AR113918.1 GI:14094240  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 364 17-OCT-2000;  
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Query Match 0.3%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAT 2589  
Db 14 AAAAAAAAAAAT 1

RESULT 586  
AR113918/c  
LOCUS AR113918 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 364 from patent US 6132967.  
ACCESSION AR113918  
VERSION AR113918.1 GI:14094240  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 364 17-OCT-2000;  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2801 TGAATAAAAAAAAAA 2814
Db 15 TGAATAAAAAAAAAA 2

RESULT 587
ARL13919/c
LOCUS ARL13919 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 365 from patent US 6132967.
ACCESSION ARL13919
VERSION ARL13919.1 GI:14094241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 365 17-OCT-2000;
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Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814
Db 14 TGAATAAAAAAAAAA 1

RESULT 588
BD207266/c
LOCUS BD207266 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207266.1 GI:33017036
VERSION JP 2002512791-A/856.
KEYWORDS unidentified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 856 08-MAY-2002;
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/856
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K48/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT virus)'
FT Location/Qualifiers

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            /db_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGAGGCT 3223
Db 15 TGCCCAAGAGGCT 2

RESULT 589
BD207267/c
LOCUS BD207267 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207267.1 GI:33017037
VERSION JP 2002512791-A/857.
KEYWORDS unidentified
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 857 08-MAY-2002;
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/857
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT virus)'
FT Location/Qualifiers

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            /mol_type="genomic RNA"
            /db_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 TGCCCAAGAGGCT 3223
Db 14 TGCCCAAGAGGCT 1

RESULT 590
IS7762/c
LOCUS IS7762 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 299 from patent US 5610054.
ACCESSION IS7762
VERSION IS7762.1 GI:2482826
KEYWORDS Unknown.
SOURCE
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ORGANISM      Unknown.
Unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Draper,K.G.
TITLE          Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL        Patent: US 5610054-A 299 11-MAR-1997;
FEATURES       Location/Qualifiers
source         1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match    0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3210 TGCCGAGAGGCCT 3223
Db      15 TGCCGAGAGGCCT 2

RESULT 591
157763/c
LOCUS      157763              15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 300 from patent US 5610054.
ACCESSION  157763
VERSION    157763.1 GI:2482827
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1
AUTHORS    Draper,K.G.
TITLE      Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL    Patent: US 5610054-A 300 11-MAR-1997;
FEATURES   Location/Qualifiers
source     1..15
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match    0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3210 TGCCGAGAGGCCT 3223
Db      14 TGCCGAGAGGCCT 1

RESULT 592
AX633193/c
LOCUS      AX633193              15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 332 from Patent EP1260586.
ACCESSION  AX633193
VERSION    AX633193.1 GI:28468807
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE      Method and reagent for inhibiting the expression of disease related
            genes
JOURNAL    Patent: EP 1260586-A 332 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   Location/Qualifiers
source     1..15
           /organism="unassigned RNA"
           /db_xref="taxon:32644"

Query Match    0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3210 TGCCGAGAGGCCT 3223
Db      14 TGCCGAGAGGCCT 1

RESULT 593
AX633195/c
LOCUS      AX633195              15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 334 from Patent EP1260586.
ACCESSION  AX633195
VERSION    AX633195.1 GI:28468809
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE      Method and reagent for inhibiting the expression of disease related
            genes
JOURNAL    Patent: EP 1260586-A 334 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   Location/Qualifiers
source     1..15
           /organism="unassigned RNA"
           /db_xref="taxon:32644"

Query Match    0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3210 TGCCGAGAGGCCT 3223
Db      14 TGCCGAGAGGCCT 1

RESULT 594
AX633203/c
LOCUS      AX633203              15 bp      RNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 342 from Patent EP1260586.
ACCESSION  AX633203
VERSION    AX633203.1 GI:28468817
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE      Method and reagent for inhibiting the expression of disease related
            genes
JOURNAL    Patent: EP 1260586-A 342 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES   Location/Qualifiers
source     1..15
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           /db_xref="taxon:32644"

Query Match    0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3210 TGCCGAGAGGCCT 3223
Db      14 TGCCGAGAGGCCT 1
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAAGAAAAA 2814
Db 15 TGAAGAAAAA 2

RESULT 595
AX633205/c
LOCUS
DEFINITION Sequence 344 from Patent EP1260586.
ACCESSION AX633205
VERSION AX633205.1 GI:28468819
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggan,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL Patent: EP 1260586-A 344 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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source
1..15
/organism="unidentified"
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Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAAGAAAAA 2814
Db 14 TGAAGAAAAA 1

RESULT 596
AX769806
LOCUS
DEFINITION Sequence 17 from Patent WO03020980.
ACCESSION AX769806
VERSION AX769806.1 GI:32437503
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Kaytes,P.S. and Teng,C.H.
TITLE Single nucleotide polymorphisms diagnostic for schizophrenia
JOURNAL Patent: WO 03020980-A 17 13-MAR-2003;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
source
1..15
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Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3718 CCCTGCCTGTATT 3731
Db 1 CCCTGCCTGTATT 14

RESULT 597

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BD065951/c
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065951
VERSION BD065951.1 GI:22611554
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Schlengersiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 586 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/586
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..15
FT /organism='Unknown'.
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/db_xref="taxon:32644"

Query Match 0.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1917 TCTAATAATTACAT 1930
Db 14 TCTAATAATTACAT 1

RESULT 598
I28577/c
LOCUS
DEFINITION Sequence 30 from patent US 5571937.
ACCESSION I28577
VERSION I28577.1 GI:1819353
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5571937-A 30 05-NOV-1996;
FEATURES
source
1..16
/organism="unassigned DNA"

Query Match 0.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1169 TTTTTCCTTACTTT 1182
Db 15 TTTTTCCTTACTTT 2

RESULT 599
I58739/c
LOCUS
DEFINITION Sequence 30 from patent US 5652350.
ACCESSION I58739

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[illegible]

PI GOZO TSUJIMOTO,EIKI TAKAHASHI  
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC  
C12Q1/68,  
PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,  
PC G01N33/15,  
PC G01N33/50//C12P21/08,C12N5/10,C12R1/91),(C12P21/02,C12R1:91)  
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer  
CC key Location/Qualifiers  
FH key 1..17  
FT source /organism='Artificial Sequence'.  
FT Location/Qualifiers

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/db\_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588

DB 17 TAAAAA 4

RESULT 604  
BD143834/C  
LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method of examining allergic disease.  
ACCESSION BD143834  
VERSION BD143834.1 GI:27849592  
KEYWORDS JP 2002095500-A/2.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Tsujimoto,K.  
TITLE Method of examining allergic disease  
JOURNAL Patent: JP 2002095500-A 2 02-APR-2002;  
GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL  
COMMENT OS Artificial Sequence  
PN JP 2002095500-A/2  
PD 02-APR-2002  
PF 25-SEP-2000 JP 2000291316  
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI  
PI TAKESHI NAGASU,  
PI KOZO TSUJIMOTO  
PC C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC  
C07K14/47,  
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC  
,C12N15/09,C12P21/02,  
PC C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC  
C12N15/00  
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer  
CC key Location/Qualifiers  
FH key 1..17  
FT source /organism='Artificial Sequence'.  
FT Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2575 TAAAAA 2588  
DB 17 TAAAAA 4

RESULT 605  
BD167835/C  
LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method for examination of allergosis.  
ACCESSION BD167835  
VERSION BD167835.1 GI:27873647  
KEYWORDS WO 0233122-A/2.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E.  
TITLE Method for examination of allergosis  
JOURNAL Patent: WO 0233122-A 2 25-APR-2002;  
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI  
HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA  
SAITO,EIKI TAKAHASHI  
COMMENT OS Artificial Sequence  
PN WO 0233122-A/2  
PD 25-APR-2002  
PF 11-OCT-2001 WO 2001JP008937  
PR 13-OCT-2000 JP 00P 314093  
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI  
PI TAKESHI NAGASU,  
PI HIROHISA SAITO,EIKI TAKAHASHI  
PC C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC  
A61K39/395,  
PC A01K67/027//C07K16/18,C12N5/10  
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/db\_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588

DB 17 TAAAAA 4

RESULT 606  
BD167907/C  
LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method of examining allergic disease.  
ACCESSION BD167907  
VERSION BD167907.1 GI:27873719  
KEYWORDS WO 0226962-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.  
TITLE Method of examining allergic disease

CC primer sequence anchor  
CC key Location/Qualifiers  
FH key 1..17  
FT source /organism='Artificial Sequence'.  
FT Location/Qualifiers  
1..17  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588

DB 17 TAAAAA 4

RESULT 606  
BD167907/C  
LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method of examining allergic disease.  
ACCESSION BD167907  
VERSION BD167907.1 GI:27873719  
KEYWORDS WO 0226962-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.  
TITLE Method of examining allergic disease

CC primer sequence anchor  
CC key Location/Qualifiers  
FH key 1..17  
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FT Location/Qualifiers  
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/mol\_type="genomic DNA"  
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Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588

DB 17 TAAAAA 4

RESULT 606  
BD167907/C  
LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method of examining allergic disease.  
ACCESSION BD167907  
VERSION BD167907.1 GI:27873719  
KEYWORDS WO 0226962-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.  
TITLE Method of examining allergic disease

CC primer sequence anchor  
CC key Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588

DB 17 TAAAAA 4

RESULT 606  
BD167907/C  
LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method of examining allergic disease.  
ACCESSION BD167907  
VERSION BD167907.1 GI:27873719  
KEYWORDS WO 0226962-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.  
TITLE Method of examining allergic disease

CC primer sequence anchor  
CC key Location/Qualifiers  
FH key 1..17  
FT source /organism='Artificial Sequence'.  
FT Location/Qualifiers  
1..17  
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/mol\_type="genomic DNA"  
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JOURNAL Patent: WO 0226962-A 6 04-APR-2002;  
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI  
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI  
NAGASU, HIROHISA SAITO  
OS Artificial Sequence  
PN WO 0226962-A/6  
PD 04-APR-2002  
PF 21-SEP-2001 WO 2001JP008247  
PR 26-SEP-2000 JP 00P 293021  
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI  
TAKESHI NAGASU,  
PI HIROHISA SAITO  
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC  
C12Q1/68,  
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,  
PC G01N33/15,  
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)  
CC Description of Artificial Sequence: an artificially synthesized

CC primer  
CC sequence 0.3%; Score 14; DB 1; Length 17;  
FH Key Location/Qualifiers  
FT source 1. .17  
FT /organism='Artificial Sequence'.  
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/db\_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588  
Db 17 TAAAAA 4

RESULT 608  
BD171177/c  
LOCUS 17 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method of examining allergic disease.  
ACCESSION BD171177  
VERSION BD171177.1 GI:27876989  
KEYWORDS WO 0250269-A/2.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
AUTHORS 1 (bases 1 to 17)  
Matsumoto, Y., Imai, Y., Oshida, T., Sugita, Y., Nagasu, T. and  
Tsujiimoto, G.  
TITLE Method of examining allergic disease  
JOURNAL Patent: WO 0250269-A 2 27-JUN-2002;  
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO  
MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,  
GOZO TSUJIMOTO  
OS Artificial Sequence  
PN WO 0250269-A/2  
PD 27-JUN-2002  
PF 21-DEC-2001 WO 2001JP011286  
PR 21-DEC-2000 JP 00P 389476  
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI  
TAKESHI NAGASU,  
PI GOZO TSUJIMOTO  
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,  
PC A61P37/08,  
PC C12Q1/68, G01N33/50  
CC Description of Artificial Sequence: 'GT15A', an artificially  
synthesized  
CC primer sequence  
FH Key Location/Qualifiers  
FT source 1. .17  
FT /organism='Artificial Sequence'.  
FEATURES  
source  
1. .17  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA 2588  
Db 17 TAAAAA 4

RESULT 609  
E02988  
LOCUS 17 bp DNA linear PAT 29-SEP-1997

JOURNAL Patent: WO 023069-A 18 25-APR-2002;  
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO  
MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU  
OGAWA, MASAYA OBYASHI, TAKESHI NAGASU, HIROHISA SAITO  
OS Artificial Sequence  
PN WO 023069-A/18  
PD 25-APR-2002  
PF 28-SEP-2001 WO 2001JP008574  
PR 13-OCT-2000 JP 00P 314093  
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBYASHI, PI  
TAKESHI NAGASU,  
PI HIROHISA SAITO  
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC  
A61K39/395,  
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08  
CC Description of Artificial Sequence: an artificially synthesized

CC anchor



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DEFINITION   DNA encoding DNA primer for typing DR antigen of human leukocyte
antigen.
ACCESSION    E02988
VERSION      E02988.1  GI:2171210
KEYWORDS     JP 1991164180-A/5.
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kashiwagi,N., Obata,B. and Abe,A.
TITLE        NEW DNA BASE SEQUENCE AND USE THEREOF
JOURNAL      Patent: JP 1991164180-A 5 16-JUL-1991;
COMMENT      KASHIWAGI NOBORU, KITASATO INST:THE
OS           Artificial gene
OC           Artificial sequence; Genes.
PN           JP 1991164180-A/5
PD           16-JUL-1991
PE           07-AUG-1990  JP 1990208901
PF           10-AUG-1989  JP 89P 207153
PI           KASHIWAGI NOBORU, OBATA BUNYA, ABE AKIO
PC           C12N15/12,C12N15/11,C12Q1/68;
CC           strandedness: Single;
CC           topology: Linear;
CC           hypothetical: No;
CC           anti-sense: No;
CC           *source: clone=PPR5;
FH           Key          Location/Qualifiers
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FT           /note='DNA primer for typing DR antigen of leukocyte antigen'
FT           /note='PPR5'.
FEATURES     Location/Qualifiers
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              /organism='synthetic construct'
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Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  31 GCAGAGCTGCTGAA 44
Db   4 GCAGAGCTGCTGAA 17

RESULT 610
E34258/c
LOCUS      E34258
DEFINITION Pollinosis-associated gene.
ACCESSION  E34258
VERSION     E34258.1  GI:18624263
KEYWORDS    JP 2000106879-A/2.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE       Pollinosis-associated gene
JOURNAL     Patent: JP 2000106879-A 2 18-APR-2000;
COMMENT     GENOX RESEARCH INC
OS           Artificial Sequence
PN           JP 2000106879-A/2
PD           18-APR-2000
PE           06-OCT-1998  JP 1998284610
PF           TAKESHI NAGASU YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI           MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI, YUKIHO IMAI,
PI           NING NO,
PI           KAORU OGAWA

DNA encoding DNA primer for typing DR antigen of human leukocyte
antigen.
ACCESSION    E02988
VERSION      E02988.1  GI:2171210
KEYWORDS     JP 1991164180-A/5.
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Kashiwagi,N., Obata,B. and Abe,A.
TITLE        NEW DNA BASE SEQUENCE AND USE THEREOF
JOURNAL      Patent: JP 1991164180-A 5 16-JUL-1991;
COMMENT      KASHIWAGI NOBORU, KITASATO INST:THE
OS           Artificial gene
OC           Artificial sequence; Genes.
PN           JP 1991164180-A/5
PD           16-JUL-1991
PE           07-AUG-1990  JP 1990208901
PF           10-AUG-1989  JP 89P 207153
PI           KASHIWAGI NOBORU, OBATA BUNYA, ABE AKIO
PC           C12N15/12,C12N15/11,C12Q1/68;
CC           strandedness: Single;
CC           topology: Linear;
CC           hypothetical: No;
CC           anti-sense: No;
CC           *source: clone=PPR5;
FH           Key          Location/Qualifiers
FT           misc_feature 1..17
FT           /note='DNA primer for typing DR antigen of leukocyte antigen'
FT           /note='PPR5'.
FEATURES     Location/Qualifiers
source       1..17
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              /mol_type='genomic DNA'
              /db_xref='taxon:32630'

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  31 GCAGAGCTGCTGAA 44
Db   4 GCAGAGCTGCTGAA 17

RESULT 610
E34258/c
LOCUS      E34258
DEFINITION Pollinosis-associated gene.
ACCESSION  E34258
VERSION     E34258.1  GI:18624263
KEYWORDS    JP 2000106879-A/2.
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE       Pollinosis-associated gene
JOURNAL     Patent: JP 2000106879-A 2 18-APR-2000;
COMMENT     GENOX RESEARCH INC
OS           Artificial Sequence
PN           JP 2000106879-A/2
PD           18-APR-2000
PE           06-OCT-1998  JP 1998284610
PF           TAKESHI NAGASU YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI           MASAYA ODAYASHI, SHIGEMICHI GUNJI, IZUMI ODAYASHI, YUKIHO IMAI,
PI           NING NO,
PI           KAORU OGAWA

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PC  C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC
FH   Key          Location/Qualifiers
FT   source       1..17
FT   /organism='Artificial Sequence'.
FEATURES     Location/Qualifiers
source       1..17
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              /db_xref='taxon:32630'

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2575 TAAAAA
Db   17 TAAAAA

RESULT 611
AR266625/c
LOCUS      AR266625
DEFINITION Sequence 63 from patent US 6495319.
ACCESSION  AR266625
VERSION     AR266625.1  GI:29695689
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     McClelland,M., Welsh,J. and Trenkle,T.
TITLE       Reduced complexity nucleic acid targets and methods of using same
JOURNAL     Patent: US 6495319-A 63 17-DEC-2002;
COMMENT     Location/Qualifiers
FEATURES     Location/Qualifiers
source       1..17
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Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2575 TAAAAA
Db   17 TAAAAA

RESULT 612
AX215415/c
LOCUS      AX215415
DEFINITION Sequence 857 from Patent WO0159103.
ACCESSION  AX215415
VERSION     AX215415.1  GI:15525458
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE       Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
JOURNAL     Patent: WO 0159103-A 857 16-AUG-2001;
COMMENT     RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ;
            Mcswiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES     Location/Qualifiers
source       1..17
              /organism='synthetic construct'
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Query Match      0.3%; Score 14; DB 1; Length 17;

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Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCCGCTCCGGGGCG 578  
 Db 17 GCCGCTCCGGGGCG 4

RESULT 613  
 AX216957/c  
 LOCUS AX216957 17 bp RNA linear PAT 07-SEP-2001  
 DEFINITION Sequence 2399 from Patent WO0159103.  
 ACCESSION AX216957  
 VERSION AX216957.1 GI:15527018  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B. M.  
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
 JOURNAL Patent: WO 0159103-A 2399 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
 Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"  
 /note="Nucleic Acid"

Query Match 0.3%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCCGCTCCGGGGCG 578  
 Db 16 GCCGCTCCGGGGCG 3

RESULT 614  
 AX216958/c  
 LOCUS AX216958 17 bp RNA linear PAT 07-SEP-2001  
 DEFINITION Sequence 2400 from Patent WO0159103.  
 ACCESSION AX216958  
 VERSION AX216958.1 GI:15527019  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B. M.  
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
 JOURNAL Patent: WO 0159103-A 2400 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES  
 Location/Qualifiers  
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 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"  
 /note="Nucleic Acid"

Query Match 0.3%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCCGCTCCGGGGCG 578  
 Db 15 GCCGCTCCGGGGCG 2

RESULT 615  
 AX532502/c  
 LOCUS AX532502 17 bp DNA linear PAT 22-NOV-2002  
 DEFINITION Sequence 2011 from Patent EP1239051.  
 ACCESSION AX532502  
 VERSION AX532502.1 GI:25256775  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Shannon, M.  
 TITLE Human posh-like protein 1  
 JOURNAL Patent: EP 1239051-A 2011 11-SEP-2002;  
 Aeomica, Inc. (US)

FEATURES  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 0.3%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1890 CACTGCCCTCTGCTG 1903  
 Db 17 CACTGCCCTCTGCTG 4

RESULT 616  
 AX532503/c  
 LOCUS AX532503 17 bp DNA linear PAT 22-NOV-2002  
 DEFINITION Sequence 2012 from Patent EP1239051.  
 ACCESSION AX532503  
 VERSION AX532503.1 GI:25256777  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Shannon, M.  
 TITLE Human posh-like protein 1  
 JOURNAL Patent: EP 1239051-A 2012 11-SEP-2002;  
 Aeomica, Inc. (US)

FEATURES  
 Location/Qualifiers  
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Query Match 0.3%; Score 14; DB 1; Length 17;  
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QY 1890 CACTGCCCTCTGCTG 1903  
 Db 16 CACTGCCCTCTGCTG 3

RESULT 617  
 AX532504/c  
 LOCUS AX532504 17 bp DNA linear PAT 22-NOV-2002  
 DEFINITION Sequence 2013 from Patent EP1239051.  
 ACCESSION AX532504  
 VERSION AX532504.1 GI:25256779  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



[illegible]

PI KAORU OGAWA,KEIKO MATSUI  
PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50  
CC Description of Artificial Sequence:Artificially Synthesized CC  
Primer Sequence

PH Key Location/Qualifiers.

FEATURES  
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/mol\_type="genomic DNA"  
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Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA AAAAAAAAAA 2588  
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Db 17 TAAAAA AAAAAAAAAA 4

RESULT 626  
BD091750/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

465, a novel gene related to pollen allergy.  
BD091750 17 bp DNA linear PAT 27-AUG-2002  
465, a novel gene related to pollen allergy  
BD091750  
BD091750.1 GI:22637361  
WO 0073439-A/2.  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 17)  
/organism="synthetic construct"  
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,  
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,  
Takahashi,E. and Yokoi,A.  
465, a novel gene related to pollen allergy  
Patent: WO 0073439-A 2 07-DEC-2000;  
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,  
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,  
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI  
TAKAHASHI,AKIRA YOKOI  
OS Artificial Sequence  
PN WO 0073439-A/2  
PD 07-DEC-2000  
PF 18-MAY-2000 WO 2000JP003191  
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,  
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,  
PI NEI YOSHIDA,  
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC  
C12N15/12,C12Q1/68,A61P37/08,A61K39/36,A61K45/00 CC Description  
of Artificial Sequence:Artificially Synthesized CC Primer  
Sequence

PH Key Location/Qualifiers.

FEATURES  
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/mol\_type="genomic DNA"  
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Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA AAAAAAAAAA 2588  
|||||  
Db 17 TAAAAA AAAAAAAAAA 4

RESULT 627  
BD091773/c  
LOCUS  
DEFINITION  
ACCESSION

787, a novel gene related to pollen allergy.  
BD091773 17 bp DNA linear PAT 27-AUG-2002  
787, a novel gene related to pollen allergy.  
BD091773

BD091773.1 GI:22637384  
WO 0073440-A/2.  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 17)  
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,  
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,  
Takahashi,E. and Yokoi,A.  
787, a novel gene related to pollen allergy  
Patent: WO 0073440-A 2 07-DEC-2000;  
GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,  
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,  
YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI  
TAKAHASHI,AKIRA YOKOI  
OS Artificial Sequence  
PN WO 0073440-A/2  
PD 07-DEC-2000  
PF 18-MAY-2000 WO 2000JP003192  
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,  
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,  
PI NEI YOSHIDA,  
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC  
C12N15/12,C12Q1/68,C12N5/08,C12N5/06,C07K14/415 CC Description of  
Artificial Sequence:Artificially Synthesized CC Primer Sequence  
FH Key Location/Qualifiers.

FEATURES  
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/mol\_type="genomic DNA"  
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Query Match 0.3%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAA AAAAAAAAAA 2588  
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Db 17 TAAAAA AAAAAAAAAA 4

RESULT 628  
BD097334/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Method for examination for allergosis.  
BD097334 17 bp DNA linear PAT 27-AUG-2002  
BD097334  
BD097334.1 GI:22642908  
WO 0165259-A/5.  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 17)  
Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.  
Patent: WO 0165259-A 5 07-SEP-2001;  
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA  
FUJIKI,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI  
OBAYASHI,KEIKO MATSUI, HIROHISA SAITO  
OS Artificial Sequence  
PN WO 0165259-A/5  
PD 07-SEP-2001  
PF 23-FEB-2001 WO 2001JP001372  
PI TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI  
HIROHISA SAITO  
PC G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,  
CC Description of Artificial Sequence:Artificially Synthesized CC  
Primer Sequence  
FH Key Location/Qualifiers  
FT source 1. .17

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FT /organism='Artificial Sequence'.
source Location/Qualifiers
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  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

Query Match      0.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2575 TAAAAAAAAAAAAA 2588
Db 17 TAAAAAAAAAAAAA 4

RESULT 629
AR266625
LOCUS AR266625 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 63 from patent US 6495319.
ACCESSION AR266625
VERSION AR266625.1 GI:29695689
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 63 17-DEC-2002;
FEATURES
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    /organism="unknown"
    /mol_type="genomic DNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3263 ATTTTTCCTTTTA 3279
Db 1 ATTTTTCCTTTTA 17

RESULT 630
AR8312
LOCUS AR8312 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 460 from Patent WO9833904.
ACCESSION AR8312
VERSION AR8312.1 GI:6736882
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 460 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2570 GTGTTTAAAAA 2586
Db 1 GTCTTTAAAAA 17

RESULT 633
AR053084
LOCUS AR053084 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 54 from patent US 5834181.
ACCESSION AR053084
VERSION AR053084.1 GI:5977946
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic alterations in nucleic acids
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RESULT 631
A90279
LOCUS A90279 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 460 from Patent EP0856579.
ACCESSION A90279
VERSION A90279.1 GI:6738793
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 460 05-AUG-1998;
BIOGOSTIK GES (DE)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2570 GTGTTTAAAAA 2586
Db 1 GTCTTTAAAAA 17

RESULT 632
AR040485
LOCUS AR040485 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1333 from patent US 5807743.
ACCESSION AR040485
VERSION AR040485.1 GI:5959848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 1333 15-SEP-1998;
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
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QY 3761 ACCTGGGTCCATCCTC 3777
Db 1 ACCTGGGTCCATCCTC 17

RESULT 633
AR053084
LOCUS AR053084 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 54 from patent US 5834181.
ACCESSION AR053084
VERSION AR053084.1 GI:5977946
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic alterations in nucleic acids
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JOURNAL Patent: US 5834181-A 54 10-NOV-1998;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
Db 1 GATTGTTTTTTGTTTC 17

RESULT 634
LOCUS AR065045 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 54 from patent US 5849483.
ACCESSION AR065045
VERSION AR065045.1 GI:5995261
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic
alterations in nucleic acids
JOURNAL Patent: US 5849483-A 54 15-DEC-1998;
FEATURES
  source      1. .17
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3620 GATTGTATATTGTTTC 3636
Db 1 GATTGTTTTTTGTTTC 17

RESULT 635
AR164696
LOCUS AR164696 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 7 from patent US 6274332.
ACCESSION AR164696
VERSION AR164696.1 GI:16237815
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human minK which cause
arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6274332-A 7 14-AUG-2001;
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCTCTGACCAAGCT 1360
Db 1 CAGATCTCTGAGGATGCT 17

RESULT 636
BD142809/c
LOCUS BD142809 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142809
VERSION BD142809.1 GI:23237754
KEYWORDS WO 0224903-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 3 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0224903-A/3
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP 00P 231318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
GOZO TSUJIMOTO, EIKI TAKAHASHI
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
C12Q1/68,
A01K67/027,A61K31/713,A61K45/00,A61P17/00,A61P37/08,
PC GOIN33/15,
PC GOIN33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized
primer
CC sequence
FH key Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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              Location/Qualifiers
Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 GAAAAAACAACCAACC 946
Db 17 GAAAAAACAACCAACC 1

RESULT 637
BD143835/c
LOCUS BD143835 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD143835
VERSION BD143835.1 GI:27849593
KEYWORDS JP 2002095500-A/3.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Tsujimoto,K.
TITLE Method of examining allergic disease
JOURNAL Patent: JP 2002095500-A 3 02-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT OS Artificial Sequence
PN JP 2002095500-A/3
PD 02-APR-2002
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PF 25-SEP-2000 JP 2000291316
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI KOZO TSUJINOTO
PC
C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
C07K14/47,
PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
,C12N15/09,C12P21/02,
PC C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
C12N15/00
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
/organism='Artificial Sequence'.

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Location/Qualifiers
/organism='synthetic construct'
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 GAAAAAAACAAACC 946
Db 17 GAAAAAAACAAACC 1

RESULT 638
BD167908/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167908
VERSION BD167908.1 GI:27873720
KEYWORDS WO 0226962-A/7,
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 7 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
C12Q1/68,
PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
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CC sequence primer
CC sequence Location/Qualifiers
FH Key 1..17
FT source /organism='Artificial Sequence'.

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 GAAAAAAACAAACC 946
Db 17 GAAAAAAACAAACC 1

RESULT 640
BD168112/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168112
VERSION BD168112
KEYWORDS WO 0233069-A/19,
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 GAAAAAAACAAACC 946
Db 17 GAAAAAAACAAACC 1

RESULT 639
BD167908/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167908
VERSION BD167908.1 GI:27873720
KEYWORDS WO 0226962-A/7,
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 7 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
C12Q1/68,
PC A01K67/027,A61K31/713,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
PC G01N33/15,
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CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
CC sequence Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 GAAAAAAACAAACC 946
Db 17 GAAAAAAACAAACC 1

RESULT 640
BD168112/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168112
VERSION BD168112
KEYWORDS WO 0233069-A/19,
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SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 17)  
Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.  
Method for examination for allergosis  
Patent: WO 023069-A 19 25-APR-2002;  
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA ODAYASHI, TAKESHI NAGASU, HIROHISA SAITO  
OS Artificial Sequence  
PN WO 023069-A/19  
PD 25-APR-2002  
PF 28-SEP-2001 WO 2001JP008574  
PR 13-OCT-2000 JP ODP 314093  
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA ODAYASHI, PI TAKESHI NAGASU,  
PI HIROHISA SAITO  
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC A61K39/395,  
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08  
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CC primer anchor  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 GAAAAAAACAAACC 946  
DB 17 GAAAAAAACAAACC 1

RESULT 641  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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BD171178  
Method of examining allergic disease.  
BD171178  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD171178 17 bp DNA linear PAT 17-JAN-2003  
Method of examining allergic disease.  
BD171178  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD171178.1 GI:27876990  
WO 0250269-A/3.  
synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 17)  
Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.  
Method of examining allergic disease  
Patent: WO 0250269-A 3 27-JUN-2002;  
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU, GOZO TSUJIMOTO  
OS Artificial Sequence  
PN WO 0250269-A/3  
PD 27-JUN-2002  
PF 21-DEC-2001 WO 2001JP011286  
PR 21-DEC-2000 JP ODP 389476  
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI TAKESHI NAGASU,  
PI GOZO TSUJIMOTO  
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,

PC A61P37/08,  
PC C12Q1/68, G01N33/50  
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
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QY 930 GAAAAAAACAAACC 946  
DB 17 GAAAAAAACAAACC 1

RESULT 642  
BD177281/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD177281  
Sulfotransferase for nonreducing beta-galactose and nucleic acid en coding the same.  
BD177281  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD177281.1 GI:30014542  
JP 2002300879-A/2.  
synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 17)  
Motoie,K.  
Sulfotransferase for nonreducing beta-galactose and nucleic acid en coding the same  
Patent: JP 2002300879-A 2 15-OCT-2002;  
J G S INC  
OS Artificial Sequence  
PN JP 2002300879-A/2  
PD 15-OCT-2002  
PF 03-APR-2001 JP 2001105201  
PI KOICHI MOTOIE  
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/10, C12Q1/68, C12N15/00,  
PC C12N5/00  
CC Oligonucleotide forward primer used in PCR for amplifying CC GP3ST cDNA  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2526 GACCATGATGTTTGCA 2542  
DB 17 GAACATGATGTTTGCA 1

RESULT 643  
BD201512  
LOCUS  
DEFINITION

BD201512  
Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.

ACCESSION BD201512  
VERSION BD201512.1 GI:33011282  
KEYWORDS JP 2002509721-A/4538.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.  
TITLE Method and reagent for treating diseases or conditions concerning  
molecule participating in vasculogenic response  
JOURNAL RIBOZYME PHARMACEUTICALS INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002509721-A/4538  
PD 02-APR-2002  
PF 24-MAR-1999 JP 2000541291  
PR 27-MAR-1998 US 60/079678  
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,  
PI JAMES A MCSWIGGEN  
PC  
C12N15/09, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC  
A61P29/00,  
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC  
C12N5/00  
CC Method and reagent for treating diseases or conditions CC  
CC participating in vasculogenic response  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3600 TTTTTCATGATCAT 3616  
Db 1 TTTTTCATGATCAT 17  
RESULT 644  
BD222807  
LOCUS  
DEFINITION KVLQTI-QT extension syndrome.  
ACCESSION BD222807  
VERSION BD222807.1 GI:33032577  
KEYWORDS JP 2002521045-A/5.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Keating, M.T., Sanguinetti, M.C., Karan, M.E., Landes, G.M.,  
Conners, T.D., Burn, T.C. and Splawski, I.  
TITLE KVLQTI-QT extension syndrome  
JOURNAL Patent: JP 2002521045-A 5 16-JUL-2002;  
UNIVERSITY OF UTAH RESEARCH FOUNDATION, GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002521045-A/5  
PD 16-JUL-2002  
PF 12-MAY-1999 JP 2000562052  
PR 29-JUL-1998 US 60/094477, 17-AUG-1998 US 09/135010 PI  
MARK T KEATING, MICHAEL C SANGUINETTI, MARK E KARAN, GREGORY M PI  
LANDES,  
PI TIMOTHY D CONNORS, TIMOTHY C BURN IGOR SPLAWSKI PC  
C12N15/09, A01K67/027, C07K14/46, C07K14/47, C07K16/18, C12N1/15, PC  
C12N1/19,

PC C12N1/21, C12N5/10, C12P21/08, C12Q1/02, C12Q1/68, G01N33/15, G01N33/PC  
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PC G01N33/53, G01N33/53, G01N33/566, G01N33/577, G01N33/58, G01N33/68,  
PC C12N15/00,  
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1344 CAGATCCTGAGCAAGCT 1360  
Db 1 CAGATCCTGAGGATGCT 17  
RESULT 645  
BD235082/c  
LOCUS  
DEFINITION A method for stimulating the immune system.  
ACCESSION BD235082  
VERSION BD235082.1 GI:33044852  
KEYWORDS JP 2002517434-A/186.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Schlingensiepen, K.H., Schlingensiepen, R. and Brysch, W.  
TITLE A method for stimulating the immune system  
JOURNAL Patent: JP 2002517434-A 186 18-JUN-2002;  
BIOLOGISTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Homo sapiens (human)  
PN JP 2002517434-A/186  
PD 18-JUN-2002  
PF 10-JUN-1999 JP 2000553044  
PR 10-JUN-1998 EP 98110709.7, 25-JUL-1998 EP 98113974.4 PI  
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI  
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PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/  
PC 00, A61P35/00,  
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1320 AAGCGATCGAGCCAT 1336  
Db 17 AAGCGATCGAGCCAT 1  
RESULT 646  
BD254578  
LOCUS  
DEFINITION A method for stimulating the immune system.  
ACCESSION BD254578  
VERSION BD254578.1 GI:33044852  
KEYWORDS JP 2002517434-A/186.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Schlingensiepen, K.H., Schlingensiepen, R. and Brysch, W.  
TITLE A method for stimulating the immune system  
JOURNAL Patent: JP 2002517434-A 186 18-JUN-2002;  
BIOLOGISTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Homo sapiens (human)  
PN JP 2002517434-A/186  
PD 18-JUN-2002  
PF 10-JUN-1999 JP 2000553044  
PR 10-JUN-1998 EP 98110709.7, 25-JUL-1998 EP 98113974.4 PI  
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI  
BRYSCH  
PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/  
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PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A  
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Db 17 AAGCGATCGAGCCAT 1  
RESULT 646  
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LOCUS  
DEFINITION A method for stimulating the immune system.  
ACCESSION BD254578  
VERSION BD254578.1 GI:33044852  
KEYWORDS JP 2002517434-A/186.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Schlingensiepen, K.H., Schlingensiepen, R. and Brysch, W.  
TITLE A method for stimulating the immune system  
JOURNAL Patent: JP 2002517434-A 186 18-JUN-2002;  
BIOLOGISTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT OS Homo sapiens (human)  
PN JP 2002517434-A/186  
PD 18-JUN-2002  
PF 10-JUN-1999 JP 2000553044  
PR 10-JUN-1998 EP 98110709.7, 25-JUL-1998 EP 98113974.4 PI  
KARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI  
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PC A61K45/06, A61K31/7088, A61K38/00, A61K39/395, A61K39/395, A61P31/  
PC 00, A61P35/00,  
PC A61P35/02, A61P37/02, C12N15/09, A61K37/02, C12N15/00 CC A  
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DEFINITION Regulation of repressor genes using nucleic acid molecules.  
 ACCESSION BD254578  
 VERSION BD254578.1 GI:33064348  
 KEYWORDS JP 2002541795-A/2371.  
 SOURCE unidentified  
 ORGANISM unidentified  
 1 (bases 1 to 17)  
 REFERENCE Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.  
 AUTHORS Regulation of repressor genes using nucleic acid molecules  
 TITLE Patent: JP 2002541795-A 2371 10-DEC-2002;  
 JOURNAL RIBOZYME PHARMACEUTICALS INC  
 COMMENT OS Eukaryote  
 PN JP 2002541795-A/2371  
 PD 10-DEC-2002  
 PF 11-APR-2000 JP 2000611654  
 PR 12-APR-1999 US 60/129390  
 PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC  
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC  
 C12P21/02,  
 PC  
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 C12R1:91),  
 PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,  
 PC A61K37/02,  
 PC (C12N5/00, C12R1:91)  
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 QY 3631 TGTTCCTTTAGCTGGC 3647  
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 Db 1 TGTTCCTTTAGCTGGC 17  
 RESULT 647  
 BD254579  
 LOCUS 17 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Regulation of repressor genes using nucleic acid molecules.  
 ACCESSION BD254579  
 VERSION BD254579.1 GI:33064349  
 KEYWORDS JP 2002541795-A/2372.  
 SOURCE unidentified  
 ORGANISM unidentified  
 1 (bases 1 to 17)  
 REFERENCE Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.  
 AUTHORS Regulation of repressor genes using nucleic acid molecules  
 TITLE Patent: JP 2002541795-A 2372 10-DEC-2002;  
 JOURNAL RIBOZYME PHARMACEUTICALS INC  
 COMMENT OS Eukaryote  
 PN JP 2002541795-A/2372  
 PD 10-DEC-2002  
 PF 11-APR-2000 JP 2000611654  
 PR 12-APR-1999 US 60/129390  
 PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC  
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC  
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 PC  
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 C12R1:91),  
 PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,  
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 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3632 GTTTCCTTTAGCTGGCC 3648  
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 Db 1 GTTTCCTTTAGCTGGCC 17  
 RESULT 648  
 BD254580  
 LOCUS 17 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Regulation of repressor genes using nucleic acid molecules.  
 ACCESSION BD254580  
 VERSION BD254580.1 GI:33064350  
 KEYWORDS JP 2002541795-A/2373.  
 SOURCE unidentified  
 ORGANISM unidentified  
 1 (bases 1 to 17)  
 REFERENCE Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.  
 AUTHORS Regulation of repressor genes using nucleic acid molecules  
 TITLE Patent: JP 2002541795-A 2373 10-DEC-2002;  
 JOURNAL RIBOZYME PHARMACEUTICALS INC  
 COMMENT OS Eukaryote  
 PN JP 2002541795-A/2373  
 PD 10-DEC-2002  
 PF 11-APR-2000 JP 2000611654  
 PR 12-APR-1999 US 60/129390  
 PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC  
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC  
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 PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,  
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 PC (C12N5/00, C12R1:91)  
 CC Regulation of repressor genes using nucleic acid molecules FH  
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 /db\_xref='taxon:32644'  
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 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
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 QY 3633 TTTTCCTTTAGCTGGCCA 3649  
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 Db 1 TTTTCCTTTAGCTGGCCA 17  
 RESULT 649  
 BD254790  
 LOCUS 17 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Regulation of repressor genes using nucleic acid molecules.  
 ACCESSION BD254790

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BD254790.1 GI:33064560
KEYWORDS JP 2002541795-A/2583.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2583 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2583
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
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C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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CC Regulation of repressor genes using nucleic acid molecules FH
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2593 AGAAAAAATCGGTAC 2609
Db 17 AGAAAAAATCTGAAC 1

RESULT 651
BD256406/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256406
VERSION BD256406.1 GI:33066176
KEYWORDS JP 2002541795-A/4199.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4199 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/4199
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
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C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,C12R1:91)
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
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Location/Qualifiers
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 TTTGCTCGGAGCAGAGC 37
Db 17 TTTGCTCGGAGTAGAGC 1

RESULT 652
BD256854/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256854
VERSION BD256854.1 GI:33066624
KEYWORDS JP 2002541795-A/4647.

BD255536
KEYWORDS JP 2002541795-A/3329.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3329 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/3329
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
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C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH

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SOURCE  
ORGANISM  
unidentified  
unclassified.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
TITLE  
Regulation of repressor genes using nucleic acid molecules  
JOURNAL  
Patent: JP 2002541795-A 4647 10-DEC-2002;  
RIBOZYME PHARMACEUTICALS INC  
COMMENT  
OS Eukaryote  
FN JP 2002541795-A/4647  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC  
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C12P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC  
C12R1:91),  
PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
PC A61K37/02,  
PC (C12N5/00,C12R1:91)  
CC Regulation of repressor genes using nucleic acid molecules FH  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 TTGTCTGGAGCAGAC 37  
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DB 17 TTGCTTGGAGTAGAC 1

RESULT 653  
BD257113/C  
LOCUS  
BD257113  
DEFINITION  
Regulation of repressor genes using nucleic acid molecules.  
ACCESSION  
BD257113  
VERSION  
BD257113.1 GI:33066883  
KEYWORDS  
JP 2002541795-A/4906.  
SOURCE  
unidentified  
unclassified.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
TITLE  
Regulation of repressor genes using nucleic acid molecules  
JOURNAL  
Patent: JP 2002541795-A 4906 10-DEC-2002;  
RIBOZYME PHARMACEUTICALS INC  
COMMENT  
OS Eukaryote  
FN JP 2002541795-A/4906  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC  
C12P21/02,  
PC  
C12P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC  
C12R1:91),  
PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
PC A61K37/02,  
PC (C12N5/00,C12R1:91)  
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1858 AAGACAGGAACCTGGGG 1874  
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DB 17 AAGACATGAACACGGGG 1

RESULT 654  
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LOCUS  
BD257474  
DEFINITION  
Regulation of repressor genes using nucleic acid molecules.  
ACCESSION  
BD257474  
VERSION  
BD257474.1 GI:33067244  
KEYWORDS  
JP 2002541795-A/5267.  
SOURCE  
unidentified  
unclassified.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
TITLE  
Regulation of repressor genes using nucleic acid molecules  
JOURNAL  
Patent: JP 2002541795-A 5267 10-DEC-2002;  
RIBOZYME PHARMACEUTICALS INC  
COMMENT  
OS Eukaryote  
FN JP 2002541795-A/5267  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PR 12-APR-1999 US 60/129390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC  
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C12P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC  
C12R1:91),  
PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
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PC (C12N5/00,C12R1:91)  
CC Regulation of repressor genes using nucleic acid molecules FH  
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QY 2338 CTTCCGCTTCCCTTGC 2354  
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DB 1 CTTCCCTTCCCTTCC 17

RESULT 655  
BD258338/c  
LOCUS  
BD258338  
DEFINITION  
Regulation of repressor genes using nucleic acid molecules.  
ACCESSION  
BD258338  
VERSION  
BD258338.1 GI:33068108  
KEYWORDS  
JP 2002541795-A/6131.  
SOURCE  
unidentified  
unclassified

|                       |  |        |        |                          |       |     |        |                 |
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| unclassified.         | 1. .17   | source | 1. .17 | /organism="unidentified" | 17 bp | DNA | linear | PAT 17-JUL-2003 |
| REFERENCE             | 1 (bases 1 to 17)  |        |        | /mol_type="genomic DNA"  |       |     |        |                 |
| AUTHORS               | Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.                      |        |        | /db_xref="taxon:32644"   |       |     |        |                 |
| TITLE                 | Regulation of repressor genes using nucleic acid molecules         |        |        |                          |       |     |        |                 |
| JOURNAL               | Patent: JP 2002541795-A 6131 10-DEC-2002;                          |        |        |                          |       |     |        |                 |
| COMMENT               | OS Eukaryote   |        |        |                          |       |     |        |                 |
|                       | FN JP 2002541795-A/6131  |        |        |                          |       |     |        |                 |
|                       | PD 10-DEC-2002   |        |        |                          |       |     |        |                 |
|                       | PF 11-APR-2000 JP 2000611654                                       |        |        |                          |       |     |        |                 |
|                       | PR 12-APR-1999 US 60/129390  |        |        |                          |       |     |        |                 |
|                       | PI LAWRENCE BLATT,MICHAEL,ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC    |        |        |                          |       |     |        |                 |
|                       | C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC     |        |        |                          |       |     |        |                 |
|                       | C12P21/02,   |        |        |                          |       |     |        |                 |
| PC                    | C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC |        |        |                          |       |     |        |                 |
|                       | C12R1:91),   |        |        |                          |       |     |        |                 |
| PC                    | (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,      |        |        |                          |       |     |        |                 |
| PC                    | A61K37/02,   |        |        |                          |       |     |        |                 |
| PC                    | (C12N5/00,C12R1:91)  |        |        |                          |       |     |        |                 |
| CC                    | Regulation of repressor genes using nucleic acid molecules FH      |        |        |                          |       |     |        |                 |
| Key                   | Location/Qualifiers  |        |        |                          |       |     |        |                 |
| FT                    | source   |        |        |                          |       |     |        |                 |
|                       | 1. .17   |        |        |                          |       |     |        |                 |
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| FEATURES              | Location/Qualifiers  |        |        |                          |       |     |        |                 |
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|                       | /mol_type="genomic DNA"  |        |        |                          |       |     |        |                 |
|                       | /db_xref="taxon:32644"   |        |        |                          |       |     |        |                 |
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| Best Local Similarity | 88.2%; Pred. No. 4.1e+02;  |        |        |                          |       |     |        |                 |
| Matches               | 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;                |        |        |                          |       |     |        |                 |
| Qy                    | 2812 AAACATCAAAACAAAC 2828   |        |        |                          |       |     |        |                 |
|                       |  |        |        |                          |       |     |        |                 |
| Db                    | 17 AAACAAACAAACAAAGC 1   |        |        |                          |       |     |        |                 |
| RESULT 656            |  |        |        |                          |       |     |        |                 |
| BD258340/C            |  |        |        |                          |       |     |        |                 |
| LOCUS                 | BD258340   |        |        |                          |       |     |        |                 |
| DEFINITION            | Regulation of repressor genes using nucleic acid molecules.        |        |        |                          |       |     |        |                 |
| ACCESSION             | BD258340   |        |        |                          |       |     |        |                 |
| VERSION               | BD258340.1 GI:33068110   |        |        |                          |       |     |        |                 |
| KEYWORDS              | JP 2002541795-A/6133.  |        |        |                          |       |     |        |                 |
| SOURCE                | unidentified   |        |        |                          |       |     |        |                 |
| ORGANISM              | unclassified.  |        |        |                          |       |     |        |                 |
| REFERENCE             | 1 (bases 1 to 17)  |        |        |                          |       |     |        |                 |
| AUTHORS               | Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.                      |        |        |                          |       |     |        |                 |
| TITLE                 | Regulation of repressor genes using nucleic acid molecules         |        |        |                          |       |     |        |                 |
| JOURNAL               | Patent: JP 2002541795-A 6133 10-DEC-2002;                          |        |        |                          |       |     |        |                 |
| COMMENT               | OS Eukaryote   |        |        |                          |       |     |        |                 |
|                       | FN JP 2002541795-A/6133  |        |        |                          |       |     |        |                 |
|                       | PD 10-DEC-2002   |        |        |                          |       |     |        |                 |
|                       | PF 11-APR-2000 JP 2000611654                                       |        |        |                          |       |     |        |                 |
|                       | PR 12-APR-1999 US 60/129390  |        |        |                          |       |     |        |                 |
|                       | PI LAWRENCE BLATT,MICHAEL,ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC    |        |        |                          |       |     |        |                 |
|                       | C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC     |        |        |                          |       |     |        |                 |
|                       | C12P21/02,   |        |        |                          |       |     |        |                 |
| PC                    | C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC |        |        |                          |       |     |        |                 |
|                       | C12R1:91),   |        |        |                          |       |     |        |                 |
| PC                    | (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,      |        |        |                          |       |     |        |                 |
| PC                    | A61K37/02,   |        |        |                          |       |     |        |                 |
| PC                    | (C12N5/00,C12R1:91)  |        |        |                          |       |     |        |                 |
| CC                    | Regulation of repressor genes using nucleic acid molecules FH      |        |        |                          |       |     |        |                 |
| Key                   | Location/Qualifiers  |        |        |                          |       |     |        |                 |
| FT                    | source   |        |        |                          |       |     |        |                 |
|                       | 1. .17   |        |        |                          |       |     |        |                 |
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| FEATURES              | Location/Qualifiers  |        |        |                          |       |     |        |                 |
| source                | 1. .17   |        |        |                          |       |     |        |                 |
|                       | /organism="unidentified"   |        |        |                          |       |     |        |                 |
|                       | /mol_type="genomic DNA"  |        |        |                          |       |     |        |                 |
|                       | /db_xref="taxon:32644"   |        |        |                          |       |     |        |                 |
| Query Match</         |  |        |        |                          |       |     |        |                 |

AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
 TITLE Regulation of repressor genes using nucleic acid molecules  
 JOURNAL Patent: JP 2002541795-A 6305 10-DEC-2002;  
 RIBOZYME PHARMACEUTICALS INC

COMMENT OS Eukaryote

PN JP 2002541795-A/6305  
 PD 10-DEC-2002  
 PF 11-APR-2000 JP 2000611654  
 PR 12-APR-1999 US 60/129390  
 PI LAWRENCE BLATT,MICHAEL,ZWICK,PAMELA,PAVCO,JAMES MCSWIGGEN PC  
 C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC  
 C12P21/02,

PC  
 C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC  
 C12R1:91),

PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
 PC A61K37/02,

PC (C12N5/00,C12R1:91)

CC Regulation of repressor genes using nucleic acid molecules FH

Key Location/Qualifiers

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FEATURES source

1..17 Location/Qualifiers  
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 /db\_xref="taxon:32644"

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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2572 GTTTAAAAA 2588

DB 17 GTATATAATAAAAA 1

RESULT 659  
 BD258513/c  
 LOCUS 17 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Regulation of repressor genes using nucleic acid molecules.

ACCESSION BD258513

VERSION BD258513.1 GI:33068283

KEYWORDS JP 2002541795-A/6306.

SOURCE unidentified

ORGANISM unclassified.

1 (bases 1 to 17)

REFERENCE Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

AUTHORS Regulation of repressor genes using nucleic acid molecules

TITLE Patent: JP 2002541795-A 6306 10-DEC-2002;

JOURNAL RIBOZYME PHARMACEUTICALS INC

COMMENT OS Eukaryote

PN JP 2002541795-A/6306

PD 10-DEC-2002

PF 11-APR-2000 JP 2000611654

PR 12-APR-1999 US 60/129390

PI LAWRENCE BLATT,MICHAEL,ZWICK,PAMELA,PAVCO,JAMES MCSWIGGEN PC

C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC

C12P21/02,

PC

C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC  
 C12R1:91),

PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,

PC A61K37/02,

PC (C12N5/00,C12R1:91)

CC Regulation of repressor genes using nucleic acid molecules FH

Key Location/Qualifiers

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FEATURES source

1..17 Location/Qualifiers  
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/mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
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QY 2571 TGTAAAAA 2587

DB 17 TGTATAATAATAAAAA 1

RESULT 660  
 BD258574

LOCUS

BD258574 17 bp DNA linear PAT 17-JUL-2003

DEFINITION Regulation of repressor genes using nucleic acid molecules.

ACCESSION BD258574

VERSION BD258574.1 GI:33068344

KEYWORDS JP 2002541795-A/6367.

SOURCE unidentified

ORGANISM unclassified.

1 (bases 1 to 17)

REFERENCE Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

AUTHORS Regulation of repressor genes using nucleic acid molecules

TITLE Patent: JP 2002541795-A 6367 10-DEC-2002;

JOURNAL RIBOZYME PHARMACEUTICALS INC

COMMENT OS Eukaryote

PN JP 2002541795-A/6367

PD 10-DEC-2002

PF 11-APR-2000 JP 2000611654

PR 12-APR-1999 US 60/129390

PI LAWRENCE BLATT,MICHAEL,ZWICK,PAMELA,PAVCO,JAMES MCSWIGGEN PC

C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC

C12P21/02,

PC

C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC  
 C12R1:91),

PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,

PC A61K37/02,

PC (C12N5/00,C12R1:91)

CC Regulation of repressor genes using nucleic acid molecules FH

Key Location/Qualifiers

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ORGANISM /organism='Eukaryote'.

FEATURES source

1..17 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"

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QY 3594 GGACATTTTAAAT 3610

DB 1 GCACATTTTAAAT 17

RESULT 661  
 BD258575

LOCUS

BD258575 17 bp DNA linear PAT 17-JUL-2003

DEFINITION Regulation of repressor genes using nucleic acid molecules.

ACCESSION BD258575

VERSION BD258575.1 GI:33068345

KEYWORDS JP 2002541795-A/6368.

SOURCE unidentified

ORGANISM unclassified.

1 (bases 1 to 17)

REFERENCE Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

AUTHORS Regulation of repressor genes using nucleic acid molecules

TITLE Patent: JP 2002541795-A 6368

JOURNAL Patent: JP 2002541795-A 6368 10-DEC-2002;  
 RIBOZYME PHARMACEUTICALS INC  
 COMMENT OS Eukaryote  
 PN JP 2002541795-A/6368  
 PD 10-DEC-2002  
 PF 11-APR-2000 JP 2000611654  
 PR 12-APR-1999 US 60/129390  
 PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
 C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC  
 C12P21/02,  
 PC  
 C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1.91),(C12P21/02, PC  
 C12R1.91),  
 PC (C12P21/02,C12R1.91),(C12P21/02,C12R1.91),C12N15/00,C12N5/00,  
 PC A61K37/02  
 PC (C12N5/00,C12R1.91)  
 CC Regulation of repressor genes using nucleic acid molecules FH  
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 FT source 1..17  
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 /organism='unidentified'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'  
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 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4074 CACCTTTTCTTTAATT 4090  
 Db 1 CACATTTTCTTTAATT 17  
 RESULT 662  
 CQ615503  
 LOCUS 17 bp DNA linear PAT 02-FEB-2004  
 DEFINITION Sequence 243 from Patent WO0192524.  
 ACCESSION CQ615503  
 VERSION CQ615503.1 GI:41665721  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Myosin-like gene expressed in human heart and muscle  
 JOURNAL Patent: WO 0192524-A 243 06-DEC-2001;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism='Homo sapiens'  
 /mol\_type='unassigned DNA'  
 /db\_xref='taxon:9606'  
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 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 496 ATCCTCGCCGCTGCTC 512  
 Db 1 ATCCTCGCCCTCTCTC 17  
 RESULT 663  
 CQ616325/c  
 LOCUS 17 bp DNA linear PAT 02-FEB-2004  
 DEFINITION Sequence 1065 from Patent WO0192524.  
 ACCESSION CQ616325  
 VERSION CQ616325.1 GI:41666543

KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Myosin-like gene expressed in human heart and muscle  
 JOURNAL Patent: WO 0192524-A 1065 06-DEC-2001;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
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 /organism='Homo sapiens'  
 /mol\_type='unassigned DNA'  
 /db\_xref='taxon:9606'  
 Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2713 CTACTTCTTAAGAGACA 2729  
 Db 17 CTAGTCCTTAGAGACA 1  
 RESULT 664  
 CQ616326/c  
 LOCUS 17 bp DNA linear PAT 02-FEB-2004  
 DEFINITION Sequence 1066 from Patent WO0192524.  
 ACCESSION CQ616326  
 VERSION CQ616326.1 GI:41666544  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Myosin-like gene expressed in human heart and muscle  
 JOURNAL Patent: WO 0192524-A 1066 06-DEC-2001;  
 Aeomica, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism='Homo sapiens'  
 /mol\_type='unassigned DNA'  
 /db\_xref='taxon:9606'  
 Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2712 CCTACTTCTTAAGAGAC 2728  
 Db 17 CCTACGTCCTTAGAGAC 1  
 RESULT 665  
 CQ617482  
 LOCUS 17 bp DNA linear PAT 02-FEB-2004  
 DEFINITION Sequence 2222 from Patent WO0192524.  
 ACCESSION CQ617482  
 VERSION CQ617482.1 GI:41667700  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
 TITLE Myosin-like gene expressed in human heart and muscle



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JOURNAL Patent: WO 0192524-A 2222 06-DEC-2001;
FEATURES   Location/Qualifiers
source     1..17
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 675 GTGTGAAGCGAGGCC 691
Db 1 GTGTGATGCAGGGTC 17

RESULT 666
LOCUS      CQ623817      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 8557 from Patent WO0192524.
ACCESSION  CQ623817
VERSION    CQ623817.1 GI:41674035
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE     Myosin-like gene expressed in human heart and muscle
JOURNAL   Patent: WO 0192524-A 8557 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
source     1..17
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2519 CGATGACGACCATGATG 2535
Db 1 CGATGAGGACCGAGTG 17

RESULT 667
LOCUS      CQ624486      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 9226 from Patent WO0192524.
ACCESSION  CQ624486
VERSION    CQ624486.1 GI:41674704
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE     Myosin-like gene expressed in human heart and muscle
JOURNAL   Patent: WO 0192524-A 9226 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
source     1..17
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2519 CGATGACGACCATGATG 2535
Db 1 CGATGAGGACCGAGTG 17

RESULT 668
LOCUS      CQ625768      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 10508 from Patent WO0192524.
ACCESSION  CQ625768
VERSION    CQ625768.1 GI:41675986
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE     Myosin-like gene expressed in human heart and muscle
JOURNAL   Patent: WO 0192524-A 10508 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
source     1..17
            /organism="Homo sapiens"
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2928 CTCCCGTCCTTCCTC 2944
Db 17 CTCCCGTCCTTCCTC 1

RESULT 669
LOCUS      CQ625769      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 10509 from Patent WO0192524.
ACCESSION  CQ625769
VERSION    CQ625769.1 GI:41675987
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  1
AUTHORS   Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
            Shannon, M.E.
TITLE     Myosin-like gene expressed in human heart and muscle
JOURNAL   Patent: WO 0192524-A 10509 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
source     1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2927 CCTCCCGTCCTTCCT 2943
Db 17 CCTCCCGTCCTTCCT 1

RESULT 670
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CQ868213  
 LOCUS CQ868213 17 bp DNA linear PAT 13-SEP-2004  
 DEFINITION Sequence 7 from Patent EP1454915.  
 ACCESSION CQ868213  
 VERSION CQ868213.1 GI:51998263  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Canis familiaris (dog)  
 Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1  
 Murayama,M. and Ito,S.  
 Polynucleotides, polypeptides and method for screening for  
 useful dog candidates  
 Patent: EP 1454915-A 7 08-SEP-2004;  
 President of Gifu University (JP)  
 JOURNAL  
 FEATURES  
 source  
 1..17  
 Location/Qualifiers  
 intron  
 1..17  
 /note="Polymorphic region of Dopamine Receptor D4 Intron"  
 Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
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 QY 589 CCGCGGCTGCCAGGC 605  
 Db 1 CCGCGGCTGCCAGGC 17  
 RESULT 671  
 E34259/c  
 LOCUS E34259 17 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Pollinosis-associated gene.  
 ACCESSION E34259  
 VERSION E34259.1 GI:18624264  
 KEYWORDS JP 2000106879-A/3.  
 SOURCE  
 ORGANISM  
 synthetic construct  
 synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 17)  
 Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,  
 Gunji,S., Obayashi,I., Imai,Y., No.N. and Ogawa,K.  
 Pollinosis-associated gene  
 Patent: JP 2000106879-A 3 18-APR-2000;  
 GENOX RESEARCH INC  
 COMMENT  
 OS Artificial Sequence  
 PN JP 2000106879-A/3  
 PD 18-APR-2000  
 PE 06-OCT-1998 JP 1998284610  
 PR  
 PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,  
 PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,  
 PI NING NO,  
 PI KAORU OGAWA  
 PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC  
 FH Key Location/Qualifiers  
 FT source 1..17  
 FT /organism='Artificial Sequence'.  
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 /db\_xref="taxon:32630"  
 Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 GAAAAAACAACACC 946  
 Db 17 GAAAAAACAACACC 1  
 RESULT 672  
 I32590  
 LOCUS I32590 17 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 54 from patent US 5589330.  
 ACCESSION I32590  
 VERSION I32590.1 GI:1823381  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Unknown.  
 Unknow.  
 Unclassified.  
 1 (bases 1 to 17)  
 Shuber,A.P.  
 High-throughput screening method for sequence or genetic  
 alterations in nucleic acids using elution and sequencing of  
 complementary oligonucleotides  
 Patent: US 5589330-A 54 31-DEC-1996;  
 Location/Qualifiers  
 1..17  
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 Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3620 GATTGTATTTGTTTC 3636  
 Db 1 GATTGTATTTGTTTC 17  
 RESULT 673  
 AR186202/c  
 LOCUS AR186202 17 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 1690 from patent US 6346398.  
 ACCESSION AR186202  
 VERSION AR186202.1 GI:20232167  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Unknown.  
 Unknow.  
 Unclassified.  
 1 (bases 1 to 17)  
 Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
 Method and reagent for the treatment of diseases or conditions  
 related to levels of vascular endothelial growth factor receptor  
 Patent: US 6346398-A 1690 12-FEB-2002;  
 Location/Qualifiers  
 1..17  
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 Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
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 QY 4228 AGGTTTTCAGACACATT 4244  
 Db 17 AGGTTTTCAGACACATT 1  
 RESULT 674  
 AR186698/c  
 LOCUS AR186698 17 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 2186 from patent US 6346398.  
 ACCESSION AR186698  
 VERSION AR186698.1 GI:20232663  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Unknown.  
 Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 2186 12-FEB-2002;  
FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2800 GTCAAAAAAAAAAACA 2816  
Db 17 GTCAAAAAAAAAAGCA 1

RESULT 675  
AR186827  
LOCUS 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2315 from patent US 6346398.  
ACCESSION AR186827  
VERSION AR186827.1 GI:20232792  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 2315 12-FEB-2002;  
FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 862 ACTGAACCTCAATTCCTT 878  
Db 1 ACTTAACCAATTCCTT 17

RESULT 676  
AR187056/c  
LOCUS 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2544 from patent US 6346398.  
ACCESSION AR187056  
VERSION AR187056.1 GI:20233021  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 2544 12-FEB-2002;  
FEATURES Location/Qualifiers  
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1. .17  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2579 AAAAAAAAAAATTGGAGA 2595  
Db 17 AAAAAAAAAAAGTAGAGA 1

RESULT 677  
AR187057/c  
LOCUS 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2545 from patent US 6346398.  
ACCESSION AR187057  
VERSION AR187057.1 GI:20233022  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 2545 12-FEB-2002;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2578 AAAAAAAAAAATTGGAG 2594  
Db 17 AAAAAAAAAAAGTAGAG 1

RESULT 678  
AR187058/c  
LOCUS 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2546 from patent US 6346398.  
ACCESSION AR187058  
VERSION AR187058.1 GI:20233023  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 2546 12-FEB-2002;  
FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAAAAAATTGGA 2593  
Db 17 AAAAAAAAAAAGTAGA 1

RESULT 679  
AR187059/c  
LOCUS 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2547 from patent US 6346398.  
ACCESSION AR187059  
VERSION AR187059.1 GI:20233024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.



AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 4005 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1811 GCTCTCTTTCGACGTGA 1827  
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Db 1 GATCTCTTCCACGTGA 17  
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RESULT 685  
LOCUS AR188526 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 4014 from patent US 6346398.  
ACCESSION AR188526  
VERSION AR188526.1 GI:20234491  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 4014 12-FEB-2002;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1849 TTCACCACAAAGACAGG 1865  
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Db 17 TGCACCACAAAGACAGC 1  
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RESULT 686  
LOCUS AR188812 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 4300 from patent US 6346398.  
ACCESSION AR188812  
VERSION AR188812.1 GI:20234777  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 4300 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4030 TATGAGCTCTCTTTGCC 4046  
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Db 1 TCTGGACTCTCTCTGCC 17  
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RESULT 687  
LOCUS AR190075 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 5563 from patent US 6346398.  
ACCESSION AR190075  
VERSION AR190075.1 GI:20236040  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 5563 12-FEB-2002;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 246 TGGAGCTAGGAGAGC 262  
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Db 1 TGCACCTAGAGAGAGC 17  
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RESULT 688  
LOCUS AR190475 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 5963 from patent US 6346398.  
ACCESSION AR190475  
VERSION AR190475.1 GI:20236440  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 5963 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4035 ACTCTCTTTGGCGTTCA 4051  
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Db 1 ACTCTCTTTCCATTCA 17  
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RESULT 689  
LOCUS AR192138 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 7626 from patent US 6346398.  
ACCESSION AR192138  
VERSION AR192138.1 GI:20238103  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.

|                         |                            |   |                      |  |  |
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| TITLE                   |                            | Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor |                      |  |  |
| JOURNAL                 |                            | Patent: US 6346398-A 7626 12-FEB-2002;  |                      |  |  |
| FEATURES                | source                     | Location/Qualifiers   |                      |  |  |
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| Query Match             |                            | 0.3%; Score 13.8; DB 1; Length 17;  |                      |  |  |
| Best Local Similarity   |                            | 88.2%; Pred. No. 4.1e+02;   |                      |  |  |
| Matches                 | 15;                        | Conservative  | 0; Gaps 0; Indels 0; |  |  |
| Qy                      |                            | 34 GAGCTGCTGAAACTGCC 50   |                      |  |  |
| Db                      | 17                         | GAGCTGCTGACACTGTC 1   |                      |  |  |
| RESULT 690              |                            | AR196413  |                      |  |  |
| LOCUS                   | DEFINITION                 | Sequence 878 from patent US 6350934.  |                      |  |  |
| ACCESSION               |                            | AR196413  |                      |  |  |
| VERSION                 | KEYWORDS                   | AR196413.1 GI:20245850  |                      |  |  |
| SOURCE                  |                            | Unknown.  |                      |  |  |
| ORGANISM                | REFERENCE                  | Unclassified.   |                      |  |  |
| 1 (bases 1 to 17)       |                            | Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens., Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.      |                      |  |  |
| AUTHORS                 | TITLE                      | Nucleic acid encoding delta-9 desaturase  |                      |  |  |
| JOURNAL                 |                            | Patent: US 6350934-A 878 26-FEB-2002;   |                      |  |  |
| FEATURES                | Location/Qualifiers        |   |                      |  |  |
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| Query Match             | Best Local Similarity      | 0.3%; Score 13.8; DB 1; Length 17;  |                      |  |  |
| Matches                 |                            | 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;   |                      |  |  |
| Qy                      | 931                        | AAAAAAAAAACCAACCT 947   |                      |  |  |
| Db                      |                            | 17 AAAAAATAAAAAACAAGCT 1  |                      |  |  |
| RESULT 691              | LOCUS                      | AR218660  |                      |  |  |
| DEFINITION              |                            | Sequence 7 from patent US 6420124.  |                      |  |  |
| ACCESSION               | VERSION                    | AR218660  |                      |  |  |
| KEYWORDS                |                            | AR218660.1 GI:23319555  |                      |  |  |
| SOURCE                  | ORGANISM                   | Unknown.  |                      |  |  |
| Unclassified.           |                            | 1 (bases 1 to 17)   |                      |  |  |
| REFERENCE               | AUTHORS                    | Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.                               |                      |  |  |
| TITLE                   |                            | KVLQT1--a long qt syndrome gene   |                      |  |  |
| JOURNAL                 | FEATURES                   | Patent: US 6420124-A 7 16-JUL-2002;   |                      |  |  |
| source                  |                            | Location/Qualifiers   |                      |  |  |
| 1..17                   | /organism="unknown"        |   |                      |  |  |
| /mol_type="genomic DNA" |                            |   |                      |  |  |
| Query Match             | Best Local Similarity      | 0.3%; Score 13.8; DB 1; Length 17;  |                      |  |  |
| Matches                 |                            | 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;   |                      |  |  |
| Qy                      | 1344                       | CAGATCCTGAGCAAGCT 1360  |                      |  |  |
| Db                      |                            | 1 CAGATCCTGAGGATGCT 17  |                      |  |  |
| RESULT 694              | LOCUS                      | AR241830/c  |                      |  |  |
| DEFINITION              |                            | Sequence 118 from patent US 6472154.  |                      |  |  |
| ACCESSION               | VERSION                    | AR241830  |                      |  |  |
| KEYWORDS                |                            | AR241830.1 GI:27287642  |                      |  |  |
| SOURCE                  | ORGANISM                   | Unknown.  |                      |  |  |
| Unclassified.           |                            | 1 (bases 1 to 17)   |                      |  |  |
| REFERENCE               | AUTHORS                    | Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.   |                      |  |  |
| TITLE                   |                            | Polymorphic repeats in human genes  |                      |  |  |

|                       |   |                                      |       |     |        |                 |
|-----------------------|---|--------------------------------------|-------|-----|--------|-----------------|
| RESULT 692            | AR223075  | Sequence 7 from patent US 6432644.   | 17 bp | DNA | linear | PAT 26-SEP-2002 |
| LOCUS                 | AR223075  |                                      |       |     |        |                 |
| DEFINITION            | Sequence 7 from patent US 6432644.  |                                      |       |     |        |                 |
| ACCESSION             | AR223075  |                                      |       |     |        |                 |
| VERSION               | AR223075.1  | GI:23330928                          |       |     |        |                 |
| KEYWORDS              | Unknown.  |                                      |       |     |        |                 |
| SOURCE                | Unknown.  |                                      |       |     |        |                 |
| ORGANISM              | Unclassified.   |                                      |       |     |        |                 |
| REFERENCE             | 1 (bases 1 to 17)   |                                      |       |     |        |                 |
| AUTHORS               | Keating,M.T., Sanguinetti,M.C. and Splawski,I.  |                                      |       |     |        |                 |
| TITLE                 | Mutations in the KCNE1 gene encoding human minK which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene |                                      |       |     |        |                 |
| JOURNAL               | Patent: US 6432644-A 7 13-AUG-2002;   |                                      |       |     |        |                 |
| FEATURES              | Location/Qualifiers   |                                      |       |     |        |                 |
|                       | 1..17   | /organism="unknown"                  |       |     |        |                 |
| source                | /mol_type="genomic DNA"   |                                      |       |     |        |                 |
| Query Match           | 0.3%; Score 13.8; DB 1; Length 17;  |                                      |       |     |        |                 |
| Best Local Similarity | 88.2%; Pred. No. 4.1e+02;   |                                      |       |     |        |                 |
| Matches               | 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;   |                                      |       |     |        |                 |
| Qy                    | 1344 CAGATCCTGAGCAAGCT 1360   |                                      |       |     |        |                 |
| Db                    | 1 CAGATCCTGAGGATGCT 17  |                                      |       |     |        |                 |
| RESULT 693            | AR229837  | Sequence 7 from patent US 6451534.   | 17 bp | DNA | linear | PAT 20-DEC-2002 |
| LOCUS                 | AR229837  |                                      |       |     |        |                 |
| DEFINITION            | Sequence 7 from patent US 6451534.  |                                      |       |     |        |                 |
| ACCESSION             | AR229837  |                                      |       |     |        |                 |
| VERSION               | AR229837.1  | GI:27269715                          |       |     |        |                 |
| KEYWORDS              | Unknown.  |                                      |       |     |        |                 |
| SOURCE                | Unknown.  |                                      |       |     |        |                 |
| ORGANISM              | Unclassified.   |                                      |       |     |        |                 |
| REFERENCE             | 1 (bases 1 to 17)   |                                      |       |     |        |                 |
| AUTHORS               | Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.                               |                                      |       |     |        |                 |
| TITLE                 | KVLQT1--a long QT syndrome gene   |                                      |       |     |        |                 |
| JOURNAL               | Patent: US 6451534-A 7 17-SEP-2002;   |                                      |       |     |        |                 |
| FEATURES              | Location/Qualifiers   |                                      |       |     |        |                 |
|                       | 1..17   | /organism="unknown"                  |       |     |        |                 |
| source                | /mol_type="genomic DNA"   |                                      |       |     |        |                 |
| Query Match           | 0.3%; Score 13.8; DB 1; Length 17;  |                                      |       |     |        |                 |
| Best Local Similarity | 88.2%; Pred. No. 4.1e+02;   |                                      |       |     |        |                 |
| Matches               | 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;   |                                      |       |     |        |                 |
| Qy                    | 1344 CAGATCCTGAGCAAGCT 1360   |                                      |       |     |        |                 |
| Db                    | 1 CAGATCCTGAGGATGCT 17  |                                      |       |     |        |                 |
| RESULT 694            | AR241830/c  | Sequence 118 from patent US 6472154. | 17 bp | DNA | linear | PAT 20-DEC-2002 |
| LOCUS                 | AR241830  |                                      |       |     |        |                 |
| DEFINITION            | Sequence 118 from patent US 6472154.  |                                      |       |     |        |                 |
| ACCESSION             | AR241830  |                                      |       |     |        |                 |
| VERSION               | AR241830.1  | GI:27287642                          |       |     |        |                 |
| KEYWORDS              | Unknown.  |                                      |       |     |        |                 |
| SOURCE                | Unknown.  |                                      |       |     |        |                 |
| ORGANISM              | Unclassified.   |                                      |       |     |        |                 |
| REFERENCE             | 1 (bases 1 to 17)   |                                      |       |     |        |                 |
| AUTHORS               | Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.   |                                      |       |     |        |                 |
| TITLE                 | Polymorphic repeats in human genes  |                                      |       |     |        |                 |

JOURNAL Patent: US 6472154-A 118 29-OCT-2002;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGAGRAAAAAAAAAACA 943  
Db 17 GGAAAAAAAAAAAAAAAAA 1

RESULT 695  
AR262093 AR262093 17 bp DNA linear PAT 29-JAN-2003  
LOCUS Sequence 7 from patent US 6323026.  
DEFINITION AR262093  
ACCESSION AR262093  
VERSION AR262093.1 GI:28073454  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.  
TITLE Mutations in the KCNE1 gene encoding human mink which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene  
JOURNAL Patent: US 6323026-A 7 27-NOV-2001;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCCTGAGCAAGCT 1360  
Db 1 CAGATCCTGAGGATGCT 17

RESULT 696  
AR286385/c AR286385 17 bp RNA linear PAT 10-APR-2003  
LOCUS Sequence 757 from patent US 6528640.  
DEFINITION AR286385  
ACCESSION AR286385  
VERSION AR286385.1 GI:29723981  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Synthetic ribonucleic acids with RNase activity  
JOURNAL Patent: US 6528640-A 757 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3204 GCCATATGCCAGAAG 3220  
Db 17 GGCAGATGCCAGAAG 1

RESULT 697  
AR322833/c AR322833 17 bp RNA linear PAT 17-AUG-2003  
LOCUS Sequence 235 from patent US 6566127.  
DEFINITION AR322833  
ACCESSION AR322833  
VERSION AR322833.1 GI:33708641  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 235 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4228 AGGTTTGAAGACATT 4244  
Db 17 AGGTTTGAAGACATT 1

RESULT 698  
AR323329/c AR323329 17 bp RNA linear PAT 17-AUG-2003  
LOCUS Sequence 731 from patent US 6566127.  
DEFINITION AR323329  
ACCESSION AR323329  
VERSION AR323329.1 GI:33709137  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 731 20-MAY-2003;  
FEATURES Location/Qualifiers  
source 1. .17  
/organism="unknown"  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2800 GTGAAAAAAAAAAAAACA 2816  
Db 17 GTCAAAAAAAAAAAGCA 1

RESULT 699  
AR323458 AR323458 17 bp RNA linear PAT 17-AUG-2003  
LOCUS Sequence 860 from patent US 6566127.  
DEFINITION AR323458  
ACCESSION AR323458  
VERSION AR323458.1 GI:33709266  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 860 20-MAY-2003;

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FEATURES.  
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        /mol_type="unassigned RNA"  
  
Query Match      0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 862 ACTGAAGTCCATTCTT 878  
Db 1 ACTTAAGTCAATTCTT 17  
  
RESULT 700  
AR323666/c  
LOCUS AR323666 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1068 from patent US 6566127.  
ACCESSION AR323666  
VERSION AR323666.1 GI:33709474  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1068 20-MAY-2003;  
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        /mol_type="unassigned RNA"  
  
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2579 AAAAAAAATTCGAGA 2595  
Db 17 AAAAAAAAGTAGAGA 1  
  
RESULT 701  
AR323667/c  
LOCUS AR323667 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1069 from patent US 6566127.  
ACCESSION AR323667  
VERSION AR323667.1 GI:33709475  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1069 20-MAY-2003;  
FEATURES  
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        /mol_type="unassigned RNA"  
  
Query Match      0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2578 AAAAAAAATTCGAG 2594  
Db 17 AAAAAAAAGTAGAG 1  
  
RESULT 702  
AR323668/c  
LOCUS AR323668 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1070 from patent US 6566127.  
ACCESSION AR323668  
VERSION AR323668.1 GI:33709476  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1070 20-MAY-2003;  
FEATURES  
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        /mol_type="unassigned RNA"  
  
Query Match      0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2577 AAAAAAAATTCGA 2593  
Db 17 AAAAAAAAGTAGA 1  
  
RESULT 703  
AR323669/c  
LOCUS AR323669 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1071 from patent US 6566127.  
ACCESSION AR323669  
VERSION AR323669.1 GI:33709477  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1071 20-MAY-2003;  
FEATURES  
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    Location/Qualifiers  
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        /mol_type="unassigned RNA"  
  
Query Match      0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2576 AAAAAAAATTCG 2592  
Db 17 AAAAAAAAGTAG 1  
  
RESULT 704  
AR323673/c  
LOCUS AR323673 17 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 1075 from patent US 6566127.  
ACCESSION AR323673  
VERSION AR323673.1 GI:33709481  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 1075 20-MAY-2003;  
FEATURES  
  source  
    Location/Qualifiers
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source 1..17
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/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 GAGAAAAAACAACAA 944
Db 17 GAAAAAACAACAA 1

RESULT 705
AR323674/c
LOCUS AR323674 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1076 from patent US 6566127.
ACCESSION AR323674
VERSION AR323674.1 GI:33709482
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 927 GGAGAAAAAACAACAA 943
Db 17 GGAGAAAAAACAACAA 1

RESULT 706
AR323678/c
LOCUS AR323678 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1080 from patent US 6566127.
ACCESSION AR323678
VERSION AR323678.1 GI:33709486
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1080 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2798 ATGTGAAAAAACAACAA 2814
Db 17 ATTTGAAAAAACAACAA 1

RESULT 707
AR323849
LOCUS AR323849 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1251 from patent US 6566127.
ACCESSION AR323849
VERSION AR323849.1 GI:33709657
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1251 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3702 TTTTATATATCTTC 3718
Db 1 TTTGTATACCATCTTC 17

RESULT 708
AR324370
LOCUS AR324370 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1772 from patent US 6566127.
ACCESSION AR324370
VERSION AR324370.1 GI:33710178
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1772 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
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Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 GCTCTCTTTCGACGTGA 1827
Db 1 GATCTCTTCCACGTGA 17

RESULT 709
AR324379/c
LOCUS AR324379 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1781 from patent US 6566127.
ACCESSION AR324379
VERSION AR324379.1 GI:33710187
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1781 20-MAY-2003;
FEATURES Location/Qualifiers
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Query Match
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1849 TTCACCAACAAAGACAGG 1865
Db 17 TGCACCAACAAAGACAG 1

RESULT 710
LOCUS AR324665 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2067 from patent US 6566127.
ACCESSION AR324665
VERSION AR324665.1 GI:33710473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2067 20-MAY-2003;
FEATURES
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    /mol_type="unassigned RNA"

Query Match
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTTGCCGTTCA 4051
Db 1 ACTCTCTTTTCCATTCA 17

RESULT 713
LOCUS AR326016/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3418 from patent US 6566127.
ACCESSION AR326016
VERSION AR326016.1 GI:33711824
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3418 20-MAY-2003;
FEATURES
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Query Match
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4030 TATGGACTCTCTTGCC 4046
Db 1 TCTGGACTCTCTTGCC 17

RESULT 711
LOCUS AR325051 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2453 from patent US 6566127.
ACCESSION AR325051
VERSION AR325051.1 GI:33710859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2453 20-MAY-2003;
FEATURES
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Query Match
  0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 246 TGGAGCTAGGAGAAGC 262
Db 1 TGGAGCTAGGAGAAGC 17

RESULT 712
LOCUS AR325398 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5235 from patent US 6566127.
ACCESSION AR325398
VERSION AR325398.1 GI:33713641
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5235 20-MAY-2003;
FEATURES
  Location/Qualifiers
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    /mol_type="unassigned RNA"

DEFINITION Sequence 2800 from patent US 6566127.
ACCESSION AR325398
VERSION AR325398.1 GI:33711206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2800 20-MAY-2003;
FEATURES
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Query Match
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4035 ACTCTCTTTGCCGTTCA 4051
Db 1 ACTCTCTTTTCCATTCA 17

RESULT 713
LOCUS AR326016/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3418 from patent US 6566127.
ACCESSION AR326016
VERSION AR326016.1 GI:33711824
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3418 20-MAY-2003;
FEATURES
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    /mol_type="unassigned RNA"

Query Match
  0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAAACTGCC 50
Db 17 GAGCTGCTGACACTGTC 1

RESULT 714
LOCUS AR327833 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5235 from patent US 6566127.
ACCESSION AR327833
VERSION AR327833.1 GI:33713641
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5235 20-MAY-2003;
FEATURES
  Location/Qualifiers
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/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 861 CACTGAACCTCCATTCT 877
Db 1 CACTTAACCTCAATTCT 17

RESULT 715
AR328033/c
LOCUS AR328033 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5435 from patent US 6566127.
ACCESSION AR328033
VERSION AR328033.1 GI:33713841
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5435 20-MAY-2003;
FEATURES Location/Qualifiers
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAATGTGAGAA 2596
Db 17 AAAAAAAAGTAGAGAA 1

RESULT 716
AR328180/c
LOCUS AR328180 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5582 from patent US 6566127.
ACCESSION AR328180
VERSION AR328180.1 GI:33713988
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5582 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2750 TTTTAAAGGAAAAAA 2766
Db 17 TTATTTTAGGAAAAAA 1

RESULT 717
AR328181/c
LOCUS AR328181 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5583 from patent US 6566127.

/mol_type="unassigned RNA"

ACCESSION AR328181 GI:33713989
VERSION AR328181.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5583 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2749 TTTTAAAGGAAAAAA 2765
Db 17 TTATTTTAGGAAAAAA 1

RESULT 718
AR329412
LOCUS AR329412 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6814 from patent US 6566127.
ACCESSION AR329412
VERSION AR329412.1 GI:33715220
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6814 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4029 TTATGGACTCTCTTTC 4045
Db 1 TTCTGGACTCTCTCTGC 17

RESULT 719
AR344531
LOCUS AR344531 17 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 7 from patent US 6582913.
ACCESSION AR344531
VERSION AR344531.1 GI:33740600
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M., Connors,T.D., Burn,T.C. and Splawski,I.
TITLE Diagnostic method for KVLQT1--a long QT syndrome gene
JOURNAL Patent: US 6582913-A 7 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1344 CAGATCTCTGACGAGCT 1360  
|||||  
Db 1 CAGATCTCTGAGGATGCT 17

RESULT 720  
AR398375/c  
LOCUS AR398375 17 bp RNA linear PAT 18-DEC-2003  
DEFINITION Sequence 756 from patent US 6617438.  
ACCESSION AR398375  
VERSION AR398375.1 GI:40136135  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Oligoribonucleotides with enzymatic activity  
JOURNAL Patent: US 6617438-A 756 09-SEP-2003;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3204 GCCATATGCCCCAGAAGG 3220  
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Db 17 GGCAGATGCCAGAAGG 1

RESULT 721  
AR402307/c  
LOCUS AR402307 17 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 647 from patent US 6623962.  
ACCESSION AR402307  
VERSION AR402307.1 GI:40149757  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.  
TITLE Enzymatic nucleic acid treatment of diseases of conditions related  
to levels of epidermal growth factor receptors  
JOURNAL Patent: US 6623962-A 647 23-SEP-2003;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3058 GATGGCTTAAGGATTT 3074  
|||||  
Db 17 GATGGCTAAAGGAGATT 1

RESULT 722  
AR456566  
LOCUS AR456566 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 243 from patent US 6686188.  
ACCESSION AR456566

AR456566.1 GI:42691623  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed  
predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 243 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 496 ATCTCTCGCGCCTGCTC 512  
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Db 1 ATCTCTCGCGCCTCTCTC 17

RESULT 723  
AR457388/c  
LOCUS AR457388 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 1065 from patent US 6686188.  
ACCESSION AR457388  
VERSION AR457388.1 GI:42692445  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed  
predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 1065 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2713 CTACTTCTCTAAGAGACA 2729  
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Db 17 CTACGTCCTTAGAGACA 1

RESULT 724  
AR457389/c  
LOCUS AR457389 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 1066 from patent US 6686188.  
ACCESSION AR457389  
VERSION AR457389.1 GI:42692446  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed  
predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 1066 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1..17

/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2712 CCTACTTCCTTAAGAGAC 2728  
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Db 17 CCTACGTCCTTAGAGAC 1

RESULT 725  
AR458545  
LOCUS AR458545 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 2222 from patent US 6686188.  
ACCESSION AR458545  
VERSION AR458545.1 GI:42693602  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 2222 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1..17  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 675 GTGTGAAGCAGGGCC 691  
||||| ||||| |||||  
Db 1 GTGTGGATGGCAGGGTC 17

RESULT 726  
AR464880  
LOCUS AR464880 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 8557 from patent US 6686188.  
ACCESSION AR464880  
VERSION AR464880.1 GI:42699937  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 8557 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1..17  
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/mol\_type="genomic DNA"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2519 CGATGACGACCATGATG 2535  
||||| ||||| |||||  
Db 1 CGATGAGACCATGATG 17

RESULT 727

AR465549  
LOCUS AR465549 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 9226 from patent US 6686188.  
ACCESSION AR465549  
VERSION AR465549.1 GI:42700606  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 9226 03-FEB-2004;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1462 CAAGCCGAGGGCAGCC 1478  
||||| ||||| |||||  
Db 1 CCAGCCAGAGGGCAGCC 17

RESULT 728  
AR466831/c  
LOCUS AR466831 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 10508 from patent US 6686188.  
ACCESSION AR466831  
VERSION AR466831.1 GI:42701888  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 10508 03-FEB-2004;  
FEATURES Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2928 CTCCCGTCCTTCCTC 2944  
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Db 17 CTCCCGTCCTTCGGCTC 1

RESULT 729  
AR466832/c  
LOCUS AR466832 17 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 10509 from patent US 6686188.  
ACCESSION AR466832  
VERSION AR466832.1 GI:42701889  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed

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predominantly in heart and muscle
Patent: US 6686188-A 10509 03-FEB-2004;
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2927 CCTCCCGTCCTTCCT 2943
Db 17 CCTCCCGTCCTTCGCT 1

RESULT 730
AX009153/c
LOCUS AX009153 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 186 from Patent WO9963975.
ACCESSION AX009153
VERSION AX009153.1 GI:9996527
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE A method for stimulating the immune system
JOURNAL Patent: WO 9963975-A 186 16-DEC-1999;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1320 AAGAGCATCGAGCCAT 1336
Db 17 AAGCGCATCGAGCCAT 1

RESULT 731
AX214795
LOCUS AX214795 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 237 from Patent WO0159103.
ACCESSION AX214795
VERSION AX214795.1 GI:15524838
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 237 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1320 TCAGACCTTTTTCCT 1250
Db 1 TGAGACCTTTTTCCT 17

predominantly in heart and muscle
Patent: US 6686188-A 10509 03-FEB-2004;
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2582 AAAAAAATTGGAGAAA 2598
Db 1 AAAAAAATAGAGAAA 17

RESULT 732
AX215493
LOCUS AX215493 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 935 from Patent WO0159103.
ACCESSION AX215493
VERSION AX215493.1 GI:15525536
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 935 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 973 CCCCCCCCCCGCCGCC 989
Db 1 CCCCCCTCCACCGCCGCC 17

RESULT 733
AX215509
LOCUS AX215509 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 951 from Patent WO0159103.
ACCESSION AX215509
VERSION AX215509.1 GI:15525552
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 951 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1234 TCAGACCTTTTTCCT 1250
Db 1 TGAGACCTTTTTCCT 17
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RESULT 734  
AX215783  
LOCUS AX215783 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 1225 from Patent WO0159103.  
ACCESSION AX215783  
VERSION AX215783.1 GI:15525826  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 1225 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source Location/Qualifiers  
1. .17  
/organism="synthetic construct"  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 934 AAAAAACAAACCTTTC 950  
|||||  
Db 1 AAAGAAACCAAGCTTTC 17  
RESULT 735  
AX216730  
LOCUS AX216730 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 2172 from Patent WO0159103.  
ACCESSION AX216730  
VERSION AX216730.1 GI:15526791  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 2172 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2580 AAAAAAAATTTGAGAA 2596  
|||||  
Db 1 AAAAAAATAGAGAA 17  
RESULT 736  
AX217212/c  
LOCUS AX217212 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 2654 from Patent WO0159103.  
ACCESSION AX217212  
VERSION AX217212.1 GI:15527273

KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 2654 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1182 TAAATAACAACATCAAC 1198  
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Db 17 TAAATACCAATCAAC 1  
RESULT 737  
AX217483/c  
LOCUS AX217483 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 2925 from Patent WO0159103.  
ACCESSION AX217483  
VERSION AX217483.1 GI:15527544  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 2925 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 72 GAAAGAGAGAGCGCT 88  
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Db 17 GTAAGAGAGAGGAGCT 1  
RESULT 738  
AX217485  
LOCUS AX217485 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 2927 from Patent WO0159103.  
ACCESSION AX217485  
VERSION AX217485.1 GI:15527546  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and

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nogo gene expression
Patent: WO 0159103-A 2927 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
1. .17
/organism="synthetic construct"
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/note="Nucleic Acid"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2384 CATTCTCTTACATTG 2400
Db 1 CCTTCTCTTACATTG 17

RESULT 739
AX217486 AX217486 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 2928 from Patent WO0159103.
ACCESSION AX217486
VERSION AX217486.1 GI:15527547
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 2928 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2386 TTCTCTTACATTGGA 2402
Db 1 TTCTCTTACATTGAA 17

RESULT 740
AX217558/c
LOCUS
DEFINITION Sequence 3000 from Patent WO0159103.
ACCESSION AX217558
VERSION AX217558.1 GI:15527619
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 3000 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
1. .17
/organism="synthetic construct"

nogo gene expression
Patent: WO 0159103-A 2927 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2798 ATCTGAAAAA 2814
Db 17 ATGTGGAATAAAAAA 1

RESULT 741
AX217577 AX217577 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 3019 from Patent WO0159103.
ACCESSION AX217577
VERSION AX217577.1 GI:15527638
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Blatt, L., McSwiggen, J. and Chowrira, B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and
TITLE nogo gene expression
JOURNAL Patent: WO 0159103-A 3019 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4251 AGGCTGATTAAAAA 4267
Db 1 AGGATGATAAAAAA 17

RESULT 742
AX226925/c
LOCUS
DEFINITION Sequence 297 from Patent WO0157206.
ACCESSION AX226925
VERSION AX226925.1 GI:15556066
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
AUTHORS Method and reagent for the inhibition of checkpoint kinase-1 (chk
TITLE 1) enzyme
JOURNAL Patent: WO 0157206-A 297 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2577 AAAAAAATAATTGGA 2593
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|----------------------------|--|--------------------|------------------------------------|
| Db                         | 17   | AAACAAATAAATTGGA   | 1                                  |
| RESULT 743                 |  |                    |                                    |
| AX226959/c                 |  |                    |                                    |
| LOCUS                      | AX226959   | 17 bp              | RNA                                |
| DEFINITION                 | Sequence 331 from Patent WO0157206.                                |                    |                                    |
| ACCESSION                  | AX226959   |                    |                                    |
| VERSION                    | AX226959.1   | GI:15556100        |                                    |
| KEYWORDS                   | synthetic construct  |                    |                                    |
| SOURCE                     | synthetic construct  |                    |                                    |
| ORGANISM                   | other sequences; artificial sequences.                             |                    |                                    |
| REFERENCE                  | 1  |                    |                                    |
| AUTHORS                    | Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S. |                    |                                    |
| TITLE                      | Method and reagent for the inhibition of checkpoint kinase-1 (chk  |                    |                                    |
| JOURNAL                    | 1) enzyme  |                    |                                    |
| FEATURES                   | Patent: WO 0157206-A 331 09-AUG-2001;                              |                    |                                    |
| source                     | RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)         |                    |                                    |
| Location/Qualifiers        | 1. .17   |                    |                                    |
| ORGANISM                   | /organism="synthetic construct"                                    |                    |                                    |
| /mol_type="unassigned RNA" | /db_xref="taxon:32630"   |                    |                                    |
| Query Match                | 0.3%;  | Score 13.8;        | DB 1;                              |
| Best Local Similarity      | 88.2%;   | Pred. No. 4.1e+02; |                                    |
| Matches                    | 15;  | Conservative       | 0; Mismatches 2; Indels 0; Gaps 0; |
| Qy                         | 2283   | TCAGACACTCAACACAC  | 2299                               |
| Db                         | 17   | TCAGATACTAAACACAC  | 1                                  |
| RESULT 744                 |  |                    |                                    |
| AX227129                   |  |                    |                                    |
| LOCUS                      | AX227129   | 17 bp              | RNA                                |
| DEFINITION                 | Sequence 501 from Patent WO0157206.                                |                    |                                    |
| ACCESSION                  | AX227129   |                    |                                    |
| VERSION                    | AX227129.1   | GI:15556270        |                                    |
| KEYWORDS                   | synthetic construct  |                    |                                    |
| SOURCE                     | synthetic construct  |                    |                                    |
| ORGANISM                   | other sequences; artificial sequences.                             |                    |                                    |
| REFERENCE                  | 1  |                    |                                    |
| AUTHORS                    | Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S. |                    |                                    |
| TITLE                      | Method and reagent for the inhibition of checkpoint kinase-1 (chk  |                    |                                    |
| JOURNAL                    | 1) enzyme  |                    |                                    |
| FEATURES                   | Patent: WO 0157206-A 501 09-AUG-2001;                              |                    |                                    |
| source                     | RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)         |                    |                                    |
| Location/Qualifiers        | 1. .17   |                    |                                    |
| ORGANISM                   | /organism="synthetic construct"                                    |                    |                                    |
| /mol_type="unassigned RNA" | /db_xref="taxon:32630"   |                    |                                    |
| Query Match                | 0.3%;  | Score 13.8;        | DB 1;                              |
| Best Local Similarity      | 88.2%;   | Pred. No. 4.1e+02; |                                    |
| Matches                    | 15;  | Conservative       | 0; Mismatches 2; Indels 0; Gaps 0; |
| Qy                         | 4148   | AAAGGGGAAAAGTCC    | 4164                               |
| Db                         | 1  | AAAGGGGCAAAAAGGCC  | 17                                 |
| RESULT 745                 |  |                    |                                    |
| AX227513/c                 |  |                    |                                    |
| LOCUS                      | AX227513   | 17 bp              | RNA                                |
| DEFINITION                 | Sequence 885 from Patent WO0157206.                                |                    |                                    |
| ACCESSION                  | AX227513   |                    |                                    |
| VERSION                    | AX227513.1   | GI:15556654        |                                    |
| KEYWORDS                   | synthetic construct  |                    |                                    |
| SOURCE                     | synthetic construct  |                    |                                    |
| ORGANISM                   | other sequences; artificial sequences.                             |                    |                                    |
| REFERENCE                  | 1  |                    |                                    |
| AUTHORS                    | Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S. |                    |                                    |
| TITLE                      | Method and reagent for the inhibition of checkpoint kinase-1 (chk  |                    |                                    |
| JOURNAL                    | 1) enzyme  |                    |                                    |
| FEATURES                   | Patent: WO 0157206-A 885 09-AUG-2001;                              |                    |                                    |
| source                     | RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)         |                    |                                    |
| Location/Qualifiers        | 1. .17   |                    |                                    |
| ORGANISM                   | /organism="synthetic construct"                                    |                    |                                    |
| /mol_type="unassigned RNA" | /db_xref="taxon:32630"   |                    |                                    |
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| Best Local Similarity      | 88.2%;   | Pred. No. 4.1e+02; |                                    |
| Matches                    | 15;  | Conservative       | 0; Mismatches 2; Indels 0; Gaps 0; |
| Qy                         | 2428   | CCAATATGATTGTCAG   | 2444                               |
| Db                         | 1  | CCAATATGTTTTCAG    | 17                                 |
| RESULT 747                 |  |                    |                                    |
| AX264281/c                 |  |                    |                                    |
| LOCUS                      | AX264281   | 17 bp              | DNA                                |
| DEFINITION                 | Sequence 1672 from Patent WO0173002.                               |                    |                                    |
| ACCESSION                  | AX264281   |                    |                                    |
| VERSION                    | AX264281.1   | GI:16513080        |                                    |
| KEYWORDS                   | Homo sapiens (human)   |                    |                                    |
| SOURCE                     | Homo sapiens   |                    |                                    |
| ORGANISM                   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                    |                                    |
|                            | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.         |                    |                                    |
| REFERENCE                  | 1  |                    |                                    |
| AUTHORS                    | Knies,E.B., Gamper,H.B. and Rice,M.C.                              |                    |                                    |
| TITLE                      | Targeted chromosomal genomic alterations with modified single      |                    |                                    |
| JOURNAL                    | stranded oligonucleotides  |                    |                                    |
| FEATURES                   | Patent: WO 0173002-A 1672 04-OCT-2001;                             |                    |                                    |
| source                     | UNIVERSITY OF DELAWARE (US)  |                    |                                    |
| Location/Qualifiers        | 1. .17   |                    |                                    |
| ORGANISM                   | /organism="Homo sapiens"   |                    |                                    |
| /mol_type="unassigned DNA" | /db_xref="taxon:9606"  |                    |                                    |
| Query Match                | 0.3%;  | Score 13.8;        | DB 1;                              |
| Best Local Similarity      | 88.2%;   | Pred. No. 4.1e+02; |                                    |
| Matches                    | 15;  | Conservative       | 0; Mismatches 2; Indels 0; Gaps 0; |
| Qy                         | 2428   | CCAATATGATTGTCAG   | 2444                               |
| Db                         | 1  | CCAATATGTTTTCAG    | 17                                 |
| RESULT 749                 |  |                    |                                    |
| AX264281/c                 |  |                    |                                    |
| LOCUS                      | AX264281   | 17 bp              | DNA                                |
| DEFINITION                 | Sequence 1672 from Patent WO0173002.                               |                    |                                    |
| ACCESSION                  | AX264281   |                    |                                    |
| VERSION                    | AX264281.1   | GI:16513080        |                                    |
| KEYWORDS                   | Homo sapiens (human)   |                    |                                    |
| SOURCE                     | Homo sapiens   |                    |                                    |
| ORGANISM                   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                    |                                    |
|                            | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.         |                    |                                    |
| REFERENCE                  | 1  |                    |                                    |
| AUTHORS                    | Knies,E.B., Gamper,H.B. and Rice,M.C.                              |                    |                                    |
| TITLE                      | Targeted chromosomal genomic alterations with modified single      |                    |                                    |
| JOURNAL                    | stranded oligonucleotides  |                    |                                    |

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FEATURES
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Query Match
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  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2428 CCAATATGATGTCACAG 2444
Db 17 CCAATATGTTTTCACAG 1

RESULT 748
AX265075/c
LOCUS AX265075 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 2466 from Patent WO0173002.
ACCESSION AX265075
VERSION AX265075.1 GI:16513874
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Kmiec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
PATENT: WO 0173002-A 2466 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
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        /mol_type="unassigned DNA"
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Query Match
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  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 859 CACACTGAATCCATTT 875
Db 17 CACACTGATCTCATCT 1

RESULT 749
AX265076
LOCUS AX265076 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 2467 from Patent WO0173002.
ACCESSION AX265076
VERSION AX265076.1 GI:16513875
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Kmiec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
PATENT: WO 0173002-A 2467 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
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        /mol_type="unassigned DNA"
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Query Match
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QY 859 CACACTGAATCCATTT 875
Db 17 CACACTGATCTCATCT 1

RESULT 750
AX273239
LOCUS AX273239 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 808 from Patent WO0162911.
ACCESSION AX273239
VERSION AX273239.1 GI:16545976
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and
  Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 808 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
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        /mol_type="unassigned RNA"
        /db_xref="taxon:9606"

Query Match
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QY 2716 CTTCTTAAGACACAA 2732
Db 1 CTTCTTAGACAGAA 17

RESULT 751
AX326509/c
LOCUS AX326509 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2647 from Patent WO0192512.
ACCESSION AX326509
VERSION AX326509.1 GI:18097273
KEYWORDS
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
  1
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
PATENT: WO 0192512-A 2647 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
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        /mol_type="unassigned DNA"
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Query Match
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QY 501 CGCCGCTCTCTCCGCC 517
Db 17 CGCCTCTCTACTCCGCC 1

RESULT 752
AX326510

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LOCUS AX326510 17 bp DNA linear PAT 02-SEP-2002  
DEFINITION Sequence 2648 from Patent WO0192512.  
ACCESSION AX326510  
VERSION AX326510.1 GI:18097274  
KEYWORDS Triticum aestivum (bread wheat)  
SOURCE Triticum aestivum  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
REFERENCE 1  
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.  
TITLE Targeted chromosomal genomic alterations in plants using modified  
single stranded oligonucleotides  
JOURNAL Patent: WO 0192512-A 2648 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:4565"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 501 CGCGCGCTGCTCGGCG 517  
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Db 1 CGCCTCTACTCGGCG 17  
RESULT 753  
AX361606/c  
LOCUS AX361606 17 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 24 from Patent WO0208461.  
ACCESSION AX361606  
VERSION AX361606.1 GI:18694225  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.  
TITLE A method and an algorithm for mrna expression analysis  
JOURNAL Patent: WO 0208461-A 24 31-JAN-2002;  
Global Genomics AB (SE)  
FEATURES  
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1. .17  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Double-stranded product DNA"  
Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
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QY 928 GAGAAAAAAACAAA 944  
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Db 17 GAAAAAAACAAAAA 1  
RESULT 754  
AX422617/c  
LOCUS AX422617 17 bp RNA linear PAT 18-JUN-2002  
DEFINITION Sequence 953 from Patent WO0188124.  
ACCESSION AX422617  
VERSION AX422617.1 GI:121525999  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and  
Randi,A.M.  
TITLE Method and reagent for the inhibition of erg  
JOURNAL Patent: WO 0188124-A 953 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
FEATURES  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3774 CCTCCCCAACCCCGT 3790  
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Db 17 CCTCCCCAGCCCCAGT 1  
RESULT 755  
AX423623/c  
LOCUS AX423623 17 bp RNA linear PAT 18-JUN-2002  
DEFINITION Sequence 1959 from Patent WO0188124.  
ACCESSION AX423623  
VERSION AX423623.1 GI:21527005  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and  
Randi,A.M.  
TITLE Method and reagent for the inhibition of erg  
JOURNAL Patent: WO 0188124-A 1959 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3773 TCCTCCCCAACCCCG 3789  
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Db 17 TCCTCCCCAGCCCCAG 1  
RESULT 756  
AX423624/c  
LOCUS AX423624 17 bp RNA linear PAT 18-JUN-2002  
DEFINITION Sequence 1960 from Patent WO0188124.  
ACCESSION AX423624  
VERSION AX423624.1 GI:21527006  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and  
Randi,A.M.  
TITLE Method and reagent for the inhibition of erg  
JOURNAL Patent: WO 0188124-A 1960 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)  
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3772 TTCCTCCCCCAACCCCA 3788
17 TTCCTCCCCCAACCCCA 1

RESULT 757
AX530538
LOCUS AX530538 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 47 from Patent EP1239051.
ACCESSION AX530538
VERSION AX530538.1 GI:25252453
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 47 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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1.17
/mol_type="unassigned RNA"
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Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 425 GGCAGCAGCGGGCGCTG 441
1 GGCAGCAGCGGGCGCTG 17

RESULT 758
AX530550/c
LOCUS AX530550 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 59 from Patent EP1239051.
ACCESSION AX530550
VERSION AX530550.1 GI:25252477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 59 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
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Qy 2933 CGTCCTTCTCTCAAGC 2949
17 CGTCCTTCTCTCAAGC 1

RESULT 761
AX532047
LOCUS AX532047 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1556 from Patent EP1239051.
ACCESSION AX532047
VERSION AX532047.1 GI:25255857
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Shannon,M.
TITLE Human poeh-like protein 1
JOURNAL Patent: EP 1239051-A 1556 11-SEP-2002;
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1920 AATAATTACATCATCCC 1936
Db 1 AACAAATTACGTCATCCC 17

RESULT 762
AX544872/c
LOCUS AX544872 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 385 from Patent EP1243660.
ACCESSION AX544872
VERSION AX544872.1 GI:25810083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Zhang,J., Gu,Y. and Nguyen,C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 385 25-SEP-2002;
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3857 AGCCTTTTCTGCTCAG 3873
Db 17 AGCCTTTTCTTCTTCAG 1

RESULT 763
AX579530
LOCUS AX579530 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1368 from Patent WO0211674.
ACCESSION AX579530
VERSION AX579530.1 GI:27648732
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1368 14-FEB-2002;
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source
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/organism="Homo sapiens"
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Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1031 ATTTTCTTTTAAAGG 1047
Db 1 ATTTTCTTGTAAAGG 17

RESULT 764
AX580100
LOCUS AX580100 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1938 from Patent WO0211674.
ACCESSION AX580100
VERSION AX580100.1 GI:27649302
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1938 14-FEB-2002;
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
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Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 163 CATCTCGGAGAGAGG 179
Db 1 CAACTGTGGAGAGAGG 17

RESULT 765
AX616011/c
LOCUS AX616011 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 818 from Patent EP1262488.
ACCESSION AX616011
VERSION AX616011.1 GI:28447057
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Gu,Y. and Nguyen,C.T.
TITLE Human lcll-domain containing protein
JOURNAL Patent: EP 1262488-A 818 04-DEC-2002;
FEATURES
source
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/organism="Homo sapiens"
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Query Match
Best Local Similarity 0.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Db                    | 17   | TCCCCATCCCTTCTCCTG | 1                          |
| RESULT 766            |  |                    |                            |
| AX648557/c            |  |                    |                            |
| LOCUS                 | AX648557   | 17 bp              | DNA linear PAT 22-MAR-2003 |
| DEFINITION            | Sequence 397 from Patent EP1273660.  |                    |                            |
| ACCESSION             | AX648557   |                    |                            |
| VERSION               | AX648557.1   | GI:29151375        |                            |
| KEYWORDS              | Homo sapiens (human)   |                    |                            |
| SOURCE                | Homo sapiens   |                    |                            |
| ORGANISM              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |                    |                            |
| REFERENCE             | Gu, Y.   |                    |                            |
| AUTHORS               | Human sodium-hydrogen exchanger like protein 1   |                    |                            |
| TITLE                 | Patent: EP 1273660-A 397 08-JAN-2003;  |                    |                            |
| JOURNAL               | Aeomica, Inc. (US)   |                    |                            |
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| Query Match           | 0.3%; Score 13.8; DB 1; Length 17;   |                    |                            |
| Best Local Similarity | 88.2%; Pred. No. 4.1e+02;  |                    |                            |
| Matches               | 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  |                    |                            |
| QY                    | 1154   | TCTTTTATATATT      | 1170                       |
| Db                    | 17   | TCTTTTGATTTATAT    | 1                          |
| RESULT 767            |  |                    |                            |
| AX671693/c            |  |                    |                            |
| LOCUS                 | AX671693   | 17 bp              | DNA linear PAT 27-MAR-2003 |
| DEFINITION            | Sequence 138 from Patent WO03004526.   |                    |                            |
| ACCESSION             | AX671693   |                    |                            |
| VERSION               | AX671693.1   | GI:293330041       |                            |
| KEYWORDS              | Homo sapiens (human)   |                    |                            |
| SOURCE                | Homo sapiens   |                    |                            |
| ORGANISM              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |                    |                            |
| REFERENCE             | Teleman,A., Anson,R. and Tuijnder,M.   |                    |                            |
| AUTHORS               | Sequences involved in phenomena of tumour suppression, tumour  |                    |                            |
| TITLE                 | reversion, apoptosis and/or resistance to viruses and their use as   |                    |                            |
|                       | medicines  |                    |                            |
| JOURNAL               | Patent: WO 03004526-A 138 16-JAN-2003;   |                    |                            |
|                       | Molecular Engines Laboratories (FR)  |                    |                            |
| FEATURES              | Location/Qualifiers  |                    |                            |
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| Query Match           | 0.3%; Score 13.8; DB 1; Length 17;   |                    |                            |
| Best Local Similarity | 88.2%; Pred. No. 4.1e+02;  |                    |                            |
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| QY                    | 3361   | TGAAGTGGCTGTGATC   | 3377                       |
| Db                    | 17   | TGGAGTGGCGGTGATC   | 1                          |
| RESULT 768            |  |                    |                            |
| AX672167              |  |                    |                            |
| LOCUS                 | AX672167   | 17 bp              | DNA linear PAT 27-MAR-2003 |
| DEFINITION            | Sequence 612 from Patent WO03004526.   |                    |                            |

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| QY                    | 2929   | TCCCCGTCCTTCTCCTCC | 2945                       |
| Db                    | 17   | TCCCCATCCCTCTCTGC  | 1                          |
| RESULT 766            |  |                    |                            |
| AX648557/c            |  |                    |                            |
| LOCUS                 | AX648557   | 17 bp              | DNA linear PAT 22-MAR-2003 |
| DEFINITION            | Sequence 397 from Patent EP1273660.  |                    |                            |
| ACCESSION             | AX648557   |                    |                            |
| VERSION               | AX648557.1   | GI:29151375        |                            |
| KEYWORDS              | Homo sapiens (human)   |                    |                            |
| SOURCE                | Homo sapiens   |                    |                            |
| ORGANISM              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |                    |                            |
| REFERENCE             | Gu, Y.   |                    |                            |
| AUTHORS               | Human sodium-hydrogen exchanger like protein 1   |                    |                            |
| TITLE                 | Patent: EP 1273660-A 397 08-JAN-2003;  |                    |                            |
| JOURNAL               | Aeomica, Inc. (US)   |                    |                            |
| FEATURES              | Location/Qualifiers  |                    |                            |
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| Matches               | 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  |                    |                            |
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| Db                    | 17   | TCCTTTGTATTATATT   | 1                          |
| RESULT 767            |  |                    |                            |
| AX671693/c            |  |                    |                            |
| LOCUS                 | AX671693   | 17 bp              | DNA linear PAT 27-MAR-2003 |
| DEFINITION            | Sequence 138 from Patent WO03004526.   |                    |                            |
| ACCESSION             | AX671693   |                    |                            |
| VERSION               | AX671693.1   | GI:293330041       |                            |
| KEYWORDS              | Homo sapiens (human)   |                    |                            |
| SOURCE                | Homo sapiens   |                    |                            |
| ORGANISM              | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |                    |                            |
| REFERENCE             | Teleman,A., Amson,R. and Tuijnder,M.   |                    |                            |
| AUTHORS               | Sequences involved in phenomena of tumour suppression, tumour  |                    |                            |
| TITLE                 | reversion, apoptosis and/or resistance to viruses and their use as   |                    |                            |
|                       | medicines  |                    |                            |
| JOURNAL               | Patent: WO 03004526-A 138 16-JAN-2003;   |                    |                            |
|                       | Molecular Engines Laboratories (FR)  |                    |                            |
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| Query Match           | 0.3%; Score 13.8; DB 1; Length 17;   |                    |                            |
| Best Local Similarity | 88.2%; Pred. No. 4.1e+02;  |                    |                            |
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| QY                    | 3361   | TGAAGTGCGCTGTGATC  | 3377                       |
| Db                    | 17   | TGGAGTGGCGGTGATC   | 1                          |
| RESULT 768            |  |                    |                            |
| AX672167              |  |                    |                            |
| LOCUS                 | AX672167   | 17 bp              | DNA linear PAT 27-MAR-2003 |
| DEFINITION            | Sequence 612 from Patent WO03004526.   |                    |                            |

REFERENCE 1  
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
medicines reversion, apoptosis and/or resistance to viruses and their use as  
JOURNAL Patent: WO 03004526-A 1278 16-JAN-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2189 TGATTTTAAGAGGATC 2205  
Db 17 TGATTGAAGATGGATC 1

RESULT 771  
LOCUS AX674271/c 17 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 2716 from Patent WO03004526.  
ACCESSION AX674271  
VERSION AX674271.1 GI:29332619  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour  
medicines reversion, apoptosis and/or resistance to viruses and their use as  
JOURNAL Patent: WO 03004526-A 2716 16-JAN-2003;  
FEATURES Molecular Engines Laboratories (FR)  
source Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1714 TTGAAGTGTATCAGATC 1730  
Db 17 TTGTGCTGTATCAGATC 1

RESULT 772  
LOCUS AX691837/c 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 4569 from Patent EP1281758.  
ACCESSION AX691837  
VERSION AX691837.1 GI:29414778  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
JOURNAL Patent: EP 1281758-A 4569 05-FEB-2003;  
FEATURES Aeomica, Inc. (US)  
source Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 121 GGAGAGAAGTATTAGGG 137  
Db 17 GGAGAGAAGTCTTAGGG 1

RESULT 773  
LOCUS AX692519/c 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5251 from Patent EP1281758.  
ACCESSION AX692519  
VERSION AX692519.1 GI:29415477  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
JOURNAL Patent: EP 1281758-A 5251 05-FEB-2003;  
FEATURES Aeomica, Inc. (US)  
source Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACAACT 947  
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RESULT 774  
LOCUS AX692530/c 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5262 from Patent EP1281758.  
ACCESSION AX692530  
VERSION AX692530.1 GI:29415488  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
JOURNAL Patent: EP 1281758-A 5262 05-FEB-2003;  
FEATURES Aeomica, Inc. (US)  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 931 AAAAAAAAAACAACT 947  
Db 17 AAAAAAAAAAGATCCT 1

RESULT 774  
LOCUS AX692530/c 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 5262 from Patent EP1281758.  
ACCESSION AX692530  
VERSION AX692530.1 GI:29415488  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
JOURNAL Patent: EP 1281758-A 5262 05-FEB-2003;  
FEATURES Aeomica, Inc. (US)  
source Location/Qualifiers  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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| Db                    | 17  | GTCTCAAAAAA        | 1               |
| RESULT 775            |   |                    |                 |
| AX692531/C            |   |                    |                 |
| LOCUS                 | AX692531  | 17 bp              | DNA             |
| DEFINITION            | Sequence 5263 from Patent EP1281758.  |                    | linear          |
| ACCESSION             | AX692531  |                    |                 |
| VERSION               | AX692531.1  | GI:29415489        |                 |
| KEYWORDS              | .   |                    |                 |
| SOURCE                | Homo sapiens (human)  |                    |                 |
| ORGANISM              | Homo sapiens  |                    |                 |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.          |                    |                 |
| AUTHORS               | Shannon,M., Gu,Y. and Nguyen,C.T.   |                    |                 |
| TITLE                 | Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12   |                    |                 |
| JOURNAL               | Patent: EP 1281758-A 5263 05-FEB-2003;  |                    |                 |
| FEATURES              | Acemica, Inc. (US)  |                    |                 |
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| Matches               | 15;   | Conservative 0;    | Mismatches 2;   |
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| Db                    | 17  | TGTTCAAAAAA        | 1               |
| RESULT 776            |   |                    |                 |
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| LOCUS                 | AX722447  | 17 bp              | DNA             |
| DEFINITION            | Sequence 134 from Patent WO03025176.  |                    | linear          |
| ACCESSION             | AX722447  |                    |                 |
| VERSION               | AX722447.1  | GI:30422948        |                 |
| KEYWORDS              | .   |                    |                 |
| SOURCE                | Mus musculus (house mouse)  |                    |                 |
| ORGANISM              | Mus musculus  |                    |                 |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |                    |                 |
| AUTHORS               | Telerman,A., Amson,R. and Tuijnder,M.   |                    |                 |
| TITLE                 | Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines |                    |                 |
| JOURNAL               | Patent: WO 03025176-A 134 27-MAR-2003;  |                    |                 |
| FEATURES              | Molecular Engines Laboratories (FR)   |                    |                 |
| source                | 1. .17  |                    |                 |
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| Query Match           | 0.3%;   | Score 13.8;        | DB 1;           |
| Best Local Similarity | 88.2%;  | Pred. No. 4.1e+02; |                 |
| Matches               | 15;   | Conservative 0;    | Mismatches 2;   |
|                       |   | Indels 0;          | Gaps 0;         |
| QY                    | 2373  | GAACCACTGACCATTC   | 2389            |
| Db                    | 1   | GATCCAGTGACCATTC   | 17              |
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| AX723926/C            |   |                    |                 |
| LOCUS                 | AX723926  | 17 bp              | DNA             |
|                       |   |                    | linear          |
|                       |   |                    | PAT 08-MAY-2003 |



Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS  
TITLE  
Telerman, A., Anson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL  
Patent: WO 03025176-A 5339 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3262 GATTTTTCCTTTT 3278  
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Db 1 GATCTTTTTCCTTAT 17  
RESULT 780  
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LOCUS  
DEFINITION  
Sequence 5952 from Patent WO03025176.  
ACCESSION  
AX728265  
VERSION  
AX728265.1 GI:30507608  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS  
TITLE  
Telerman, A., Anson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL  
Patent: WO 03025176-A 5952 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
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Db 17 GGACTGGAGTTTCAGATC 1  
RESULT 781  
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LOCUS  
DEFINITION  
Sequence 790 from Patent WO03025175.  
ACCESSION  
AX729156  
VERSION  
AX729156.1 GI:30508499  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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REFERENCE  
AUTHORS  
TITLE  
Telerman, A., Anson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL  
Patent: WO 03025175-A 790 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
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REFERENCE  
AUTHORS  
TITLE  
Telerman, A., Anson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL  
Patent: WO 03025176-A 5339 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3230 AAAGAAAACCTTGGATC 3246  
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Db 17 AAAGAAAACCTTGGATC 1  
RESULT 782  
AX730368  
LOCUS  
DEFINITION  
Sequence 2002 from Patent WO03025175.  
ACCESSION  
AX730368  
VERSION  
AX730368.1 GI:30509711  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS  
TITLE  
Telerman, A., Anson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL  
Patent: WO 03025175-A 2002 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 34 GAGTCTGTAACCTGCC 50  
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Db 1 GATCTGCTGAAGTGCC 17  
RESULT 783  
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LOCUS  
DEFINITION  
Sequence 2131 from Patent WO03025175.  
ACCESSION  
AX730497  
VERSION  
AX730497.1 GI:30509840  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS  
TITLE  
Telerman, A., Anson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
JOURNAL  
Patent: WO 03025175-A 2131 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
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Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3611 GATCATTTCAGATTGTAT 3627
Db 1 GATCATTCAAATTGAAT 17

RESULT 784
AX730996/c
LOCUS AX730996 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2630 from Patent WO03025175.
ACCESSION AX730996
VERSION AX730996.1 GI:30510339
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 2630 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3230 AAAGAAAACCTTGAATC 3246
Db 17 AAAGAAAACCTTGTATC 1

RESULT 785
AX731845/c
LOCUS AX731845 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3479 from Patent WO03025175.
ACCESSION AX731845
VERSION AX731845.1 GI:30511188
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3479 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTNTTTTAAATGATC 3614
Db 17 TTTTNTTTTAAATGATC 1

RESULT 786
AX732633/c
LOCUS AX732633 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4267 from Patent WO03025175.
ACCESSION AX732633
VERSION AX732633.1 GI:30511976
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4267 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match          0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3262 GATTTTTCCTCTTTT 3278
Db 1 GATCTTTTCCTCTTTT 17

RESULT 788
AX733744
LOCUS AX733744 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5378 from Patent WO03025175.
ACCESSION AX733744
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VERSION      AX733744.1 GI:30513087
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS      Telerman,A., Anson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 5378 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     source
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Query Match  0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 GAGCTGCTGAAACTGCC 50
Db 1 GATCTGCTGAAATGCC 17

RESULT 789
AX734489/c
LOCUS       AX734489          17 bp    DNA          linear    PAT 08-MAY-2003
DEFINITION Sequence 79 from Patent WO03025177.
ACCESSION  AX734489
VERSION    AX734489.1 GI:30513766
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL    Patent: WO 03025177-A 79 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   source
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTCTTTTAAATGATC 3614
Db 17 TTTATTTTCTACTGATC 1

RESULT 790
AX734527/c
LOCUS       AX734527          17 bp    DNA          linear    PAT 08-MAY-2003
DEFINITION Sequence 117 from Patent WO03025177.
ACCESSION  AX734527
VERSION    AX734527.1 GI:30513804
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL    Patent: WO 03025177-A 1460 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   source
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTCTTTTAAATGATC 3614
Db 17 TTTATTTTCTACTGATC 1

RESULT 792
AX735870/c
LOCUS       AX735870          17 bp    DNA          linear    PAT 08-MAY-2003
DEFINITION Sequence 1460 from Patent WO03025177.
ACCESSION  AX735870
VERSION    AX735870.1 GI:30515147
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL    Patent: WO 03025177-A 1460 27-MAR-2003;
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FEATURES   source
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 17 TTGTGATGCAATGGATC 1

RESULT 792
AX735870/c
LOCUS       AX735870          17 bp    DNA          linear    PAT 08-MAY-2003
DEFINITION Sequence 1460 from Patent WO03025177.
ACCESSION  AX735870
VERSION    AX735870.1 GI:30515147
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Telerman,A., Anson,R. and Tuijnder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL    Patent: WO 03025177-A 1460 27-MAR-2003;
            Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTTCATTTTAATGATC 3614
Db      ||| ||||| ||||| |||||
17 TTTTCATTTTAATGATC 1

RESULT 795
AX737376/c AX737376 17 bp DNA linear PAT 08-MAY-2003
LOCUS      Sequence 2966 from Patent WO03025177.
DEFINITION AX737376
ACCESSION  AX737376
VERSION    AX737376.1 GI:30516664
KEYWORDS   . Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Telerman,A., Anson,R. and Tuijnder,M.
TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL   Patent: WO 03025177-A 2966 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTTCATTTTAATGATC 3614
Db      ||| ||||| ||||| |||||
17 TTTTTCATTTTAATGATC 1

RESULT 796
AX737499/c AX737499 17 bp DNA linear PAT 08-MAY-2003
LOCUS      Sequence 3089 from Patent WO03025177.
DEFINITION AX737499
ACCESSION  AX737499
VERSION    AX737499.1 GI:30516787
KEYWORDS   . Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Telerman,A., Anson,R. and Tuijnder,M.
TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL   Patent: WO 03025177-A 3089 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTTCATTTTAATGATC 3614
Db      ||| ||||| ||||| |||||
17 TTTTTCATTTTAATGATC 1

RESULT 794
AX736541/c AX736541 17 bp DNA linear PAT 08-MAY-2003
LOCUS      Sequence 2131 from Patent WO03025177.
DEFINITION AX736541
ACCESSION  AX736541
VERSION    AX736541.1 GI:30515829
KEYWORDS   . Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Telerman,A., Anson,R. and Tuijnder,M.
TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL   Patent: WO 03025177-A 2131 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTTCATTTTAATGATC 3614
Db      ||| ||||| ||||| |||||
17 TTTTTCATTTTAATGATC 1

RESULT 794
AX736541/c AX736541 17 bp DNA linear PAT 08-MAY-2003
LOCUS      Sequence 2131 from Patent WO03025177.
DEFINITION AX736541
ACCESSION  AX736541
VERSION    AX736541.1 GI:30515829
KEYWORDS   . Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Telerman,A., Anson,R. and Tuijnder,M.
TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL   Patent: WO 03025177-A 2131 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
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Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTTCATTTTAATGATC 3614
Db      ||| ||||| ||||| |||||
17 TTTTTCATTTTAATGATC 1
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RESULT 797
AX738113/c
LOCUS
DEFINITION Sequence 3703 from Patent WO03025177.
ACCESSION AX738113
VERSION AX738113.1 GI:30517401
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTGTGTTGAATGATC 3614
Db 17 TTTTGTGTTGAATGATC 1

RESULT 798
AX738194
LOCUS
DEFINITION Sequence 3784 from Patent WO03025177.
ACCESSION AX738194
VERSION AX738194.1 GI:30517482
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2202 GATCTTGGATGGAATG 2218
Db 1 GATCTTGGATGGAATG 17

RESULT 799
AX738406/c
LOCUS
DEFINITION Sequence 3996 from Patent WO03025177.
ACCESSION AX738406
VERSION AX738406.1 GI:30517694
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2354 CTGTGTGCCAGGATC 2370
Db 17 CTATGTGCCAGGATC 1

RESULT 800
AX739252
LOCUS
DEFINITION Sequence 4842 from Patent WO03025177.
ACCESSION AX739252
VERSION AX739252.1 GI:30518549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 821 GATCGAGTTCAGATCA 837
Db 1 GATCTGAGTTCAGAAC 17

RESULT 801
AX739583/c
LOCUS
DEFINITION Sequence 5173 from Patent WO03025177.
ACCESSION AX739583
VERSION AX739583.1 GI:30518880
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
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reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
Patent: WO 03025177-A 5173 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/organism="Homo sapiens"
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTCTTTTAAATGATC 3614
Db 17 TTTTCTTTTCTGATC 1

RESULT 802
AX739654
LOCUS AX739654 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5244 from Patent WO03025177.
ACCESSION AX739654
VERSION AX739654.1 GI:30518951
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
Patent: WO 03025177-A 5244 27-MAR-2003;
Molecular Engines Laboratories (FR)
JOURNAL Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2572 GTTTAAAAAATAAAAAA 2588
Db 1 GATCAAAAAAATAAAAAA 17

RESULT 803
AX739654/c
LOCUS AX739654 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5244 from Patent WO03025177.
ACCESSION AX739654
VERSION AX739654.1 GI:30518951
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
Patent: WO 03025177-A 5244 27-MAR-2003;
Molecular Engines Laboratories (FR)
JOURNAL Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3598 TTTTCTTTTAAATGATC 3614
Db 17 TTTTCTTTTCTGATC 1

RESULT 804
AX745430/c
LOCUS AX745430 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 1395 from Patent WO03031621.
ACCESSION AX745430
VERSION AX745430.1 GI:30724097
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang,J.
TITLE A human G protein coupled receptor
Patent: WO 03031621-A 1395 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
JOURNAL Location/Qualifiers
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Db 17 GTTCTCTTTATATCTAT 1

RESULT 805
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LOCUS AX757514 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 835 from Patent WO03040369.
ACCESSION AX757514
VERSION AX757514.1 GI:32252130
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
Patent: WO 03040369-A 835 15-MAY-2003;
Molecular Engines Laboratories (FR)
JOURNAL Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 0.3%; Score 13.8; DB 1; Length 17;
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| DB                    | 1  | CGAGCAGACGCGCACAC  | 17            |            |
| LOCUS                 | AX814938/c   |                    |               |            |
| DEFINITION            | Sequence 24 from Patent WO03064691.  | 17 bp              | DNA           | linear     |
| ACCESSION             | AX814938   |                    |               |            |
| VERSION               | AX814938.1   | GI:39104076        |               |            |
| KEYWORDS              |  |                    |               |            |
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| ORGANISM              |  |                    |               |            |
| REFERENCE             |  |                    |               |            |
| AUTHORS               | Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and Montelius,A.  |                    |               |            |
| TITLE                 | Methods and means for manipulating nucleic acid  |                    |               |            |
| JOURNAL               | Patent: WO 03064691-A 24 07-AUG-2003;  |                    |               |            |
| FEATURES              | Global Genomics AB (SE)  |                    |               |            |
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| DB                    | 17   | GAAAAAACAACAA      | 1             |            |
| LOCUS                 | BD011731/c   |                    |               |            |
| DEFINITION            | 795, a novel gene related to pollen allergy.   | 17 bp              | DNA           | linear     |
| ACCESSION             | BD011731   |                    |               |            |
| VERSION               | BD011731.1   | GI:22091920        |               |            |
| KEYWORDS              | WO 065050-A/3.   |                    |               |            |
| SOURCE                |  |                    |               |            |
| ORGANISM              |  |                    |               |            |
| REFERENCE             |  |                    |               |            |
| AUTHORS               | Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M., Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K., Takahashi,E. and Yokoi.A.   |                    |               |            |
| TITLE                 | 795, a novel gene related to pollen allergy  |                    |               |            |
| JOURNAL               | Patent: WO 065050-A 3 02-NOV-2000;   |                    |               |            |
|                       | GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI, NEI YOSHIDA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI |                    |               |            |
| COMMENT               | OS Artificial Sequence   |                    |               |            |
|                       | PN WO 065050-A/3   |                    |               |            |
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|                       | PP 26-APR-2000 WO 2000JP002734   |                    |               |            |
|                       | PR 27-APR-1999 JP 99P 120494   |                    |               |            |
|                       | PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,   |                    |               |            |
|                       | PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,   |                    |               |            |
|                       | PI NEI YOSHIDA,  |                    |               |            |
|                       | PI KAOBU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI  |                    |               |            |
|                       | C12N15/12, C07K14/47, C07K16/18, C12Q1/68, G01N33/50//A61K31/00, PC A61P37/00  |                    |               |            |



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Db 17 GAAAAAAACCAACC 1
RESULT 815
BD065825
LOCUS                17 bp DNA linear PAT 27-AUG-2002
DEFINITION           An antisense oligonucleotide preparation method.
ACCESSION             BD065825
VERSION               BD065825.1 GI:22611428
KEYWORDS              JP 2001511000-A/460.
SOURCE               unidentified
ORGANISM              unclassified.
REFERENCE             1 (bases 1 to 17)
AUTHORS              Schlingensiepen,K.H. and Brysch,W.
TITLES               An antisense oligonucleotide preparation method
JOURNAL              Patent: JP 2001511000-A 460 07-AUG-2001;
                    BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT              OS Unknown
PN JP 2001511000-A/460
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSTIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2570 GTGTTTAAAAA 2586
Db 1 GTCTTTAAAAAACA 17
RESULT 816
BD067807/c
LOCUS                17 bp RNA linear PAT 27-AUG-2002
DEFINITION           Enzymatic nucleic acid treatment of diseases or conditions related
                    to levels of epidermal growth factor receptors.
ACCESSION             BD067807
VERSION               BD067807.1 GI:22613410
KEYWORDS              JP 2001511003-A/647.
SOURCE               unidentified
ORGANISM              unclassified.
REFERENCE             1 (bases 1 to 17)
AUTHORS              Akhtar,S., Fell,P. and Meswiggen,J.A.
TITLES               Enzymatic nucleic acid treatment of diseases or conditions related
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to levels of epidermal growth factor receptors
Patent: JP 2001511003-A 647 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
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PN JP 2001511003-A/647
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
Topology: linear;
CC Enzymatic nucleic acid treatment of diseases or conditions
related to
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Qy 3058 GATGCTTAAGGAGTTT 3074
Db 17 GATGCTTAAGGAGATT 1
RESULT 817
BD089823
LOCUS                17 bp DNA linear PAT 27-AUG-2002
DEFINITION           A method of arraying genome clone.
ACCESSION             BD089823
VERSION               BD089823.1 GI:22635433
KEYWORDS              JP 2001321190-A/2067.
SOURCE               synthetic construct
ORGANISM              other sequences; artificial sequences.
REFERENCE             1 (bases 1 to 17)
AUTHORS              Soeda,E.
TITLES               A method of arraying genome clone
JOURNAL              Patent: JP 2001321190-A 2067 20-NOV-2001;
                    THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
COMMENT              OS Artificial Sequence
PN JP 2001321190-A/2067
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09.C12N15/09.C12M1/00.C12Q1/68.G01N33/53.G01N33/566, PC
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Db      1 CACACATGCACATGCAC 17

RESULT 818
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LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION  BD091743
VERSION     BD091743.1 GI:22637354
KEYWORDS   WO 0073435-A/3
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE      441, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073435-A 3 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
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COMMENT    OS Artificial Sequence
            PN WO 0073435-A/3
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            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI
            PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50
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RESULT 820
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LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 787, a novel gene related to pollen allergy.
ACCESSION  BD091774
VERSION     BD091774.1 GI:22637385
KEYWORDS   WO 0073440-A/3
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
TITLE      787, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073440-A 3 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT    OS Artificial Sequence
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            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003192
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
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RESULT 821
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LOCUS      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 465, a novel gene related to pollen allergy.
ACCESSION  BD091751
VERSION     BD091751.1 GI:22637362
KEYWORDS   WO 0073439-A/3
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
            Takahashi,E. and Yokoi,A.
TITLE      465, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073439-A 3 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT    OS Artificial Sequence
            PN WO 0073439-A/3
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003191

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LOCUS BD097335 17 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for examination for allergosis.  
ACCESSION BD097335  
VERSION BD097335.1 GI:22642909  
KEYWORDS WO 0169259-A/6.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.  
TITLE Method for examination for allergosis  
JOURNAL Patent: WO 0165259-A 6 07-SEP-2001;  
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF  
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA  
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI  
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO  
COMMENT OS Artificial Sequence  
PN WO 0165259-A/6  
PD 07-SEP-2001  
PF 23-FEB-2001 WO 2001JP001372  
PR 02-MAR-2000 JP 00P 61832  
PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI  
HIROHISA SAITO  
PC G01N33/53, C12Q1/68, C12N15/12, G01N33/15, A01K67/027, A61K39/395,  
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QY 930 GAAAAAAAAACACACC 946  
Db 17 GAAAAAAAAAAAAAAC 1  
RESULT 822  
BD104864 17 bp DNA linear PAT 27-AUG-2002  
LOCUS BD104864  
DEFINITION Kit and method for determining HLA type.  
ACCESSION BD104864  
VERSION BD104864.1 GI:22650438  
KEYWORDS WO 0192572-A/968.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.  
TITLE Kit and method for determining HLA type  
JOURNAL Patent: WO 0192572-A 968 06-DEC-2001;  
NISHINO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA  
COMMENT OS Artificial Sequence  
PN WO 0192572-A/968  
PD 06-DEC-2001  
PF 01-JUN-2001 WO 2001JP004662  
PR 01-JUN-2000 JP 00P 164798  
PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA  
P1 SHOGO MORIYA, MICHIO NISHIDA  
PC C12Q1/68, C12N15/00, C12N15/09, G01N33/53  
CC Description of Artificial Sequence: capture

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library RPCI-11"  
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Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 644 CACACATCCACGAC 660  
Db 1 CACACATGCACATGCAC 17  
RESULT 824  
E32456 18 bp DNA linear PAT 18-JUN-2001  
LOCUS E32456  
DEFINITION Mammal-derived tissue specific physiologically active protein.  
ACCESSION E32456  
VERSION E32456.1 GI:13018692  
KEYWORDS JP 2000037190-A/16.  
FEATURES  
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Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 4.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 547 CACCGAGTCTCCGAGTG 563  
Db 1 CACAGAGTCACCGAGTG 17  
RESULT 823  
AB068038 17 bp DNA linear SYN 21-MAY-2003  
LOCUS AB068038  
DEFINITION Synthetic construct DNA, forward primer for human STS sts-D1S2660 at 1p36.  
ACCESSION AB068038  
VERSION AB068038.1 GI:15128842  
KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K., Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H., Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A. and Soeda,E.  
TITLE A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36  
JOURNAL Genomics 74 (1), 55-70 (2001)  
MEDLINE 21269192  
PUBMED 11374902  
REFERENCE 2 (bases 1 to 17)  
AUTHORS Horii,A.  
TITLE Direct Submission  
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)

SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.  
TITLE Mammal-derived tissue specific physiologically active protein  
JOURNAL Patent: JP 2000037190-A 16 08-FEB-2000;  
JAPAN TOBACCO INC  
COMMENT OS Artificial Sequence  
PN JP 2000037190-A/16  
PD 08-FEB-2000  
PF 23-JUL-1998 JP 1998225228  
PR  
PI JUN NISHIU YUSUKE NAKAMURA TOSHIHIRO TANAKA  
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC  
C12N15/02,  
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),  
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LOCUS AX048440 20 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 39 from Patent WO0071747.  
ACCESSION AX048440  
VERSION AX048440.1 GI:12225604  
KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM  
REFERENCE 1  
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.  
TITLE Detection system for separating constituents of a sample and  
production and use of the same  
JOURNAL Patent: WO 0071747-A 39 30-NOV-2000;  
Aventis Research & Technologies GmbH & Co. KG (DE)  
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LOCUS AX048440 20 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 39 from Patent WO0071747.  
ACCESSION AX048440  
VERSION AX048440.1 GI:12225604  
KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM  
REFERENCE 1  
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.  
TITLE Detection system for separating constituents of a sample and  
production and use of the same  
JOURNAL Patent: WO 0071747-A 39 30-NOV-2000;  
Aventis Research & Technologies GmbH & Co. KG (DE)  
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LOCUS AX048441 20 bp DNA linear PAT 12-JAN-2001

DEFINITION Sequence 40 from Patent WO0071747.  
ACCESSION AX048441  
VERSION AX048441.1 GI:12225605  
KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM  
REFERENCE 1  
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.  
TITLE Detection system for separating constituents of a sample and  
production and use of the same  
JOURNAL Patent: WO 0071747-A 40 30-NOV-2000;  
Aventis Research & Technologies GmbH & Co. KG (DE)  
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LOCUS AX048442 20 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 41 from Patent WO0071747.  
ACCESSION AX048442  
VERSION AX048442.1 GI:12225606  
KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM  
REFERENCE 1  
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.  
TITLE Detection system for separating constituents of a sample and  
production and use of the same  
JOURNAL Patent: WO 0071747-A 41 30-NOV-2000;  
Aventis Research & Technologies GmbH & Co. KG (DE)  
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LOCUS AX048443 20 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 42 from Patent WO0071747.  
ACCESSION AX048443  
VERSION AX048443.1 GI:12225607  
KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM

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REFERENCE
AUTHORS Boekenkamp,D., Hoppe,H.U. and Bургstaller,P.
TITLE Detection system for separating constituents of a sample and
JOURNAL production and use of the same
PATENT: WO 0071747-A 42 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
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DEFINITION Sequence 29 from patent US 6635422.
ACCESSION AR409916
VERSION AR409916.1 GI:40161051
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 33)
AUTHORS Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
TITLE Methods for isolating and characterizing endogenous mRNA-protein
(mRNP) complexes
JOURNAL Patent: US 6635422-A 29 21-OCT-2003;
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Best Local Similarity 63.6%; Pred. No. 8e+02;
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RESULT 830
AR174027
LOCUS AR174027 14 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 17 from patent US 6306624.
ACCESSION AR174027
VERSION AR174027.1 GI:17914347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 14)
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE Retinoid metabolizing protein
JOURNAL Patent: US 6306624-A 17 23-OCT-2001;
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LOCUS BD073880 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION BD073880
VERSION BD073880.1 GI:22619483
KEYWORDS JP 2001512698-A/5.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 5 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/5
PD 28-AUG-2001
PF 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
C1201/68,C07K14/435,C07K16/18,C12N1/15,C12N15/09, PC
C12F21/02,
PC C12P21/08,C12N15/00
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LOCUS AR084519 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 8 from patent US 5981185.
ACCESSION AR084519
VERSION AR084519.1 GI:10011290
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 8 09-NOV-1999;
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Job time : 36 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-633-163-47

Perfect score: 4267

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 537 seqs, 10400 residues

Total number of hits satisfying chosen parameters: 1074

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 579 summaries

Database : fetchrng47.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| C 123 | 20   | 0.5 | 20 | 1 | ADI80189 | Human transforming | C 196 | 18   | 0.4 | 18 | 1 | AAQ78418 | TGF-beta gene phos    |
| C 124 | 20   | 0.5 | 20 | 1 | ADI80229 | Mouse transforming | C 197 | 18   | 0.4 | 18 | 1 | AAV63218 | Reverse PCR primer    |
| C 125 | 20   | 0.5 | 20 | 1 | ADI80235 | Mouse transforming | C 198 | 18   | 0.4 | 18 | 1 | AAV48953 | TGF-beta2 antisens    |
| C 126 | 20   | 0.5 | 20 | 1 | ADI80261 | Mouse transforming | C 199 | 18   | 0.4 | 18 | 1 | AAZ65457 | Immunosuppressant     |
| C 127 | 20   | 0.5 | 20 | 1 | ADI80261 | Mouse transforming | C 200 | 18   | 0.4 | 20 | 1 | AAQ05124 | Probe used to score   |
| C 128 | 20   | 0.5 | 20 | 1 | ADI80046 | Human transforming | C 201 | 17.8 | 0.4 | 21 | 1 | AAE97183 | Human gene single     |
| C 129 | 20   | 0.5 | 20 | 1 | ADI80125 | Mouse transforming | C 202 | 17.8 | 0.4 | 21 | 1 | AAE97183 | DNA sequence #3 fr    |
| C 130 | 20   | 0.5 | 20 | 1 | ADI80138 | Mouse transforming | C 203 | 17.8 | 0.4 | 21 | 1 | AAE97183 | DNA sequence #3 fr    |
| C 131 | 20   | 0.5 | 20 | 1 | ADI80151 | Mouse transforming | C 204 | 17.4 | 0.4 | 19 | 1 | AAV48945 | TGF-beta2 antisens    |
| C 132 | 20   | 0.5 | 20 | 1 | ADI80237 | Mouse transforming | C 205 | 17.4 | 0.4 | 19 | 1 | AAV48966 | TGF-beta2 antisens    |
| C 133 | 20   | 0.5 | 20 | 1 | ADI80248 | Mouse transforming | C 206 | 17.4 | 0.4 | 19 | 1 | ADO23060 | Human transforming    |
| C 134 | 20   | 0.5 | 20 | 1 | ADI80256 | Mouse transforming | C 207 | 17.4 | 0.4 | 20 | 1 | AA80354  | Human transforming    |
| C 135 | 20   | 0.5 | 20 | 1 | ADI80262 | Mouse transforming | C 208 | 17.4 | 0.4 | 20 | 1 | ADI80042 | Human transforming    |
| C 136 | 20   | 0.5 | 20 | 1 | ADI80265 | Mouse transforming | C 209 | 17.4 | 0.4 | 20 | 1 | ADI80069 | Human transforming    |
| C 137 | 20   | 0.5 | 20 | 1 | ADI80272 | Mouse transforming | C 210 | 17.4 | 0.4 | 20 | 1 | ADI80210 | Human transforming    |
| C 138 | 20   | 0.5 | 20 | 1 | ADI80097 | Mouse transforming | C 211 | 17.4 | 0.4 | 20 | 1 | ADI80200 | Human transforming    |
| C 139 | 20   | 0.5 | 20 | 1 | ADI80102 | Mouse transforming | C 212 | 17.4 | 0.4 | 20 | 1 | ADI80032 | Human transforming    |
| C 140 | 20   | 0.5 | 20 | 1 | ADI80115 | Mouse transforming | C 213 | 17.4 | 0.4 | 20 | 1 | ADI80057 | Human transforming    |
| C 141 | 20   | 0.5 | 20 | 1 | ADI80123 | Mouse transforming | C 214 | 17.4 | 0.4 | 20 | 1 | ADI80186 | Human transforming    |
| C 142 | 20   | 0.5 | 20 | 1 | ADI80145 | Mouse transforming | C 215 | 17.4 | 0.4 | 20 | 1 | ADL58461 | Human ESM-1 antisense |
| C 143 | 20   | 0.5 | 20 | 1 | ADI80161 | Mouse transforming | C 216 | 17.4 | 0.4 | 20 | 1 | ADL58461 | Human ESM-1 antisense |
| C 144 | 20   | 0.5 | 20 | 1 | ADI80249 | Mouse transforming | C 217 | 17.4 | 0.4 | 20 | 1 | AAQ09068 | Human fibrillin-1     |
| C 145 | 20   | 0.5 | 20 | 1 | ADI80258 | Mouse transforming | C 218 | 17.4 | 0.4 | 21 | 1 | AAQ09068 | Human polymorphic     |
| C 146 | 20   | 0.5 | 20 | 1 | ADI80121 | Human transforming | C 219 | 17.4 | 0.4 | 21 | 1 | AAQ26584 | Human transforming    |
| C 147 | 20   | 0.5 | 20 | 1 | ADI80183 | Mouse transforming | C 220 | 17.2 | 0.4 | 20 | 1 | AAQ26584 | TGF-beta2 antisens    |
| C 148 | 20   | 0.5 | 20 | 1 | ADI80236 | Mouse transforming | C 221 | 17   | 0.4 | 17 | 1 | AAV48933 | Immunosuppressant     |
| C 149 | 20   | 0.5 | 20 | 1 | ADI80250 | Mouse transforming | C 222 | 17   | 0.4 | 17 | 1 | AAV48933 | Immunosuppressant     |
| C 150 | 20   | 0.5 | 20 | 1 | ADI80266 | Mouse transforming | C 223 | 17   | 0.4 | 17 | 1 | AAZ65508 | TGF-beta2 antisens    |
| C 151 | 20   | 0.5 | 20 | 1 | ADI80273 | Mouse transforming | C 224 | 17   | 0.4 | 17 | 1 | AAZ65508 | Immunosuppressant     |
| C 152 | 20   | 0.5 | 20 | 1 | ADI80275 | Mouse transforming | C 225 | 17   | 0.4 | 17 | 1 | AAQ76724 | TGF-beta2 antisens    |
| C 153 | 20   | 0.5 | 20 | 1 | ADI80276 | Mouse transforming | C 226 | 17   | 0.4 | 20 | 1 | AAQ05125 | Probe used to score   |
| C 154 | 20   | 0.5 | 20 | 1 | ADI80108 | Mouse transforming | C 227 | 17   | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 155 | 20   | 0.5 | 20 | 1 | ADI80113 | Mouse transforming | C 228 | 17   | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 156 | 20   | 0.5 | 20 | 1 | ADI80155 | Mouse transforming | C 229 | 17   | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 157 | 20   | 0.5 | 20 | 1 | ADI80227 | Mouse transforming | C 230 | 17   | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 158 | 20   | 0.5 | 20 | 1 | ADI80267 | Mouse transforming | C 231 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 159 | 20   | 0.5 | 20 | 1 | AAQ41618 | TGF-beta2 sense st | C 232 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 160 | 19.4 | 0.5 | 21 | 1 | AAQ41618 | TGF-beta2 antisens | C 233 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 161 | 19.4 | 0.5 | 21 | 1 | AAQ41618 | TGF-beta2 antisens | C 234 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 162 | 19.4 | 0.5 | 21 | 1 | AAQ41618 | TGF-beta2 antisens | C 235 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 163 | 19.2 | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo | C 236 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 164 | 19.2 | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo | C 237 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 165 | 19.2 | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo | C 238 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 166 | 19.2 | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo | C 239 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 167 | 19.2 | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo | C 240 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 168 | 19.2 | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo | C 241 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 169 | 19.2 | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo | C 242 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 170 | 19.2 | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo | C 243 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 171 | 19   | 0.4 | 19 | 1 | AAZ59725 | DNA target used fo | C 244 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 172 | 19   | 0.4 | 19 | 1 | AAZ59725 | DNA target used fo | C 245 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 173 | 19   | 0.4 | 19 | 1 | AAZ59725 | DNA target used fo | C 246 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 174 | 19   | 0.4 | 19 | 1 | AAZ59725 | DNA target used fo | C 247 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 175 | 19   | 0.4 | 19 | 1 | AAZ59725 | DNA target used fo | C 248 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 176 | 19   | 0.4 | 19 | 1 | AAZ59725 | DNA target used fo | C 249 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 177 | 18.4 | 0.4 | 20 | 1 | AAZ59725 | DNA target used fo | C 250 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 178 | 18.4 | 0.4 | 20 | 1 | AAZ59725 | DNA target used fo | C 251 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |
| C 179 | 18.4 | 0.4 | 20 | 1 | AAZ59725 | DNA target used fo | C 252 | 16.8 | 0.4 | 20 | 1 | AAQ05125 | Human transforming    |



|     |      |     |    |   |          |                    |       |      |     |    |   |          |                     |
|-----|------|-----|----|---|----------|--------------------|-------|------|-----|----|---|----------|---------------------|
| 253 | 16.8 | 0.4 | 20 | 1 | ABL38811 | Immunostimulatory  | c 326 | 16   | 0.4 | 16 | 1 | AAQ78456 | TGF-beta gene phos  |
| 254 | 16.8 | 0.4 | 20 | 1 | ABL38811 | Immunostimulatory  | c 327 | 16   | 0.4 | 16 | 1 | AAV63225 | Phosphorothioate o  |
| 255 | 16.8 | 0.4 | 20 | 1 | ABA97650 | probe u. Unidenti  | 328   | 16   | 0.4 | 16 | 1 | AAV63226 | Phosphorothioate o  |
| 256 | 16.8 | 0.4 | 20 | 1 | ACH03107 | Immunostimulatory  | c 329 | 16   | 0.4 | 16 | 1 | AAV48957 | TGF-beta2 antisens  |
| 257 | 16.8 | 0.4 | 20 | 1 | ACH03107 | Immunostimulatory  | c 330 | 16   | 0.4 | 16 | 1 | AAV65460 | Immunosuppressant   |
| 258 | 16.8 | 0.4 | 20 | 1 | ACD99811 | Immunostimulatory  | c 331 | 16   | 0.4 | 16 | 1 | AA65458  | Immunosuppressant   |
| 259 | 16.8 | 0.4 | 20 | 1 | ACD99811 | Immunostimulatory  | c 332 | 16   | 0.4 | 16 | 1 | AA65458  | Immunosuppressant   |
| 260 | 16.8 | 0.4 | 20 | 1 | ADB37071 | Immunostimulatory  | 333   | 16   | 0.4 | 17 | 1 | AA200479 | Human thiodoxin     |
| 261 | 16.8 | 0.4 | 20 | 1 | ADB37071 | Immunostimulatory  | c 334 | 16   | 0.4 | 17 | 1 | AA265500 | Human thiodoxin     |
| 262 | 16.8 | 0.4 | 20 | 1 | ADB36893 | Immunostimulatory  | 335   | 16   | 0.4 | 17 | 1 | AB259896 | Immunosuppressant   |
| 263 | 16.8 | 0.4 | 20 | 1 | ADB36893 | Immunostimulatory  | c 336 | 16   | 0.4 | 17 | 1 | ADL49410 | Human K-Ras DNazym  |
| 264 | 16.8 | 0.4 | 20 | 1 | ADP86263 | Rat TGF-beta 2 PCR | c 337 | 16   | 0.4 | 17 | 1 | ADL49411 | Human PKR subestrat |
| 265 | 16.8 | 0.4 | 20 | 1 | ADP86263 | Rat TGF-beta 2 PCR | c 338 | 16   | 0.4 | 17 | 1 | AAQ38707 | First chimeric pri  |
| 266 | 16.8 | 0.4 | 20 | 1 | ABZ86060 | Human oligonucleot | c 339 | 16   | 0.4 | 18 | 1 | AAQ38707 | First chimeric pri  |
| 267 | 16.8 | 0.4 | 20 | 1 | ABZ89592 | Human oligonucleot | c 340 | 16   | 0.4 | 18 | 1 | AAQ38707 | Chimeric primer #1  |
| 268 | 16.8 | 0.4 | 20 | 1 | ABD22290 | Human stanniocalci | c 341 | 16   | 0.4 | 18 | 1 | AAQ38707 | Anti-proliferative  |
| 269 | 16.8 | 0.4 | 20 | 1 | ABD25822 | AI085559-derived o | 342   | 16   | 0.4 | 19 | 1 | ADL95318 | Oligonucleotide pr  |
| 270 | 16.8 | 0.4 | 20 | 1 | ADH67307 | Human glucocortic  | 343   | 16   | 0.4 | 19 | 1 | ADL95318 | Human IGF-1R siNA   |
| 271 | 16.8 | 0.4 | 20 | 1 | ADI80180 | Human transforming | c 344 | 16   | 0.4 | 19 | 1 | ADL95318 | Human IGF-1R trans  |
| 272 | 16.8 | 0.4 | 20 | 1 | ADI80070 | Human transforming | 345   | 16   | 0.4 | 19 | 1 | ADL95318 | AI095492-derived o  |
| 273 | 16.8 | 0.4 | 20 | 1 | ADI80187 | Human transforming | c 346 | 16   | 0.4 | 20 | 1 | AAQ75580 | Reverse transcript  |
| 274 | 16.8 | 0.4 | 20 | 1 | ADI80040 | Human transforming | 347   | 16   | 0.4 | 20 | 1 | AAQ75580 | Rat P2X 7/P2Z PCR   |
| 275 | 16.8 | 0.4 | 20 | 1 | ADI80185 | Human transforming | c 348 | 16   | 0.4 | 20 | 1 | AAQ75580 | Human S-9 derived   |
| 276 | 16.8 | 0.4 | 20 | 1 | ADI80006 | Human transforming | c 349 | 16   | 0.4 | 20 | 1 | AAQ75580 | Human S-9 derived   |
| 277 | 16.8 | 0.4 | 20 | 1 | ADI80034 | Human transforming | c 350 | 16   | 0.4 | 20 | 1 | AAQ75580 | Human S-9 derived   |
| 278 | 16.8 | 0.4 | 20 | 1 | ADI80022 | Human transforming | c 351 | 16   | 0.4 | 20 | 1 | AAQ75580 | Human S-9 derived   |
| 279 | 16.8 | 0.4 | 20 | 1 | ADI80043 | Human transforming | 352   | 16   | 0.4 | 20 | 1 | ADA09834 | Antisense nested P  |
| 280 | 16.8 | 0.4 | 20 | 1 | ADI80173 | Human transforming | 353   | 16   | 0.4 | 20 | 1 | AB291658 | Human oligonucleot  |
| 281 | 16.8 | 0.4 | 20 | 1 | ADI80045 | Human transforming | c 354 | 16   | 0.4 | 20 | 1 | AB291658 | Human CD23 + A1261  |
| 282 | 16.8 | 0.4 | 20 | 1 | ADK79195 | Chimeric phosphoro | 355   | 16   | 0.4 | 20 | 1 | AB298155 | Human oligonucleot  |
| 283 | 16.8 | 0.4 | 20 | 1 | ADOS3074 | Farnesoid X recept | 356   | 16   | 0.4 | 20 | 1 | AB289703 | Human oligonucleot  |
| 284 | 16.8 | 0.4 | 21 | 1 | AAQ73754 | Rice starch branch | 357   | 16   | 0.4 | 20 | 1 | AB288813 | Human oligonucleot  |
| 285 | 16.8 | 0.4 | 21 | 1 | AAQ73754 | Reverse transcript | 358   | 16   | 0.4 | 20 | 1 | AB288869 | Human oligonucleot  |
| 286 | 16.6 | 0.4 | 24 | 1 | ADD29304 | Molecular and biol | c 359 | 16   | 0.4 | 20 | 1 | ABD25043 | AI128305-derived o  |
| 287 | 16.4 | 0.4 | 18 | 1 | AAQ78427 | TGF-beta gene phos | 360   | 16   | 0.4 | 20 | 1 | ABD31186 | Human CD23-derived  |
| 288 | 16.4 | 0.4 | 18 | 1 | AAQ78484 | TGF-beta gene phos | c 361 | 16   | 0.4 | 20 | 1 | ABD27888 | AA258396-derived o  |
| 289 | 16.4 | 0.4 | 18 | 1 | AAZ65442 | Immunosuppressant  | c 362 | 16   | 0.4 | 20 | 1 | ADJ60020 | Oligonucleotide as  |
| 290 | 16.4 | 0.4 | 18 | 1 | AAZ65510 | Immunosuppressant  | c 363 | 16   | 0.4 | 20 | 1 | ADL58072 | Human ESM-1 antise  |
| 291 | 16.4 | 0.4 | 18 | 1 | AAZ65466 | Immunosuppressant  | c 364 | 16   | 0.4 | 20 | 1 | ADL58071 | Human ESM-1 antise  |
| 292 | 16.4 | 0.4 | 18 | 1 | ABA97624 | Probe c. Unidenti  | c 365 | 16   | 0.4 | 24 | 1 | AAZ59725 | Human oligonucleot  |
| 293 | 16.4 | 0.4 | 18 | 1 | ABA95897 | Probe c. for assay | c 366 | 16   | 0.4 | 24 | 1 | AAZ59725 | DNA target used fo  |
| 294 | 16.4 | 0.4 | 19 | 1 | AAAB5942 | Cdc 25 hs ribozyme | c 367 | 16   | 0.4 | 25 | 1 | ADH34300 | Hairpin oligonucle  |
| 295 | 16.4 | 0.4 | 19 | 1 | AAAB5941 | Cdc 25 hs ribozyme | 368   | 15.8 | 0.4 | 19 | 1 | ADH28312 | 3' untranslated re  |
| 296 | 16.4 | 0.4 | 19 | 1 | AAH61103 | Cdc25 hs ribozyme  | c 369 | 15.8 | 0.4 | 19 | 1 | AAV48959 | TGF-beta2 antisens  |
| 297 | 16.4 | 0.4 | 19 | 1 | AAH61104 | Cdc25 hs ribozyme  | c 370 | 15.8 | 0.4 | 19 | 1 | AAV48939 | TGF-beta2 antisens  |
| 298 | 16.4 | 0.4 | 19 | 1 | ADQ50911 | Anti-BMX siRNA rel | c 371 | 15.8 | 0.4 | 19 | 1 | AAZ65447 | Immunosuppressant   |
| 299 | 16.4 | 0.4 | 19 | 1 | ADQ90660 | Oligonucleotide of | 372   | 15.8 | 0.4 | 19 | 1 | AAZ65447 | PCBA HH ribozyme b  |
| 300 | 16.4 | 0.4 | 20 | 1 | AAZ32003 | MSH2 gene specific | c 373 | 15.8 | 0.4 | 19 | 1 | AAZ65447 | Immunostimulatory   |
| 301 | 16.4 | 0.4 | 20 | 1 | AAZ93327 | PCR primer used to | c 374 | 15.8 | 0.4 | 19 | 1 | AAZ65447 | Immunostimulatory   |
| 302 | 16.4 | 0.4 | 20 | 1 | ABN89197 | Human Talin antise | c 375 | 15.8 | 0.4 | 19 | 1 | AAH61643 | PCNA HH ribozyme b  |
| 303 | 16.4 | 0.4 | 20 | 1 | ADG90460 | Human talin phosph | c 376 | 15.8 | 0.4 | 19 | 1 | ABZ77654 | Angiogenesis inhib  |
| 304 | 16.4 | 0.4 | 20 | 1 | ADA45244 | Human MSH2 gene PC | c 377 | 15.8 | 0.4 | 19 | 1 | ABZ77654 | Angiogenesis inhib  |
| 305 | 16.4 | 0.4 | 20 | 1 | ABZ86070 | Human oligonucleot | c 378 | 15.8 | 0.4 | 19 | 1 | ABL38943 | Immunostimulatory   |
| 306 | 16.4 | 0.4 | 20 | 1 | ABZ89593 | Human oligonucleot | c 379 | 15.8 | 0.4 | 19 | 1 | ABL38943 | Immunostimulatory   |
| 307 | 16.4 | 0.4 | 20 | 1 | ABZ89178 | Human oligonucleot | 380   | 15.8 | 0.4 | 19 | 1 | ACD99445 | Immunostimulatory   |
| 308 | 16.4 | 0.4 | 20 | 1 | ABZ97995 | Human RANTES oligo | c 381 | 15.8 | 0.4 | 19 | 1 | ACD99445 | Immunostimulatory   |
| 309 | 16.4 | 0.4 | 20 | 1 | ABD25408 | AI122807-derived o | c 382 | 15.8 | 0.4 | 19 | 1 | ADB36515 | Immunostimulatory   |
| 310 | 16.4 | 0.4 | 20 | 1 | ABD31026 | Human RANTES-deriv | c 383 | 15.8 | 0.4 | 19 | 1 | ADB36515 | Immunostimulatory   |
| 311 | 16.4 | 0.4 | 20 | 1 | ABD22300 | Human stanniocalci | 384   | 15.8 | 0.4 | 19 | 1 | ADB42503 | Human infertility   |
| 312 | 16.4 | 0.4 | 20 | 1 | ADP25823 | AI085559-derived o | 385   | 15.8 | 0.4 | 19 | 1 | ADP50074 | Human BCL2 siNA lo  |
| 313 | 16.4 | 0.4 | 20 | 1 | ADI80176 | Human transforming | 386   | 15.8 | 0.4 | 19 | 1 | ADP49399 | Human BCL2 siNA up  |
| 314 | 16.4 | 0.4 | 20 | 1 | ADI80026 | Human transforming | c 387 | 15.8 | 0.4 | 19 | 1 | ADP49660 | Human BCL2 siNA lo  |
| 315 | 16.4 | 0.4 | 20 | 1 | ADJ59860 | Oligonucleotide as | c 388 | 15.8 | 0.4 | 19 | 1 | ADP49660 | Human BCL2 siNA up  |
| 316 | 16.4 | 0.4 | 20 | 1 | ADK81379 | Chimeric phosphoro | c 389 | 15.8 | 0.4 | 19 | 1 | ADP31627 | Human IGF-1R siNA   |
| 317 | 16.4 | 0.4 | 20 | 1 | ADL58169 | Chimeric phosphoro | 390   | 15.8 | 0.4 | 19 | 1 | ADP31627 | Human IGF-1R trans  |
| 318 | 16.4 | 0.4 | 20 | 1 | ADL58169 | Human ESM-1 antise | c 391 | 15.6 | 0.4 | 22 | 1 | ADQ14537 | TGF beta 2 3'-UTR   |
| 319 | 16.4 | 0.4 | 20 | 1 | ADL58390 | Human ESM-1 antise | 392   | 15.4 | 0.4 | 17 | 1 | AAZ63947 | Rabbit stromelysin  |
| 320 | 16.4 | 0.4 | 20 | 1 | ADQ45350 | Human oligonucleot | 393   | 15.4 | 0.4 | 17 | 1 | AAZ63947 | Rabbit stromelysin  |
| 321 | 16.4 | 0.4 | 20 | 1 | ADP85665 | Human Talin antise | 394   | 15.4 | 0.4 | 17 | 1 | AAV93710 | Human B-rat subetr  |
| 322 | 16.4 | 0.4 | 20 | 1 | ADP69475 | Human mitONEET-spe | c 395 | 15.4 | 0.4 | 17 | 1 | AAV93710 | Immunosuppressant   |
| 323 | 16.4 | 0.4 | 20 | 1 | ADP69581 | Human mitONEET-spe | 396   | 15.4 | 0.4 | 17 | 1 | ABZ59897 | Human K-Ras DNazym  |
| 324 | 16.4 | 0.4 | 20 | 1 | ADP69398 | Human mitONEET-spe | c 397 | 15.4 | 0.4 | 17 | 1 | ADL49626 | Human tumour suppr  |
| 325 | 16   | 0.4 | 16 | 1 | AAQ78464 | TGF-beta gene phos | c 398 | 15.4 | 0.4 | 17 | 1 | ADL49413 | Human PKR subestrat |

|       |      |     |    |   |          |                       |       |      |     |    |   |           |                    |
|-------|------|-----|----|---|----------|-----------------------|-------|------|-----|----|---|-----------|--------------------|
| C 399 | 15.4 | 0.4 | 17 | 1 | ADL49412 | Human PKR substrat    | c 472 | 14.8 | 0.3 | 18 | 1 | AAD18718  | Human oligonucleot |
| C 400 | 15.4 | 0.4 | 18 | 1 | AAQ78463 | TGF-beta gene phos    | c 473 | 14.8 | 0.3 | 18 | 1 | AAQ23524  | Primer #2. Uniden  |
| C 401 | 15.4 | 0.4 | 18 | 1 | AAQ57445 | Phosphorothioate o    | c 474 | 14.8 | 0.3 | 18 | 1 | ABL30793  | Human HLA genotypi |
| C 402 | 15.4 | 0.4 | 18 | 1 | ABL57541 | Nucleic acid probe    | c 475 | 14.8 | 0.3 | 18 | 1 | ACA62280  | Oligo (dC) primer. |
| C 403 | 15.4 | 0.4 | 18 | 1 | ABA97626 | Probe f. Unidenti     | c 476 | 14.8 | 0.3 | 18 | 1 | AD854824  | Hybridisation olig |
| C 404 | 15.4 | 0.4 | 18 | 1 | ABA97628 | Probe h. Unidenti     | c 477 | 14.8 | 0.3 | 18 | 1 | ADC64808  | 4B4 clone cDNA lib |
| C 405 | 15.4 | 0.4 | 18 | 1 | ABL95901 | Probe f for assayi    | c 478 | 14.8 | 0.3 | 18 | 1 | ADL06307  | Kid lingual tissue |
| C 406 | 15.4 | 0.4 | 18 | 1 | ABL95899 | Probe f for assayi    | c 479 | 14.8 | 0.3 | 18 | 1 | ADL06309  | Kid lingual tissue |
| C 407 | 15.4 | 0.4 | 18 | 1 | ABL95898 | Probe d for assayi    | c 480 | 14.8 | 0.3 | 18 | 1 | ADF31330  | Human MEGSIN gene  |
| C 408 | 15.4 | 0.4 | 18 | 1 | ABZ10862 | Haematopoietic cel    | c 481 | 14.8 | 0.3 | 18 | 1 | ADO28562  | Displacement oligo |
| C 409 | 15.4 | 0.4 | 19 | 1 | AAV40352 | Maize oligonucleot    | c 482 | 14.8 | 0.3 | 18 | 1 | ADO26670  | Synthetic leader s |
| C 410 | 15.4 | 0.4 | 19 | 1 | AAA72748 | PCR primer WB242 f    | c 483 | 14.8 | 0.3 | 18 | 1 | ADO26652  | Synthetic leader s |
| C 411 | 15.4 | 0.4 | 19 | 1 | AAA85943 | Cdc 25 hs ribozyme    | c 484 | 14.8 | 0.3 | 18 | 1 | ADO26640  | Synthetic leader s |
| C 412 | 15.4 | 0.4 | 19 | 1 | AAA85940 | Cdc 25 hs ribozyme    | c 485 | 14.8 | 0.3 | 18 | 1 | ADO26688  | Synthetic leader s |
| C 413 | 15.4 | 0.4 | 19 | 1 | AAZ70263 | Human biallelic ma    | c 486 | 14.8 | 0.3 | 18 | 1 | ADO26708  | Synthetic leader s |
| C 414 | 15.4 | 0.4 | 19 | 1 | AAZ29275 | Antisense nucleoti    | c 487 | 14.8 | 0.3 | 18 | 1 | ADO26642  | Synthetic leader s |
| C 415 | 15.4 | 0.4 | 19 | 1 | AAW1584  | Human MPROT13 forw    | c 488 | 14.8 | 0.3 | 18 | 1 | ADSO8016  | Oligonucleotide of |
| C 416 | 15.4 | 0.4 | 19 | 1 | AAQ89901 | Oligonucleotide #2    | c 489 | 14.6 | 0.3 | 15 | 1 | ABN87920  | Human GSR allele s |
| C 417 | 15.4 | 0.4 | 19 | 1 | AAH61102 | Cdc25 hs ribozyme     | c 490 | 14.4 | 0.3 | 16 | 1 | AAQ78445  | TGF-beta gene phos |
| C 418 | 15.4 | 0.4 | 19 | 1 | AAH61105 | Cdc25 hs ribozyme     | c 491 | 14.4 | 0.3 | 16 | 1 | AAV48961  | TGF-beta2 antisens |
| C 419 | 15.4 | 0.4 | 19 | 1 | ABL41198 | Human p27 gene pol    | c 492 | 14.4 | 0.3 | 16 | 1 | AAV48954  | TGF-beta2 antisens |
| C 420 | 15.4 | 0.4 | 19 | 1 | ABA97625 | Probe d. Unidenti     | c 493 | 14.4 | 0.3 | 16 | 1 | AAV18362  | RT-PCR primer of t |
| C 421 | 15.4 | 0.4 | 19 | 1 | ACA62440 | KCV core protein f    | c 494 | 14.4 | 0.3 | 16 | 1 | AAV18363  | RT-PCR primer of t |
| C 422 | 15.4 | 0.4 | 19 | 1 | ADS90818 | Oligonucleotide of    | c 495 | 14.4 | 0.3 | 16 | 1 | ABL46313  | Mouse scavenger re |
| C 423 | 15.4 | 0.4 | 19 | 1 | ADS75429 | TAK-1 gene PCR pri    | c 496 | 14.4 | 0.3 | 17 | 1 | ADL49413  | Human PKR substrat |
| C 424 | 15.4 | 0.4 | 20 | 1 | AF877713 | Human Glutathione     | c 497 | 14.4 | 0.3 | 17 | 1 | ADL49412  | Human PKR substrat |
| C 425 | 15   | 0.4 | 15 | 1 | AAV48999 | TGF-beta2 antisens    | c 498 | 14.4 | 0.3 | 17 | 1 | AAQ26183  | HLA-DR beta sub-ty |
| C 426 | 15   | 0.4 | 15 | 1 | AAV48950 | TGF-beta2 antisens    | c 499 | 14.4 | 0.3 | 17 | 1 | AAQ52216  | Neuroblastoma spec |
| C 427 | 15   | 0.4 | 15 | 1 | AAV48951 | TGF-beta2 antisens    | c 500 | 14.4 | 0.3 | 17 | 1 | AAQ51975  | B-cell mRNA ribozy |
| C 428 | 15   | 0.4 | 15 | 1 | AAV53238 | IGF-I oligonucleot    | c 501 | 14.4 | 0.3 | 17 | 1 | AAV63946  | Rabbit stromelysin |
| C 429 | 15   | 0.4 | 15 | 1 | AAV53320 | IGF-beta2 oligonucleo | c 502 | 14.4 | 0.3 | 17 | 1 | AAV63949  | Rabbit stromelysin |
| C 430 | 15   | 0.4 | 15 | 1 | AAV53237 | IGF-I oligonucleot    | c 503 | 14.4 | 0.3 | 17 | 1 | AAV71256  | Human KDR VEGF rec |
| C 431 | 15   | 0.4 | 15 | 1 | AAV60455 | Oligonucleotide c1    | c 504 | 14.4 | 0.3 | 17 | 1 | AAV5078   | Mouse flt-1 VEGF r |
| C 432 | 15   | 0.4 | 15 | 1 | ABK96652 | Interleukin-3 (IL-    | c 505 | 14.4 | 0.3 | 17 | 1 | AAV93711  | Mouse B-raf substr |
| C 433 | 15   | 0.4 | 17 | 1 | AAV18370 | RT-PCR primer of t    | c 506 | 14.4 | 0.3 | 17 | 1 | AAV93709  | Human B-raf substr |
| C 434 | 15   | 0.4 | 17 | 1 | ABT35106 | Tumour suppression    | c 507 | 14.4 | 0.3 | 17 | 1 | AAV14708  | Triple helix formi |
| C 435 | 15   | 0.4 | 17 | 1 | ADL49409 | Human PKR substrat    | c 508 | 14.4 | 0.3 | 17 | 1 | AAV14705  | Triple helix third |
| C 436 | 15   | 0.4 | 17 | 1 | ADP86176 | CpG immunostimulat    | c 509 | 14.4 | 0.3 | 17 | 1 | AAZ57107  | Human FCMQ-causing |
| C 437 | 15   | 0.4 | 18 | 1 | AAT41540 | Human apolipoprote    | c 510 | 14.4 | 0.3 | 17 | 1 | AAV05267  | Hammerhead ribozym |
| C 438 | 15   | 0.4 | 18 | 1 | AAV54164 | Nucleotide sequenc    | c 511 | 14.4 | 0.3 | 17 | 1 | AAV06339  | Hammerhead ribozym |
| C 439 | 15   | 0.4 | 18 | 1 | AAV18372 | RT-PCR primer of t    | c 512 | 14.4 | 0.3 | 17 | 1 | AAV03387  | Hammerhead ribozym |
| C 440 | 15   | 0.4 | 18 | 1 | AAZ90646 | Human adipose tiss    | c 513 | 14.4 | 0.3 | 17 | 1 | AAV06340  | Hammerhead ribozym |
| C 441 | 15   | 0.4 | 18 | 1 | ADL95317 | Anti-proliferative    | c 514 | 14.4 | 0.3 | 17 | 1 | AAV03071  | Hammerhead ribozym |
| C 442 | 15   | 0.4 | 20 | 1 | AAV32003 | MSH2 gene specific    | c 515 | 14.4 | 0.3 | 17 | 1 | AAH95613  | Human Chk1 ribozym |
| C 443 | 15   | 0.4 | 20 | 1 | ADA45244 | Human MSH2 gene PC    | c 516 | 14.4 | 0.3 | 17 | 1 | ABX00233  | Human NMOG Hammeth |
| C 444 | 15   | 0.4 | 23 | 1 | ADQ14575 | TGF beta 2 3'-UTR     | c 517 | 14.4 | 0.3 | 17 | 1 | ABQ099687 | Murine Ikbkap exon |
| C 445 | 14.8 | 0.3 | 18 | 1 | AAQ70698 | C-Rich oligonucleo    | c 518 | 14.4 | 0.3 | 17 | 1 | ABT39218  | Tumour suppression |
| C 446 | 14.8 | 0.3 | 18 | 1 | AAQ57781 | M.avium-intracellu    | c 519 | 14.4 | 0.3 | 17 | 1 | ABZ59895  | Human K-Ras DNazym |
| C 447 | 14.8 | 0.3 | 18 | 1 | AAQ79242 | Guanosine rich oli    | c 520 | 14.4 | 0.3 | 17 | 1 | ACC66553  | Murine oligonucleo |
| C 448 | 14.8 | 0.3 | 18 | 1 | AAQ79243 | Guanosine rich oli    | c 521 | 14.4 | 0.3 | 17 | 1 | ACC64890  | Murine oligonucleo |
| C 449 | 14.8 | 0.3 | 18 | 1 | AAQ78447 | TGF-beta gene phos    | c 522 | 14.4 | 0.3 | 17 | 1 | ACC67051  | Tumour suppression |
| C 450 | 14.8 | 0.3 | 18 | 1 | AAQ78430 | TGF-beta gene phos    | c 523 | 14.4 | 0.3 | 17 | 1 | ADB42062  | Tumour suppression |
| C 451 | 14.8 | 0.3 | 18 | 1 | AAQ78439 | TGF-beta gene phos    | c 524 | 14.4 | 0.3 | 17 | 1 | ADB40778  | Tumour suppression |
| C 452 | 14.8 | 0.3 | 18 | 1 | AAQ78436 | TGF-beta gene phos    | c 525 | 14.4 | 0.3 | 17 | 1 | ADB44127  | Tumour suppression |
| C 453 | 14.8 | 0.3 | 18 | 1 | AAQ78466 | TGF-beta gene phos    | c 526 | 14.4 | 0.3 | 17 | 1 | ADB42783  | Tumour suppression |
| C 454 | 14.8 | 0.3 | 18 | 1 | AAQ78423 | TGF-beta gene phos    | c 527 | 14.4 | 0.3 | 17 | 1 | ADB40065  | Tumour suppression |
| C 455 | 14.8 | 0.3 | 18 | 1 | AAQ78483 | TGF-beta gene phos    | c 528 | 14.4 | 0.3 | 17 | 1 | ADB40890  | Tumour suppression |
| C 456 | 14.8 | 0.3 | 18 | 1 | AAQ75026 | PCR primer. Synth     | c 529 | 14.4 | 0.3 | 17 | 1 | ADB31052  | Cholesterol homeos |
| C 457 | 14.8 | 0.3 | 18 | 1 | AAV1660  | Viral integrase in    | c 530 | 14.4 | 0.3 | 17 | 1 | ADP62143  | Human PCP1 DNA fr  |
| C 458 | 14.8 | 0.3 | 18 | 1 | AAV54166 | Nucleotide sequenc    | c 531 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 459 | 14.8 | 0.3 | 18 | 1 | AAV54169 | Nucleotide sequenc    | c 532 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 460 | 14.8 | 0.3 | 18 | 1 | AAV21971 | Nuclease resistant    | c 533 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 461 | 14.8 | 0.3 | 18 | 1 | AAV79242 | Oligonucleotide #3    | c 534 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 462 | 14.8 | 0.3 | 18 | 1 | AAZ65449 | Immunosuppressant     | c 535 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 463 | 14.8 | 0.3 | 18 | 1 | AAZ65505 | Immunosuppressant     | c 536 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 464 | 14.8 | 0.3 | 18 | 1 | AAZ65456 | Immunosuppressant     | c 537 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 465 | 14.8 | 0.3 | 18 | 1 | AAZ65453 | Immunosuppressant     | c 538 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 466 | 14.8 | 0.3 | 18 | 1 | AAZ90648 | Human adipose tiss    | c 539 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 467 | 14.8 | 0.3 | 18 | 1 | AAZ90645 | Human adipose tiss    | c 540 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 468 | 14.8 | 0.3 | 18 | 1 | AAZ90645 | Human adipose tiss    | c 541 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 469 | 14.8 | 0.3 | 18 | 1 | AAZ58387 | Polynucleotide # 3    | c 542 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 470 | 14.8 | 0.3 | 18 | 1 | ABL57543 | Nucleic acid probe    | c 543 | 14.4 | 0.3 | 17 | 1 | ADP62144  | Human PCP1 DNA fr  |
| C 471 | 14.8 | 0.3 | 18 | 1 | AAV33708 | Simple sequence re    | c 544 | 14.4 | 0.3 | 18 | 1 | AAZ22554  | Antisense oligonuc |
| C 472 | 14.8 | 0.3 | 18 | 1 | AAZ22554 | Antisense oligonuc    | c 545 | 14.4 | 0.3 | 18 | 1 | AAZ22554  | Antisense oligonuc |

c 545 14.4 0.3 18 1 AAX18953 Fructose:glucose r  
 c 546 14.4 0.3 18 1 AAA58386 Polynucleotide # 2  
 c 547 14.4 0.3 18 1 ABL56900 Nucleic acid probe  
 c 548 14.4 0.3 18 1 ABL57542 Nucleic acid probe  
 c 549 14.4 0.3 18 1 ABL56899 Nucleic acid probe  
 c 550 14.4 0.3 18 1 ABL57540 Nucleic acid probe  
 c 551 14.4 0.3 18 1 AAF75598 Binary encoded seq  
 c 552 14.4 0.3 18 1 ABA97627 Probe g. Unidenti  
 c 553 14.4 0.3 18 1 ABA97623 Probe b. Unidenti  
 c 554 14.4 0.3 18 1 ABL95900 Probe g for assay  
 c 555 14.4 0.3 18 1 ABL95896 Probe b for assay  
 c 556 14.4 0.3 18 1 AAL54242 RNAP recognition a  
 c 557 14.4 0.3 18 1 ABZ10926 Haematopoietic cel  
 c 558 14.4 0.3 18 1 ABZ10512 Haematopoietic cel  
 c 559 14.4 0.3 18 1 ADB54528 Hybridisation olig  
 c 560 14.4 0.3 18 1 ADB54950 Hybridisation olig  
 c 561 14.4 0.3 18 1 ADC70020 Primer oligo used  
 c 562 14.4 0.3 18 1 AAD61014 Human inhibitor-ka  
 c 563 14.4 0.3 18 1 ADE84380 Human lymphoid cel  
 c 564 14.4 0.3 18 1 ADN74905 Human CLCN2 gene 7  
 c 565 14.4 0.3 18 1 ADO79612 KIAA0783 extend pr  
 c 566 14.4 0.3 18 1 ADP46381 Extend primer 10 u  
 c 567 14.4 0.3 18 1 ADS90062 Oligonucleotide of  
 c 568 14.4 0.3 18 1 ADR78534 Human apolipoprote  
 c 569 14.2 0.3 20 1 ABZ88813 Human oligonucleot  
 c 570 14.2 0.3 20 1 ABD25043 A1128305-derived o  
 c 571 14 0.3 20 1 ABQ93687 Murine Ikbkap exon  
 c 572 14 0.3 17 1 ADB40890 Tumour suppression  
 c 573 14 0.3 17 1 ADI51580 Human tumour suppr  
 c 574 14 0.3 24 1 ABL41487 Human ATP-dependen  
 c 575 13.8 0.3 17 1 ADL49411 Human PKR substrat  
 c 576 13.8 0.3 17 1 AAX18370 RT-PCR primer of t  
 c 577 13.8 0.3 17 1 ADL49409 Human PKR substrat  
 c 578 13.8 0.3 17 1 ADP86176 Cpg immunostimulat  
 c 579 13.8 0.3 17 1 ADL49414 Human PKR substrat

## ALIGNMENTS

RESULT 1  
 AAX15250  
 ID AAX15250 standard; cDNA; 39 BP.

XX AC AAX15250;  
 XX  
 DT 20-MAR-2003 (revised)  
 DT 28-APR-1999 (first entry)  
 XX  
 XX Probe used for detection of TGF-beta-2 cDNA.  
 XX  
 KW Transforming growth factor-beta-2; TGF-beta-like protein;  
 KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;  
 KW bone repair; tissue repair; bone marrow protective agent;  
 KW cardioprotection; anti-inflammatory; immunosuppressive; ulcer; bed sore;  
 KW probe; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN EP891985-A1.  
 XX  
 XX 20-JAN-1999.  
 XX  
 XX 27-NOV-1990; 98EP-00113487.  
 XX  
 PR 06-DEC-1989; 89GB-00027546.  
 PR 27-NOV-1990; 90EP-00810922.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX  
 XX Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;

DR WPI; 1999-083520/08.  
 XX  
 PT Producing biologically active dimeric Transforming Growth Factor-beta -  
 PT by refolding new monomeric Transforming Growth Factor-beta, useful for  
 PT treatment of wounds and cancer.  
 XX  
 PS Example 1; Page 11; 32pp; English.  
 XX  
 CC The present sequence represents a probe used for the detection of cDNA  
 CC encoding the mature form of transforming growth factor-beta-2 (TGF-beta-  
 CC 2). Dimeric, biologically active TGF-beta-like protein can be produced by  
 CC subjecting the denatured monomeric form to refolding conditions. The new  
 CC monomeric S-sulphonated TGF-beta-like protein is useful for the  
 CC production of the dimeric, biologically active TGF-beta-like protein,  
 CC which is useful for the treatment of wounds (surface or internal) and  
 CC cancer in a mammal, in bone and tissue repair, as a bone marrow  
 CC protective agent, a mediator of cardioprotection, for the production of  
 CC an anti-inflammatory or immunosuppressive preparation. Treatment is  
 CC useful for animals, especially humans, and wound treatment (e.g. ulcers,  
 CC bed sores etc.) is particularly useful for the elderly. (Updated on 20-  
 CC MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to correct PR  
 CC field.)  
 XX  
 SQ Sequence 39 BP; 8 A; 6 C; 12 G; 13 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 35.8; DB 1; Length 39;  
 Best Local Similarity 94.9%; Pred. No. 0.93;  
 Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2124 GCTTTGGATGCTGCTACTGCTTTAGAAATGTCAGGAT 2162  
 DB 1 GCTTTGGATGCTGCTACTGCTTTAGAAATGTCAGGAT 39  
 |||||  
 RESULT 2  
 AAX15251/c  
 ID AAX15251 standard; cDNA; 39 BP.  
 XX  
 AC AAX15251;  
 XX  
 DT 20-MAR-2003 (revised)  
 DT 28-APR-1999 (first entry)  
 XX  
 DE Probe used for detection of TGF-beta-2 cDNA.  
 XX  
 KW Transforming growth factor-beta-2; TGF-beta-like protein;  
 KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;  
 KW bone repair; tissue repair; bone marrow protective agent;  
 KW cardioprotection; anti-inflammatory; immunosuppressive; ulcer; bed sore;  
 KW probe; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN EP891985-A1.  
 XX  
 XX 20-JAN-1999.  
 XX  
 XX 27-NOV-1990; 98EP-00113487.  
 XX  
 PR 06-DEC-1989; 89GB-00027546.  
 PR 27-NOV-1990; 90EP-00810922.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX  
 XX Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;  
 XX  
 XX WPI; 1999-083520/08.  
 XX  
 PT Producing biologically active dimeric Transforming Growth Factor-beta -  
 PT by refolding new monomeric Transforming Growth Factor-beta, useful for  
 PT treatment of wounds and cancer.  
 XX

PS Example 1; Page 11; 32pp; English.

XX The present sequence represents a probe used for the detection of cDNA

CC encoding the mature form of transforming growth factor-beta-2 (TGF-beta-

CC 2). Dimeric, biologically active TGF-beta-like protein can be produced by

CC subjecting the denatured monomeric form to refolding conditions. The new

CC monomeric S-sulphonated TGF-beta-like protein is useful for the

CC production of the dimeric, biologically active TGF-beta-like protein,

CC which is useful for the treatment of wounds (surface or internal) and

CC cancer in a mammal, in bone and tissue repair, as a bone marrow

CC protective agent, a mediator of cardioprotection, for the production of

CC an anti-inflammatory or immunosuppressive preparation. Treatment is

CC useful for animals, especially humans, and wound treatment (e.g. ulcers,

CC bed sores etc.) is particularly useful for the elderly. (Updated on 20-

CC MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to correct PR

CC field.)

XX Sequence 39 BP; 14 A; 6 C; 6 G; 13 T; 0 U; 0 Other;

SQ

Query Match 0.8%; Score 34.2; DB 1; Length 39;

Best Local Similarity 92.3%; Pred. No. 1.7;

Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2424 CTTTCAATATGATGTCAGTCTTGTAAATGACGCTAA 2462

DB 39 CTTTCAATATGATGTCAGTCTTGTAAATGACGCTAA 1

RESULT 3

AAH28309

ID AAH28309 standard; RNA; 33 BP.

XX

AC AAH28309;

XX

DT 05-SEP-2001 (first entry)

XX

DE 3' untranslated region sequence from TGF-beta gene.

XX

XX mRNA protein complex; tumour development; cell aging; death;

KW ribonomic profile; RNA-binding protein; ss.

XX

OS Unidentified.

XX

XX WO200148480-A1.

XX

XX 05-JUL-2001.

XX

XX 28-DEC-2000; 2000WO-US035583.

XX

XX 28-DEC-1999; 99US-0173338P.

XX

XX (KEEN/) KEENE J D.

XX

XX Keene JD, Tenenbaum SA, Carson C;

XX

XX WPI; 2001-425706/45.

XX

XX Partitioning endogenous mRNA-protein complexes in vivo, by contacting

PT sample comprising the complex with ligand that binds to a component of

PT the complex and separating complex by binding ligand with a binding

PT molecule.

XX

XX Example 6; Page 31; 49pp; English.

XX

XX The specification describes a method for partitioning endogenous cellular

CC mRNA-protein (mRNP) complexes. The method comprises contacting a

CC biological sample comprising mRNP complex with ligand that specifically

CC binds a component of mRNP complex, separating mRNP complex by binding the

CC ligand with a molecule specific for ligand, which is attached to the

CC solid support and then collecting the mRNP complex by removing the

CC support from the support. The method is useful for in vivo partitioning

CC of cellular mRNA protein complexes in a biological sample. The method is

CC useful for determining the ribonomic profile of a cell which has numerous

CC

CC uses including monitoring of tumour development, state of growth or state

CC of development, perturbations of a biological system such as disease,

CC drug or toxin treatment and the state of cell aging or death,

CC distinguishing ribonomic profiles among organisms, to discriminate

CC between transcriptional and post-transcriptional contributions to gene

CC expression and to track the movement of RNAs through RNP complexes, RNP

CC including the interactions of combinations of proteins with RNAs in RNP

CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'

CC untranslated region (UTR) of mRNA of various genes. The sequences contain

CC target sequences for RNA-binding proteins

XX

SQ Sequence 33 BP; 5 A; 3 C; 3 G; 0 T; 22 U; 0 Other;

Query Match 0.8%; Score 33; DB 1; Length 33;

Best Local Similarity 33.3%; Pred. No. 1.7;

Matches 11; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTAAATGTAATGTTCTTT 3296

DB 1 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 33

RESULT 4

ADQ14534

ID ADQ14534 standard; RNA; 33 BP.

XX

AC ADQ14534;

XX

DT 23-SEP-2004 (first entry)

XX

DE TGF beta 2 3'-UTR consensus sequence SEQ ID NO:29.

XX

XX metabolic state; mRNA protein complex; mRNP complex; RNA binding protein;

KW mRNA complex-associated protein; mRNP complex-associated protein;

KW mRNA target; protein target; physiological pathway;

KW TGF beta 2 3'-UTR consensus sequence; ss.

XX

OS Synthetic.

XX

XX WO2004057032-A1.

XX

XX 08-JUL-2004.

XX

XX 04-DEC-2003; 2003WO-US038475.

XX

XX 04-DEC-2002; 2002US-00309788.

XX

XX (RIBO-) RIBONOMICS INC.

XX

XX Keene JD, Tenenbaum SA, Carson CC, Phelps WC;

XX

XX WPI; 2004-525445/50.

XX

XX Assessing the metabolic state of a cell comprises isolating at least one

PT mRNP complex comprising at least one RNA binding protein, and at least

PT one mRNA or at least one mRNP complex-associated protein.

XX

XX Example 4; SEQ ID NO 29; 86pp; English.

XX

XX The present invention describes a method for assessing the metabolic

CC state of a cell. The method comprises isolating at least one mRNP complex

CC having at least one RNA binding protein, and at least one mRNA or at

CC least one mRNP complex-associated protein, and determining the expression

CC level of the mRNA or mRNP complex-associated protein, where the level of

CC expression of the at least one mRNA or the at least one mRNP complex-

CC associated protein is indicative of the metabolic state of the cell. The

CC method can be used for assessing the metabolic state in a cell, and for

CC identifying and evaluating mRNA and protein targets associated with mRNP

CC complexes and implicated in the expression of proteins involved in common

CC physiological pathways. The present sequence represents a TGF beta 2 3'-

CC UTR consensus sequence, which is used in an example from the present

CC invention.

XX

```
SQ Sequence 33 BP; 5 A; 3 C; 3 G; 0 T; 22 U; 0 Other;
Query Match 0.8%; Score 33; DB 1; Length 33;
Best Local Similarity 33.3%; Pred. No. 1.7;
Matches 11; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTTAATGTAATGCTTCTTT 3296
      ::::||||:||||:||||:||||:||||:
Db 1 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 33

RESULT 5
ADQ14572
ID ADQ14572 standard; RNA; 33 BP.
XX AC ADQ14572;
XX DT 23-SEP-2004 (first entry)
XX DE TGF beta 2 3'-UTR consensus sequence.
XX KW metabolic state; mRNA protein complex; mrnp complex; RNA binding protein;
XX KW mRNA complex-associated protein; mrnp complex-associated protein;
XX KW mRNA target; protein target; physiological pathway;
XX KW TGF beta 2 3'-UTR consensus sequence; ss.
XX OS Synthetic.
XX PN W02004057032-A1.
XX PD 08-JUL-2004.
XX PF 04-DEC-2003; 2003WO-US038475.
XX PR 04-DEC-2002; 2002US-00309788.
XX PA (RIBO-) RIBONOMICS INC.
XX PI Keene JD, Tenenbaum SA, Carson CC, Phelps WC;
XX WI; 2004-525445/50.
XX DR Assessing the metabolic state of a cell comprises isolating at least one
PT mrnp complex comprising at least one RNA binding protein, and at least
PT one mRNA or at least one mrnp complex-associated protein.
XX PS Example 4; Page 35; 86pp; English.
XX CC The present invention describes a method for assessing the metabolic
CC state of a cell. The method comprises isolating at least one mrnp complex
CC having at least one RNA binding protein, and at least one mRNA or at
CC least one mrnp complex-associated protein, and determining the expression
CC level of the mRNA or mrnp complex-associated protein, where the level of
CC expression of the at least one mRNA or the at least one mrnp complex-
CC associated protein is indicative of the metabolic state of the cell. The
CC method can be used for assessing the metabolic state in a cell, and for
CC identifying and evaluating mRNA and protein targets associated with mrnp
CC complexes and implicated in the expression of proteins involved in common
CC physiological pathways. The present sequence represents a TGF beta 2 3'-
CC UTR consensus sequence, which is used in an example from the present
CC invention.
SQ Sequence 33 BP; 5 A; 3 C; 3 G; 0 T; 22 U; 0 Other;
Query Match 0.8%; Score 33; DB 1; Length 33;
Best Local Similarity 33.3%; Pred. No. 1.7;
Matches 11; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Qy 3264 TTTTTCCTTTTAATGTAATGCTTCTTT 3296
      ::::||||:||||:||||:||||:||||:
Db 1 UUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 33

RESULT 6
AAH28311
ID AAH28311 standard; RNA; 25 BP.
XX AC AAH28311;
XX DT 05-SEP-2001 (first entry)
XX DE 3' untranslated region sequence from TGF-beta gene.
XX KW mRNA protein complex; tumour development; cell aging; death;
XX KW ribonomic profile; RNA-binding protein; ss.
XX OS Unidentified.
XX PN W0200148480-A1.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000WO-US035583.
XX PR 28-DEC-1999; 99US-0173338P.
XX PA (KEEN/) KEENE J D.
XX PI Keene JD, Tenenbaum SA, Carson C;
XX WI; 2001-425706/45.
XX DR Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX PS Example 6; Page 31; 49pp; English.
XX CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mrnp) complexes. The method comprises contacting a
CC biological sample comprising mrnp complex with ligand that specifically
CC binds a component of mrnp complex, separating mrnp complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mrnp complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
SQ Sequence 25 BP; 6 A; 3 C; 0 G; 0 T; 16 U; 0 Other;
Query Match 0.6%; Score 25; DB 1; Length 25;
Best Local Similarity 36.0%; Pred. No. 16;
Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

Qy 3693 TTCAATTTTTTTTATATATCTTCTT 3717
      :|||:||||:||||:||||:||||:
Db 1 UUCAUUUUUUUUUAUACUUCUU 25

RESULT 7
ADI80013
ID ADI80013 standard; DNA; 25 BP.
XX AC ADI80013;
XX CC
```

DT 22-APR-2004 (first entry)  
 XX Mouse transforming growth factor-beta 2 PCR probe.  
 DE  
 XX  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; mouse; murine; probe; ss.  
 XX  
 XX Mus musculus.  
 OS  
 XX US2004006030-A1.  
 PN  
 XX 08-JAN-2004.  
 XX  
 PD 02-JUL-2002; 2002US-00189267.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX Monia BP, Freier SM, Dobie KW;  
 PI WPI; 2004-081742/08.  
 XX  
 DR  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 XX Example 13; SEQ ID NO 14; 135pp; English.  
 PS  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a probe used in the exemplification of the invention.  
 XX  
 SQ Sequence 25 BP; 8 A; 4 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1789 AACACGAGCGGAGGGTGAATGGCT 1813  
 Db 1 AAACACGAGCGGAGGGTGAATGGCT 25  
 RESULT 8  
 ADQ14574  
 ID ADQ14574 standard; RNA; 25 BP.  
 XX  
 AC ADQ14574;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 XX TGF beta 2 3'-UTR consensus sequence.

XX metabolic state; mRNA protein complex; mRNP complex; RNA binding protein;  
 KW mRNA complex-associated protein; mRNP complex-associated protein;  
 KW mRNA target; protein target; physiological pathway;  
 KW TGF beta 2 3'-UTR consensus sequence; ss.  
 OS Synthetic.  
 XX WO2004057032-A1.  
 PN  
 XX 08-JUL-2004.  
 XX  
 PD 04-DEC-2003; 2003WO-US038475.  
 XX  
 PF 04-DEC-2002; 2002US-00309788.  
 XX  
 PR (RIBO-) RIBONOMICS INC.  
 XX  
 PA Keene JD, Tenenbaum SA, Carson CC, Phelps WC;  
 PI WPI; 2004-525445/50.  
 XX  
 DR Assessing the metabolic state of a cell comprises isolating at least one  
 XX mRNP complex comprising at least one RNA binding protein, and at least  
 PT one mRNA or at least one mRNP complex-associated protein.  
 PT  
 XX Example 4; Page 35; 86pp; English.  
 PS  
 XX The present invention describes a method for assessing the metabolic  
 CC state of a cell. The method comprises isolating at least one mRNP complex  
 CC having at least one RNA binding protein, and at least one mRNA or at  
 CC least one mRNP complex-associated protein, and determining the expression  
 CC level of the mRNA or mRNP complex-associated protein, where the level of  
 CC expression of the at least one mRNA or the at least one mRNP complex-  
 CC associated protein is indicative of the metabolic state of the cell. The  
 CC method can be used for assessing the metabolic state in a cell, and for  
 CC identifying and evaluating mRNA and protein targets associated with mRNP  
 CC complexes and implicated in the expression of proteins involved in common  
 CC physiological pathways. The present sequence represents a TGF beta 2 3'-  
 CC UTR consensus sequence, which is used in an example from the present  
 CC invention.  
 XX  
 SQ Sequence 25 BP; 6 A; 3 C; 0 G; 0 T; 16 U; 0 Other;  
 Query Match 0.6%; Score 25; DB 1; Length 25;  
 Best Local Similarity 36.0%; Pred. No. 16;  
 Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;  
 QY 3693 TTCAAATTTTATATATATATATCTT 3717  
 Db 1 UUCAUUUUUUUUUAUACUUCUU 25  
 RESULT 9  
 ADQ14536  
 ID ADQ14536 standard; RNA; 25 BP.  
 XX  
 AC ADQ14536;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 XX TGF beta 2 3'-UTR consensus sequence SEQ ID NO:31.  
 DE  
 XX metabolic state; mRNA protein complex; mRNP complex; RNA binding protein;  
 KW mRNA complex-associated protein; mRNP complex-associated protein;  
 KW mRNA target; protein target; physiological pathway;  
 KW TGF beta 2 3'-UTR consensus sequence; ss.  
 XX  
 OS Synthetic.  
 XX WO2004057032-A1.  
 PN  
 XX 08-JUL-2004.

XX 04-DEC-2003; 2003WO-US038475.  
 XX  
 PR 04-DEC-2002; 2002US-00309788.  
 XX  
 XX (RIBO-) RIBONOMICS INC.  
 XX  
 PI Keene JD, Tenenbaum SA, Carson CC, Phelps WC;  
 XX WPI; 2004-525445/50.  
 XX  
 XX Assessing the metabolic state of a cell comprises isolating at least one  
 PT mRNA complex comprising at least one RNA binding protein, and at least  
 PT one mRNA or at least one mRNA complex-associated protein.  
 XX  
 XX Example 4; SEQ ID NO 31; 86pp; English.  
 XX  
 CC The present invention describes a method for assessing the metabolic  
 CC state of a cell. The method comprises isolating at least one mRNA complex  
 CC having at least one RNA binding protein, and at least one mRNA or at  
 CC least one mRNA complex-associated protein, and determining the expression  
 CC level of the mRNA or mRNA complex-associated protein, where the level of  
 CC expression of the at least one mRNA or the at least one mRNA complex-  
 CC associated protein is indicative of the metabolic state of the cell. The  
 CC method can be used for assessing the metabolic state in a cell, and for  
 CC identifying and evaluating mRNA and protein targets associated with mRNA  
 CC complexes and implicated in the expression of proteins involved in common  
 CC physiological pathways. The present sequence represents a TGF beta 2 3'-  
 CC UTR consensus sequence, which is used in an example from the present  
 CC invention.  
 XX  
 SQ Sequence 25 BP; 6 A; 3 C; 0 G; 0 T; 16 U; 0 Other;  
 XX  
 Query Match 0.6%; Score 25; DB 1; Length 25;  
 Best Local Similarity 36.0%; Pred. No. 16;  
 Matches 9; Conservative 16; Mismatches 0; Indels 0; Gaps 0;  
 QY 3693 TTCAATTTTTTTATATCTATCTT 3717  
 Db 1 UUCAUUUUUUUUUAUUAUCUUCU 25  
 RESULT 10  
 ADI80005/c  
 ID ADI80005 standard; DNA; 26 BP.  
 XX  
 AC ADI80005;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human transforming growth factor-beta 2 reverse PCR primer.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotrophic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; human; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 DR  
 XX

PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 XX immune response.  
 XX  
 PS Example 13; SEQ ID NO 6; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotrophic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a primer used in the exemplification of the invention.  
 XX  
 SQ Sequence 26 BP; 10 A; 6 C; 2 G; 8 T; 0 U; 0 Other;  
 XX  
 Query Match 0.6%; Score 25; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2142 TGCCTTTAGAAATGTCAGGATAATT 2166  
 Db 25 TGCCTTTAGAAATGTCAGGATAATT 1  
 RESULT 11  
 ADJ76723  
 ID ADJ76723 standard; DNA; 23 BP.  
 XX  
 AC ADJ76723;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE TGFbeta forward PCR primer SEQ ID NO:1975.  
 XX  
 KW bronchial asthma; chronic obstructive pulmonary disease;  
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
 KW gene therapy; marker; PCR; primer; ss.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 PN EP1394274-A2.  
 XX  
 PD 03-MAR-2004.  
 XX  
 PF 04-AUG-2003; 2003EP-00254857.  
 XX  
 PR 06-AUG-2002; 2002JP-00229312.  
 XX  
 PR 20-MAR-2003; 2003JP-00077212.  
 XX  
 XX (GENO-) GENOX RES INC.  
 XX  
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;  
 XX WPI; 2004-193155/19.  
 DR  
 XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
 PT comparing the expression level of a marker gene in a biological sample  
 PT



PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.  
XX  
PS Example 11; SEQ ID NO 1975; 241pp; English.  
XX  
CC The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic  
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
CC genes (S1) whose expression levels increase when respiratory epithelial  
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
CC whose expression levels decrease when respiratory epithelial cells are  
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for  
CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
CC (2) a kit for screening for a candidate compound for a therapeutic agent  
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
CC an animal model for bronchial asthma or chronic obstructive pulmonary  
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
CC method for producing an animal model for bronchial asthma or chronic  
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
CC a marker gene or an antisense nucleic acid corresponding to a portion of  
CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
CC expression of the gene through an RNAi effect or an antibody recognising  
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
CC probe has been immobilised to assay a marker gene. (I) has respiratory  
CC and antiasthmatic activities, and can be used in gene therapy. The method  
CC is useful for testing for or screening for a therapeutic agent for  
CC bronchial asthma or chronic obstructive pulmonary disease. The present  
CC sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 23 BP; 9 A; 5 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 217 TTACCTTAAGCGAGAAAGTGCAA 239  
Db 1 TTACCTTAAGCGAGAAAGTGCAA 23  
  
RESULT 12  
AAQ41629/c  
ID AAQ41629 standard; cDNA; 26 BP.  
XX  
AC AAQ41629;  
XX  
XX 25-MAR-2003 (revised)  
DT 26-AUG-1993 (first entry)  
XX  
DE TGF-beta2 antisense strand (nucleotides 167-142) PCR primer.  
XX  
XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;  
KW cancer treatment; bone repair; growth regulation;  
KW polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
XX EP542679-A1.  
PN  
XX 19-MAY-1993.  
PD  
XX 03-NOV-1992; 92EP-00810845.  
PF  
XX 11-NOV-1991; 91EP-00810870.  
PR  
XX (CIBA ) CIBA GEIGY AG.  
PA  
XX  
PI McMaster GK, Cox D, Cerletti N, Kuhla J;  
XX  
XX WPI; 1993-161126/20.  
XX  
XX New hybrid transforming growth factor-beta molecules - comprise portions  
PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
PT antiinflammatory and immunosuppressive agents etc.  
XX  
XX Example 1; Page 40; 48pp; English.  
PS  
XX The invention covers hybrid TGF-beta molecules consisting of parts of the  
CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-  
CC beta polypeptides were constructed from the appropriate, PCR-amplified  
CC segments of the wild-type isoforms. For the construction of hybrid DNA  
CC molecules encoding TGF-beta hybrids all having the hinge points between  
CC amino acids 56 and 57, the primers AAQ41626-Q41631 (corresp. to the hinge  
CC regions) were used with the appropriate primers (see AAQ41608-Q41613)  
CC which flank the regions coding for each of the three full-length mature  
CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 26 BP; 8 A; 6 C; 6 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 22.8; DB 1; Length 26;  
Best Local Similarity 92.3%; Pred. No. 40;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2265 TGCCCATATCTATGAGTTTCAGACAC 2290  
Db 26 TGCCCGTATTATGAGTTTCAGACAC 1  
  
RESULT 13  
AAQ41628  
ID AAQ41628 standard; cDNA; 26 BP.  
XX  
AC AAQ41628;  
XX  
XX 25-MAR-2003 (revised)  
DT 26-AUG-1993 (first entry)  
XX  
DE TGF-beta2 sense strand (nucleotides 142-167) PCR primer.  
XX  
XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;  
KW cancer treatment; bone repair; growth regulation;  
KW polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
XX EP542679-A1.  
PN  
XX 19-MAY-1993.  
PD  
XX 03-NOV-1992; 92EP-00810845.  
PF  
XX 11-NOV-1991; 91EP-00810870.  
PR  
XX (CIBA ) CIBA GEIGY AG.  
PA  
XX  
PI McMaster GK, Cox D, Cerletti N, Kuhla J;  
XX  
XX WPI; 1993-161126/20.  
XX  
XX New hybrid transforming growth factor-beta molecules - comprise portions  
PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
PT antiinflammatory and immunosuppressive agents etc.  
XX  
XX Example 1; Page 40; 48pp; English.  
PS  
XX The invention covers hybrid TGF-beta molecules consisting of parts of the  
CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-

PI McMaster GK, Cox D, Cerletti N, Kuhla J;  
XX  
XX WPI; 1993-161126/20.  
XX  
XX New hybrid transforming growth factor-beta molecules - comprise portions  
PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
PT antiinflammatory and immunosuppressive agents etc.  
XX  
XX Example 1; Page 40; 48pp; English.  
PS  
XX The invention covers hybrid TGF-beta molecules consisting of parts of the  
CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-  
CC beta polypeptides were constructed from the appropriate, PCR-amplified  
CC segments of the wild-type isoforms. For the construction of hybrid DNA  
CC molecules encoding TGF-beta hybrids all having the hinge points between  
CC amino acids 56 and 57, the primers AAQ41626-Q41631 (corresp. to the hinge  
CC regions) were used with the appropriate primers (see AAQ41608-Q41613)  
CC which flank the regions coding for each of the three full-length mature  
CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 26 BP; 8 A; 6 C; 6 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 22.8; DB 1; Length 26;  
Best Local Similarity 92.3%; Pred. No. 40;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2265 TGCCCATATCTATGAGTTTCAGACAC 2290  
Db 26 TGCCCGTATTATGAGTTTCAGACAC 1  
  
RESULT 13  
AAQ41628  
ID AAQ41628 standard; cDNA; 26 BP.  
XX  
AC AAQ41628;  
XX  
XX 25-MAR-2003 (revised)  
DT 26-AUG-1993 (first entry)  
XX  
DE TGF-beta2 sense strand (nucleotides 142-167) PCR primer.  
XX  
XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;  
KW cancer treatment; bone repair; growth regulation;  
KW polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
XX EP542679-A1.  
PN  
XX 19-MAY-1993.  
PD  
XX 03-NOV-1992; 92EP-00810845.  
PF  
XX 11-NOV-1991; 91EP-00810870.  
PR  
XX (CIBA ) CIBA GEIGY AG.  
PA  
XX  
PI McMaster GK, Cox D, Cerletti N, Kuhla J;  
XX  
XX WPI; 1993-161126/20.  
XX  
XX New hybrid transforming growth factor-beta molecules - comprise portions  
PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
PT antiinflammatory and immunosuppressive agents etc.  
XX  
XX Example 1; Page 40; 48pp; English.  
PS  
XX The invention covers hybrid TGF-beta molecules consisting of parts of the  
CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-



CC beta polypeptides were constructed from the appropriate, PCR-amplified  
 CC segments of the wild-type isoforms. For the construction of hybrid DNA  
 CC molecules encoding TGF-beta hybrids all having the hinge points between  
 CC amino acids 56 and 57, the primers AAQ41626-Q41631 (corresp. to the hinge  
 CC regions) were used with the appropriate primers (see AAQ41608-Q41613)  
 CC which flank the regions coding for each of the three full-length mature  
 CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 26 BP; 6 A; 6 C; 6 G; 8 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 22.8; DB 1; Length 26;  
 Best Local Similarity 92.3%; Pred. No. 40;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2265 TGCCCATATCTATGAGGTTTCAGACAC 2290  
 Db 1 TGCCCGTATTATTGGAGTTTCAGACAC 26  
 RESULT 14  
 AAA76086  
 ID AAA76086 standard; DNA; 27 BP.  
 XX  
 AC AAA76086;  
 DT 08-DEC-2000 (first entry)  
 XX  
 DE Transforming Growth Factor-beta2 TGF-beta2 PCR primer #1.  
 XX  
 KW PCR primer; prostate cancer cell line; androgen independent; CL-1; CL-2;  
 KW LNCaP cell line; beta-actin; prostate-specific antigen;  
 KW Prostate specific membrane antigen; Basic fibroblast growth factor;  
 KW Vascular endothelial cell growth factor; Interleukin-6;  
 KW Transforming Growth Factor-beta1; transforming growth factor-beta2;  
 KW Transforming Growth Factor-beta-R; Epidermal growth factor receptor; PSA;  
 KW AR; PSAM; IL-8; VEGF; bFGF; IL-6; TGF-beta1; TGF-beta2; TGF-beta-R;  
 KW EGF-R; BCL-2; E-cadherin; p53; PTEN; Caveolin; c-myc; HER-2/neu; p27;  
 KW Androgen receptor; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200044879-A1.  
 PN  
 XX 03-AUG-2000.  
 PD  
 XX 28-JAN-2000; 2000WO-US002223.  
 PF  
 XX 28-JAN-1999; 99US-0117562P.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 PI Belldegrun AS, Teo C;  
 XX WPI; 2000-499329/44.  
 DR  
 XX Androgen independent, aggressively tumorigenic prostate cancer cell lines  
 PT designated CL-1 and CL-2, useful as tools for studying the cellular and  
 PT molecular mechanisms of prostate cancer progression.  
 XX  
 PS Example 2; Page 30; 90pp; English.  
 CC The present invention relates to androgen independent, aggressively  
 CC tumorigenic prostate cancer cell lines, CL-1 and CL-2, which are  
 CC sublines of the LNCaP cell line. The present sequence is a PCR primer  
 CC used to amplify a coding sequence expressed by the cell lines. The coding  
 CC sequences which were amplified in the present invention by the primers in  
 CC AAA76068 to AAA76107 were: beta-actin, prostate-specific antigen (PSA),  
 CC Androgen receptor (AR), Prostate specific membrane antigen (PSAM),  
 CC Interleukin-8 (IL-8), Vascular endothelial cell growth factor (VEGF),  
 CC Basic fibroblast growth factor (bFGF), Interleukin-6 (IL-6), Transforming  
 CC Growth Factor-beta1 (TGF-beta1), Transforming Growth Factor-beta2 (TGF-  
 CC beta2), Transforming Growth Factor-beta-R (TGF-beta-R), Epidermal growth

CC factor receptor (EGF-R), BCL-2, E-cadherin, p53, PTEN, Caveolin, c-myc,  
 CC HER-2/neu and p27. RT-PCR was used to monitor changes in coding sequence  
 CC expression, as the LNCaP parental lines progressed to the CL1 and CL2  
 CC sublines. The CL-1 and CL-2 sublines can be used as tools for studying  
 CC the cellular and molecular mechanisms of prostate cancer progression.  
 CC such as the expression patterns of various transcripts and proteins that  
 CC are associated with the progression of the non-metastatic, androgen-  
 CC dependent state to the metastatic androgen-independent state  
 XX  
 SQ Sequence 27 BP; 6 A; 10 C; 4 G; 7 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 22.8; DB 1; Length 27;  
 Best Local Similarity 92.3%; Pred. No. 45;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1278 CTGTCTTACCTGCAGCACCTCGACAT 1303  
 Db 2 CTGTCTTACCTGCAGCACCTCGATAT 27  
 RESULT 15  
 AAF82681/c  
 ID AAF82681 standard; DNA; 27 BP.  
 XX  
 AC AAF82681;  
 XX  
 DT 18-JUN-2001 (first entry)  
 XX  
 DE Human TGF-beta2 PCR primer #2.  
 XX  
 KW Human; androgen response element; ARE; cytostatic; gene therapy;  
 KW prostate-specific chimeric enhancer; transcriptional regulation;  
 KW Targeted gene expression; prostate cancer; prostate disorder;  
 KW prostate-specific antigen; PSA; transforming growth factor beta2;  
 KW TGF-beta2; PCR primer; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200127256-A2.  
 PN  
 XX 19-APR-2001.  
 PD  
 XX 13-OCT-2000; 2000WO-US028444.  
 PF  
 XX 14-OCT-1999; 99US-0159691P.  
 PR  
 XX 15-OCT-1999; 99US-0159730P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA SYSTEM.  
 XX  
 PI Wu L, Carey MF, Belldegrun AS;  
 XX WPI; 2001-273768/28.  
 DR  
 XX New polynucleotide, useful for treating prostatic cancer, comprises  
 PT prostate specific chimeric enhancer and proximal promoter sequence  
 PT operably linked to nucleic acid encoding heterologous polypeptide.  
 XX  
 PS Example 5; Page 73; 131pp; English.  
 XX  
 CC The present sequence was used in reverse transcriptase polymerase chain  
 CC reaction (RT-PCR) analysis of human prostate cancer cells. The invention  
 CC relates to an isolated polynucleotide comprising a prostate-specific  
 CC chimeric enhancer (PSE) sequence and a proximal promoter sequence  
 CC operably linked to a nucleic acid segment that encodes a heterologous  
 CC polypeptide. The PSE contains an ARE and specifically activates  
 CC transcription of the nucleic acid segment in a mammalian prostate cell.  
 CC The construct is useful for the treatment of a prostate disorder or a  
 CC metastasised prostate cancer, such as hyperplasia or hyperproliferation  
 CC of prostate cells. It is also useful for directing the tissue-specific  
 CC expression of a heterologous polypeptide in a human prostate cell. The  
 CC construct may be administered by injection, infection, transfection, or  
 CC liposome-mediated transfection, polybrene-mediated transfection, receptor  
 CC -mediated uptake or Ca-PO4-mediated transfection

Query Match 0.5%; Score 22; DB 1; Length 22;

```
Best Local Similarity 22.7%; Pred. No. 34;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAAATGGTTTTTTT 4099
Db 1 UUUUUUUUAUUGGUUUUUU 22

RESULT 18
AAH28312
ID AAH28312 standard; RNA; 25 BP.
XX
AC AAH28312;
XX
DT 05-SEP-2001 (first entry)
DE
DE 3' untranslated region sequence from TGP-beta gene.
XX
KW mRNA protein complex; tumour development; cell aging; death;
KW ribonomic profile; RNA-binding protein; ss.
XX
OS Unidentified.
XX
PN WO200148480-A1.
XX
PD
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035583.
XX
PR 28-DEC-1999; 99US-0173338P.
XX
PA (KEEN/) KEENE J D.
XX
PI Keene JD, Tenenbaum SA, Carson C;
XX
DR WPI; 2001-425706/45.
XX
PT Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT sample comprising the complex with ligand that binds to a component of
PT the complex and separating complex by binding ligand with a binding
PT molecule.
XX
PS Example 6; Page 31; 49pp; English.
XX
CC The specification describes a method for partitioning endogenous cellular
CC mRNA-protein (mRNP) complexes. The method comprises contacting a
CC biological sample comprising mRNP complex with ligand that specifically
CC binds a component of mRNP complex, separating mRNP complex by binding the
CC ligand with a molecule specific for ligand, which is attached to the
CC solid support and then collecting the mRNP complex by removing the
CC complex from the support. The method is useful for in vivo partitioning
CC of cellular mRNA protein complexes in a biological sample. The method is
CC useful for determining the ribonomic profile of a cell which has numerous
CC uses including monitoring of tumour development, state of growth or state
CC of development, perturbations of a biological system such as disease,
CC drug or toxin treatment and the state of cell aging or death,
CC distinguishing ribonomic profiles among organisms, to discriminate
CC between transcriptional and post-transcriptional contributions to gene
CC expression and to track the movement of RNAs through RNP complexes,
CC including the interactions of combinations of proteins with RNAs in RNP
CC complexes. AAH2831-AAH28316 represent sequences derived from the 3'
CC untranslated region (UTR) of mRNA of various genes. The sequences contain
CC target sequences for RNA-binding proteins
XX
SQ Sequence 25 BP; 2 A; 1 C; 2 G; 1 T; 17 U; 2 Other;

Query Match 0.5%; Score 22; DB 1; Length 25;
Best Local Similarity 22.7%; Pred. NO. 49;
Matches 5; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4078 TTTTCTTTAAATGGTTTTTTT 4099
Db 1 UUUUUUUUAUUGGUUUUUU 22
```

```
RESULT 19
ADJ76622
ID ADJ76622 standard; DNA; 25 BP.
XX
AC ADJ76622;
XX
DT 20-MAY-2004 (first entry)
DE
DE TGPB2 reverse PCR primer SEQ ID NO:1874.
XX
KW bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker; PCR; primer; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
PN EP1394274-A2.
XX
PD 03-MAR-2004.
XX
PF 04-AUG-2003; 2003EP-00254857.
XX
PR 06-AUG-2002; 2002JP-00293112.
PR 20-MAR-2003; 2003JP-00077212.
XX
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
PI WPI; 2004-193155/19.
XX
DR Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX
PS Example 11; SEQ ID NO 1874; 241pp; English.
XX
CC The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 25 BP; 8 A; 9 C; 5 G; 3 T; 0 U; 0 Other;
```

|                       |   |                                   |                           |            |
|-----------------------|---|-----------------------------------|---------------------------|------------|
| Query Match           | 0.5%;   | Score 21.8;                       | DB 1;                     | Length 25; |
| Best Local Similarity | 92.0%;  | Pred. NO. 52;                     |                           |            |
| Matches               | 23;   | Conservative                      | 0;                        | Mismatches |
|                       |   |                                   | 2;                        | Indels     |
|                       |   |                                   | 0;                        | Gaps       |
|                       |   |                                   | 0;                        |            |
| QY                    | 1759  | CCGAGCGCTACATCGATAGCAAGGT         | 1783                      |            |
|                       |   |                                   |                           |            |
| Db                    | 1   | CCGAGCGCTACATCGACAGCAAGT          | 25                        |            |
| RESULT 20             |   |                                   |                           |            |
| ID                    | AAF82680  | standard; DNA;                    | 24                        | BP.        |
| XX                    | AC  | AAF82680;                         |                           |            |
| XX                    | DT  | 18-JUN-2001                       | (first entry)             |            |
| XX                    | DE  | Human TGF-beta2                   | PCR primer #1.            |            |
| XX                    | Human;  | androgen response element; ARE;   | cytostatic; gene therapy; |            |
| XX                    | prostate-specific chimeric enhancer;                                      | transcriptional regulation;       |                           |            |
| XX                    | targeted gene expression; prostate cancer;                                | prostate disorder;                |                           |            |
| XX                    | prostate-specific antigen; PSA;   | transforming growth factor beta2; |                           |            |
| XX                    | TGF-beta2; PCR primer;  | ss.                               |                           |            |
| OS                    | Homo sapiens.   |                                   |                           |            |
| XX                    | WO200127256-A2.   |                                   |                           |            |
| XX                    | 19-APR-2001.  |                                   |                           |            |
| XX                    | 13-OCT-2000;  | 2000WO-US028444.                  |                           |            |
| XX                    | 14-OCT-1999;  | 99US-0159691P.                    |                           |            |
| XX                    | 15-OCT-1999;  | 99US-0159730P.                    |                           |            |
| XX                    | (REGC )   | UNIV CALIFORNIA SYSTEM.           |                           |            |
| XX                    | Wu L, Carey MF, Belldegrun AS;  |                                   |                           |            |
| XX                    | WPI;  | 2001-273768/28.                   |                           |            |
| XX                    | New polynucleotide, useful for treating prostatic cancer, comprises       |                                   |                           |            |
| XX                    | prostate specific chimeric enhancer and proximal promoter sequence        |                                   |                           |            |
| XX                    | operably linked to nucleic acid encoding heterologous polypeptide.        |                                   |                           |            |
| XX                    | Example 5; Page 73; 131pp; English.                                       |                                   |                           |            |
| XX                    | The present sequence was used in reverse transcriptase polymerase chain   |                                   |                           |            |
| XX                    | reaction (RT-PCR) analysis of human prostate cancer cells. The invention  |                                   |                           |            |
| XX                    | relates to an isolated polynucleotide comprising a prostate-specific      |                                   |                           |            |
| XX                    | chimeric enhancer (PSE) sequence and a proximal promoter sequence         |                                   |                           |            |
| XX                    | operably linked to a nucleic acid segment that encodes a heterologous     |                                   |                           |            |
| XX                    | polypeptide. The PSE contains an ARE and specifically activates           |                                   |                           |            |
| XX                    | transcription of the nucleic acid segment in a mammalian prostate cell.   |                                   |                           |            |
| XX                    | The construct is useful for the treatment of a prostate disorder or a     |                                   |                           |            |
| XX                    | metastatised prostate cancer, such as hyperplasia or hyperproliferation   |                                   |                           |            |
| XX                    | of prostate cells. It is also useful for directing the tissue-specific    |                                   |                           |            |
| XX                    | expression of a heterologous polypeptide in a human prostate cell. The    |                                   |                           |            |
| XX                    | construct may be administered by injection, infection, transformation,    |                                   |                           |            |
| XX                    | liposome-mediated transfection, polybrene-mediated transfection, receptor |                                   |                           |            |
| XX                    | -mediated uptake or Ca-PO4-mediated transformation                        |                                   |                           |            |
| XX                    | Sequence  | 24                                | BP;                       | 5          |
| XX                    |   |                                   | 10                        | C;         |
| XX                    |   |                                   | 4                         | G;         |
| XX                    |   |                                   | 5                         | T;         |
| XX                    |   |                                   | 0                         | U;         |
| XX                    |   |                                   | 0                         | Other;     |
| Query Match           |   |                                   |                           |            |
| Best Local Similarity |   | 0.5%;                             | Score 21.4;               | DB 1;      |
| Matches               |   | 22;                               | Conservative              | 0;         |
|                       |   |                                   |                           | Mismatches |
|                       |   |                                   | 1;                        | Indels     |
|                       |   |                                   | 0;                        | Gaps       |
| QY                    | 1278  | CTGCTACCTGCGAGCACCTCGA            | 1300                      |            |
|                       |   |                                   |                           |            |
| Db                    | 2   | CTGCTACCTGCGAGCACCTCGA            | 24                        |            |

KW Human; ATP-dependent serine protein hydrolase 12; recombinant production;  
KW tumour; cancer; gene therapy; human immunodeficiency virus;  
KW HIV infection; cytostatic; antiviral; reverse transcription-PCR; RT-PCR;  
KW primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1331337-A.  
XX  
XX 16-JAN-2002.  
PD  
XX  
XX 26-JUN-2000; 2000CN-00116723.  
PF  
XX  
XX 26-JUN-2000; 2000CN-00116723.  
PR  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
PI  
XX  
XX WPI; 2002-340680/38.  
DR  
XX  
XX A human ATP dependent serine protein hydrolase 12 polypeptide, and the  
PT polynucleotide encoding it, for treating e.g. cancer and HIV infection.  
PT  
XX  
PS Example 2; Page 17 (Disclosure); 32pp; Chinese.  
PS  
XX  
XX The invention relates to human ATP-dependent serine protein hydrolase 12  
CC (ABB9561) and nucleic acids encoding it (ABL41486). The protein has a  
CC molecular weight of 12 kD. The invention also relates to a method for the  
CC recombinant production of the protein, an antagonist of the protein, and  
CC the use of the protein, gene and antagonist in therapeutic applications.  
CC ATP-dependent serine protein hydrolase 12 can be used in the treatment of  
CC a variety of diseases such as cancer and HIV (human immunodeficiency  
CC virus) infection. Sequences ABL41487-ABL41488 represent reverse  
CC transcription-PCR (RT-PCR) primers used in an exemplification of the  
CC invention to isolate human ATP-dependent serine protein hydrolase 12 cDNA  
XX  
XX  
SQ Sequence 24 BP; 4 A; 11 C; 9 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 20.4; DB 1; Length 24;  
Best Local Similarity 95.5%; Pred. No. 78;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 619 GCGGCACGCGCGGCACAC 640  
Db 2 GCGGCACGCGCGGCACAC 23  
|||||  
|||||  
  
RESULT 23  
AAC96323/c  
ID AAC96323 standard; DNA; 25 BP.  
XX  
XX  
AC AAC96323;  
XX  
XX 26-FEB-2001 (first entry)  
DT  
XX  
DE HLA DPB1 gene PCR primer #55.  
XX  
XX DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200065088-A2.  
PN  
XX  
XX 02-NOV-2000.  
PD  
XX  
XX 20-APR-2000; 2000WO-EP003636.  
PF  
XX  
XX 26-APR-1999; 99EP-00303215.  
PR  
XX  
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.

XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
PT  
XX  
XX Claim 14; Page 49; 66pp; English.  
PS  
XX  
XX The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 3 A; 3 C; 5 G; 14 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 94;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 918 TCCTTCCAGGAGAGAAAAAACA 942  
Db 25 TCCTTCCAGGAGAGAAAAAACA 1  
|||||  
|||||  
  
RESULT 24  
AAC88273/c  
ID AAC88273 standard; DNA; 25 BP.  
XX  
XX AAC88273;  
AC  
XX  
XX 02-MAR-2001 (first entry)  
DT  
XX  
XX SCDNA102 DNA sequence.  
DE  
XX  
XX Drug binding site; viscosity; biomolecule interaction; drug target;  
KW electronic transducer; primer; ds.  
KW  
XX  
XX Synthetic.  
OS  
XX  
XX WO200068419-A2.  
PN  
XX  
XX 16-NOV-2000.  
PD  
XX  
XX 05-MAY-2000; 2000WO-CA000504.  
PF  
XX  
XX 05-MAY-1999; 99CA-02271179.  
PR  
XX  
XX (SENS-) SENSORCHEM INT CORP.  
PA  
XX  
XX McGovern M, Thompson M;  
PI  
XX  
XX WPI; 2001-024875/03.  
DR  
XX  
XX Monitoring/detecting small molecule-biomolecule interactions for drug  
PT screening involves contacting a solution of small molecules with  
PT immobilized biomolecules and measuring the frequency generated with an  
PT acoustic wave device.  
PT  
XX  
XX Example 4; Fig 5; 44pp; English.  
PS  
XX  
XX The present invention describes a device and method for monitoring small  
CC molecule-biomolecule interactions. These involve the measurement of the  
CC oscillation of a liquid when in contact with the biomolecule only  
CC compared with the small molecule-biomolecule complex. This uses a  
CC piezoelectric device and can be used with biomolecules such as DNA. The  
CC present sequence was used as an example. The device can be used to screen

CC for drug candidates, to determine the conditions in which small molecules  
CC will not bind to given biomolecules and to obtain information on the  
CC tertiary structure of biomolecules

Sequence 25 BP; 0 A; 13 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 94;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 614 GGCGCGCGCACGACGCGGCAC 638  
Db 25 GGCGCGCGCGCGCGCGCGCGCGC 1

RESULT 25  
AAV63217  
ID AAV63217 standard; DNA; 20 BP.

XX AAV63217;  
AC  
XX  
DT 14-JAN-1999 (first entry)

| Accession | Gene | Forward PCR primer for human transforming growth factor-beta 2 cDNA. |
|-----------|------|--|
| DE        | XX   | Human transforming growth factor-beta 2; TGF-beta3; oxygen tension;  |
| DE        | XX   | trophoblast invasion regulation; inhibitor; HIF-1 alpha;             |
| KW        | KW   | TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha; |
| KW        | KW   | pre-eclampsia; preeclampsia; choriocarcinoma; PCR primers.           |

|    |               |
|----|---------------|
| XX | Synthetic.    |
| OS | Homo sapiens. |
| OS |               |
| XX |               |
| PN | WQ9840747-A1. |

|    |                                    |                |
|----|------------------------------------|----------------|
| XX | 17-SEP-1998.                       |                |
| PD |                                    |                |
| XX |                                    |                |
| XX |                                    |                |
| PF | 05-MAR-1998;                       | 98WO-CA000180. |
| XX |                                    |                |
| XX |                                    |                |
| PR | 07-MAR-1997;                       | 97US-0039919P. |
| XX |                                    |                |
| XX |                                    |                |
| PA | (MOUN ) MOUNT SINAI HOSPITAL CORP. |                |
| PA | (HOSP-) HOSPITAL FOR SICK CHILDREN |                |

XX Caniggia I, Post M, Lye S;  
PI  
XX  
DR WPI: 1998-520837/44.

Regulation of trophoblast invasion - by, e.g. transforming growth factor-beta3 inhibitor, useful for detecting or treating preeclampsia in pregnant women.

XX  
PS  
Example 4: Page 21: 59pp: English.

PCR primers AAV63217-18 were used to amplify cDNA encoding human transforming growth factor-beta 2 (TGF-beta2). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclampsia in pregnant women or choriocarcinomas

|    |                       |         |              |      |            |      |        |          |  |
|----|-----------------------|---------|--------------|------|------------|------|--------|----------|--|
| xx | Sequence              | 20 BP;  | 1 A;         | 7 C; | 7 G;       | 5 T; | 0 U;   | 0 Other; |  |
| sq | Query Match           | 0.5%;   | Score        | 20;  | DB         | 1;   | Length | 20;      |  |
|    | Best Local Similarity | 100.0%; | Pred. No.    | 54;  |            |      |        |          |  |
|    | Matches               | 20;     | Conservative | 0;   | Mismatches | 0;   | Indels |          |  |

Qy 1254 CATCTGGTCCC GGTTGGCGCT 1273  
Db 1 CATCTGGTCCC GGTTGGCGCT 20

|           |  |
|-----------|--|
| RESULT 26 |  |
| AAV7980/c |  |
| ID        | AAV7980 standard; DNA; 20 BP.  |
| XX        |  |
| XX        |  |
| AC        | AAV7980;   |
| XX        |  |
| DT        | 24-FEB-1999 (first entry)  |
| XX        |  |
| DE        | TGF-beta 2 DNA amplifying primer.                                      |
| XX        |  |
| XX        | Transgenic; osteogenic; core binding factor; CBFA1/PBEP2-alpha-A;      |
| KW        | polyoma enhancer binding protein; runt; osteoblast; variant; TGF-beta; |
| KW        | PCR primer; ss.  |

|    |                                      |                |
|----|--------------------------------------|----------------|
| OS | Synthetic.                           |                |
| XX |                                      |                |
| XX | JF10309148-A.                        |                |
| PN |                                      |                |
| XX |                                      |                |
| XX |                                      |                |
| PD | 24-NOV-1998.                         |                |
| XX |                                      |                |
| XX | 11-SEP-1997;                         | 97JP-00247346. |
| PF |                                      |                |
| XX |                                      |                |
| XX | 10-MAR-1997;                         | 97JP-00074453. |
| PR |                                      |                |
| XX |                                      |                |
| XX | (KISH/) KISHIMOTO C.                 |                |
| PA |                                      |                |
| XX |                                      |                |
| XX | WEI; 1999-063649/06.                 |                |
| DR |                                      |                |
| XX |                                      |                |
| XX | Transgenic animal with no osteogenic |                |
| PT | in gene encoding core binding factor |                |
| PT |                                      |                |
| XX |                                      |                |
| XX |                                      |                |
| PS | Example 10; Page 7; 19pp; Japanese.  |                |

The invention provides a transgenic animal devoid of osteogenic property.  
 The transgenic animal has an introduced variation in a gene encoding for  
 core binding factor/polyoma enhancer binding protein (CBF1/PEBP2-alpha-  
 A), particularly in runt region DNA, especially prepared by introduction  
 of a variation devoid of at least a part of gene encoding CBF1/PEBP2-  
 alpha-A, leading to a disturbance in differentiation and maturation of  
 osteoblast cells. The transgenic animal can be prepared by introducing a  
 variant gene encoding for CBF1/PEBP2-alpha-A. The animal can be used to  
 elucidate the in vivo mechanism of CBF1/PEBP2-alpha-A. Sequences  
 AAU79975 to AAV80010 represent PCR primers used during the course of the  
 invention  
 Sequence 20 BP: 6 A: 5 C: 4 G: 5 T: 0 U: 0 Other:

```

Query Match          0.5%; Score
Best Local Similarity 100.0%; Pred
Matches 20; Conservative 0; Mismatches 0
Qy 1300 ACATGGATCAGTTTATGCGC 1319
Db 20 ACATGGATCAGTTTATGCGC 1

```

|          |                                |
|----------|--------------------------------|
| RESULT   | 27                             |
| AAV79979 |                                |
| ID       | AAV79979 standard; DNA; 20 BP. |
| XX       |                                |
| AC       | AAV79979;                      |
| XX       |                                |
| DT       | 24-FEB-1999 (first entry)      |
| XX       |                                |
| DE       | TGF-beta 2 DNA amplifying prim |
| XX       |                                |
| KW       | Transgenic; osteogenic; core b |
| KW       | polyoma enhancer binding prote |
| KW       | PCR primer; ss.                |
| XX       |                                |
| OS       | Synthetic.                     |



|   |   |   |  |   |  |
|---|---|---|--|---|--|
|   |   | Best Local Similarity 100.0%; Pred. No. 54; |  | Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |
| QY  | 2401 GAAATACGCCCAAGATCGAA 2420  |   |  |   |  |
| Db  | 20 GAAATACGCCCAAGATCGAA 1   |   |  |   |  |
| RESULT 30   |   |   |  |   |  |
| AD  | ADI80093/c  |   |  |   |  |
| ID  | ADI80093 standard; DNA; 20 BP.  |   |  |   |  |
| XX  | AC ADI80093;  |   |  |   |  |
| XX  | DT 22-APR-2004 (first entry)  |   |  |   |  |
| XX  | DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 94.   |   |  |   |  |
| XX  | KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;          |   |  |   |  |
| XX  | KW cytostatic; nontropic; neuroprotective; immunosuppressive;               |   |  |   |  |
| XX  | KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; |   |  |   |  |
| XX  | KW immune; ss; mouse; murine.   |   |  |   |  |
| OS  | Mus musculus.   |   |  |   |  |
| PN  | US2004006030-A1.  |   |  |   |  |
| XX  | PD 08-JAN-2004.   |   |  |   |  |
| XX  | PF 02-JUL-2002; 2002US-00189267.  |   |  |   |  |
| XX  | PR 02-JUL-2002; 2002US-00189267.  |   |  |   |  |
| XX  | PA (ISIS-) ISIS PHARM INC.  |   |  |   |  |
| PI  | Monia BP, Freier SM, Dobie KW;  |   |  |   |  |
| DR  | WPI; 2004-081742/08.  |   |  |   |  |
| XX  | New compounds, particularly antisense oligonucleotides targeted to a        |   |  |   |  |
| PT  | nucleic acid encoding TGF-beta 2, useful for treating cancer, a             |   |  |   |  |
| PT  | neurodegenerative disorder, or a disease involving hyperactivation of       |   |  |   |  |
| PT  | immune response.  |   |  |   |  |
| XX  | Example 16; SEQ ID NO 94; 135pp; English.                                   |   |  |   |  |
| XX  | The invention relates to a novel antisense compound of 8-80 nucleobases     |   |  |   |  |
| CC  | in length targeted to, and which specifically hybridizes with, a nucleic    |   |  |   |  |
| CC  | acid molecule encoding transforming growth factor (TGF)-beta 2, and         |   |  |   |  |
| CC  | inhibits the expression of TGF-beta 2. The invention further relates to:    |   |  |   |  |
| CC  | a compound 8-80 nucleobases in length that specifically hybridizes with     |   |  |   |  |
| CC  | at least an 8-nucleobase portion of an active site on a nucleic acid        |   |  |   |  |
| CC  | molecule encoding TGF-beta 2; a composition comprising the compound and a   |   |  |   |  |
| CC  | carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or     |   |  |   |  |
| CC  | tissues by contacting the cells or tissues with the compound so that        |   |  |   |  |
| CC  | expression of TGF-beta 2 is inhibited; treating an animal having a          |   |  |   |  |
| CC  | disease or condition associated with TGF-beta 2 by administering to the     |   |  |   |  |
| CC  | animal a therapeutic or prophylactic amount of the compound so that         |   |  |   |  |
| CC  | expression of TGF-beta 2 is inhibited; and screening an antisense           |   |  |   |  |
| CC  | compound. The antisense compound has cytostatic, nontropic,                 |   |  |   |  |
| CC  | neuroprotective, and immunosuppressive activities. The compound,            |   |  |   |  |
| CC  | composition and methods are useful for treating a disease or condition      |   |  |   |  |
| CC  | associated with TGF-beta 2, such as a hyperproliferative disorder e.g.      |   |  |   |  |
| CC  | cancer, a neurodegenerative disorder, or a disease or condition involving   |   |  |   |  |
| CC  | hyperactivation of an immune response. This polynucleotide sequence         |   |  |   |  |
| CC  | represents an antisense oligonucleotide of the invention.                   |   |  |   |  |
| XX  | Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;                           |   |  |   |  |
| Query Match 0.5%; Score 20; DB 1; Length 20;                |   |   |  |   |  |
| Best Local Similarity 100.0%; Pred. No. 54;                 |   |   |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |   |  |   |  |
| QY  | 914 CCTCTCCCTTCCAGGAGAAA 933  |   |  |   |  |
| Db  | 20 CCTCTCCCTTCCAGGAGAAA 1   |   |  |   |  |
| Query Match 0.5%; Score 20; DB 1; Length 20;                |   |   |  |   |  |
| Best Local Similarity 100.0%; Pred. No. 54;                 |   |   |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |   |  |   |  |

|   |   |   |  |   |  |
|---|---|---|--|---|--|
|   |   | Best Local Similarity 100.0%; Pred. No. 54; |  | Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |
| QY  | 133 TAGGGTTTAAAGAGCCATTC 152  |   |  |   |  |
| Db  | 20 TAGGGTTTAAAGAGCCATTC 1   |   |  |   |  |
| RESULT 31   |   |   |  |   |  |
| AD  | ADI80095/c  |   |  |   |  |
| ID  | ADI80095 standard; DNA; 20 BP.  |   |  |   |  |
| XX  | AC ADI80095;  |   |  |   |  |
| XX  | DT 22-APR-2004 (first entry)  |   |  |   |  |
| XX  | DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 96.   |   |  |   |  |
| XX  | KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;          |   |  |   |  |
| XX  | KW cytostatic; nontropic; neuroprotective; immunosuppressive;               |   |  |   |  |
| XX  | KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; |   |  |   |  |
| XX  | KW immune; ss; mouse; murine.   |   |  |   |  |
| OS  | Mus musculus.   |   |  |   |  |
| PN  | US2004006030-A1.  |   |  |   |  |
| XX  | PD 08-JAN-2004.   |   |  |   |  |
| XX  | PF 02-JUL-2002; 2002US-00189267.  |   |  |   |  |
| XX  | PR 02-JUL-2002; 2002US-00189267.  |   |  |   |  |
| XX  | PA (ISIS-) ISIS PHARM INC.  |   |  |   |  |
| PI  | Monia BP, Freier SM, Dobie KW;  |   |  |   |  |
| DR  | WPI; 2004-081742/08.  |   |  |   |  |
| XX  | New compounds, particularly antisense oligonucleotides targeted to a        |   |  |   |  |
| PT  | nucleic acid encoding TGF-beta 2, useful for treating cancer, a             |   |  |   |  |
| PT  | neurodegenerative disorder, or a disease involving hyperactivation of       |   |  |   |  |
| PT  | immune response.  |   |  |   |  |
| XX  | Example 16; SEQ ID NO 96; 135pp; English.                                   |   |  |   |  |
| XX  | The invention relates to a novel antisense compound of 8-80 nucleobases     |   |  |   |  |
| CC  | in length targeted to, and which specifically hybridizes with, a nucleic    |   |  |   |  |
| CC  | acid molecule encoding transforming growth factor (TGF)-beta 2, and         |   |  |   |  |
| CC  | inhibits the expression of TGF-beta 2. The invention further relates to:    |   |  |   |  |
| CC  | a compound 8-80 nucleobases in length that specifically hybridizes with     |   |  |   |  |
| CC  | at least an 8-nucleobase portion of an active site on a nucleic acid        |   |  |   |  |
| CC  | molecule encoding TGF-beta 2; a composition comprising the compound and a   |   |  |   |  |
| CC  | carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or     |   |  |   |  |
| CC  | tissues by contacting the cells or tissues with the compound so that        |   |  |   |  |
| CC  | expression of TGF-beta 2 is inhibited; treating an animal having a          |   |  |   |  |
| CC  | disease or condition associated with TGF-beta 2 by administering to the     |   |  |   |  |
| CC  | animal a therapeutic or prophylactic amount of the compound so that         |   |  |   |  |
| CC  | expression of TGF-beta 2 is inhibited; and screening an antisense           |   |  |   |  |
| CC  | compound. The antisense compound has cytostatic, nontropic,                 |   |  |   |  |
| CC  | neuroprotective, and immunosuppressive activities. The compound,            |   |  |   |  |
| CC  | composition and methods are useful for treating a disease or condition      |   |  |   |  |
| CC  | associated with TGF-beta 2, such as a hyperproliferative disorder e.g.      |   |  |   |  |
| CC  | cancer, a neurodegenerative disorder, or a disease or condition involving   |   |  |   |  |
| CC  | hyperactivation of an immune response. This polynucleotide sequence         |   |  |   |  |
| CC  | represents an antisense oligonucleotide of the invention.                   |   |  |   |  |
| XX  | Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;                           |   |  |   |  |
| Query Match 0.5%; Score 20; DB 1; Length 20;                |   |   |  |   |  |
| Best Local Similarity 100.0%; Pred. No. 54;                 |   |   |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |   |  |   |  |
| QY  | 914 CCTCTCCCTTCCAGGAGAAA 933  |   |  |   |  |
| Db  | 20 CCTCTCCCTTCCAGGAGAAA 1   |   |  |   |  |
| Query Match 0.5%; Score 20; DB 1; Length 20;                |   |   |  |   |  |
| Best Local Similarity 100.0%; Pred. No. 54;                 |   |   |  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |   |  |   |  |

|   |   |   |     |  |
|---|---|---|-----|--|
| QY  | 133                                       | TAGGCTTTAAAGAGCCATTC  | 152 |  |
| Db  | 20  | TAGGCTTTAAAGAGCCATTC  | 1   |  |
| RESULT 31   |   |   |     |  |
| ID  | ADI80095/c                                |   |     |  |
| XX  | AD  | ADI80095 standard; DNA; 20 BP.  |     |  |
| XX  | AC  | ADI80095;   |     |  |
| XX  | DT  | 22-APR-2004 (first entry)   |     |  |
| XX  | DE  | Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 96.    |     |  |
| XX  | DE  |   |     |  |
| XX  | KW  | antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;           |     |  |
| KW  | KW  | cytostatic; nontropic; neuroprotective; immunosuppressive;                |     |  |
| KW  | KW  | hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  |     |  |
| KW  | KW  | immune; ss; mouse; murine.  |     |  |
| OS  | OS  | Mus musculus.   |     |  |
| OS  | OS  |   |     |  |
| XX  | PN  | US2004006030-A1.  |     |  |
| XX  | PN  |   |     |  |
| XX  | PD  | 08-JAN-2004.  |     |  |
| XX  | PF  | 02-JUL-2002; 2002US-00189267.   |     |  |
| XX  | PF  |   |     |  |
| XX  | PR  | 02-JUL-2002; 2002US-00189267.   |     |  |
| XX  | PR  |   |     |  |
| XX  | PA  | (ISIS-) ISIS PHARM INC.   |     |  |
| XX  | PA  |   |     |  |
| XX  | PI  | Monia BP, Freier SM, Dobie KW;  |     |  |
| XX  | PI  |   |     |  |
| XX  | DR  | WPI; 2004-081742/08.  |     |  |
| XX  | XX  |   |     |  |
| PT  | PT  | New compounds, particularly antisense oligonucleotides targeted to a      |     |  |
| PT  | PT  | nucleic acid encoding TGF-beta 2, useful for treating cancer, a           |     |  |
| PT  | PT  | neurodegenerative disorder, or a disease involving hyperactivation of     |     |  |
| PT  | PT  | immune response.  |     |  |
| XX  | XX  |   |     |  |
| PS  | Example 16; SEQ ID NO 96; 135pp; English. |   |     |  |
| XX  | XX  |   |     |  |
| CC  | CC  | The invention relates to a novel antisense compound of 8-80 nucleobases   |     |  |
| CC  | CC  | in length targeted to, and which specifically hybridizes with, a nucleic  |     |  |
| CC  | CC  | acid molecule encoding transforming growth factor (TGF)-beta 2, and       |     |  |
| CC  | CC  | inhibits the expression of TGF-beta 2. The invention further relates to:  |     |  |
| CC  | CC  | a compound 8-80 nucleobases in length that specifically hybridizes with   |     |  |
| CC  | CC  | at least an 8-nucleobase portion of an active site on a nucleic acid      |     |  |
| CC  | CC  | molecule encoding TGF-beta 2; a composition comprising the compound and a |     |  |
| CC  | CC  | carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or   |     |  |
| CC  | CC  | tissues by contacting the cells or tissues with the compound so that      |     |  |
| CC  | CC  | expression of TGF-beta 2 is inhibited; treating an animal having a        |     |  |
| CC  | CC  | disease or condition associated with TGF-beta 2 by administering to the   |     |  |
| CC  | CC  | animal a therapeutic or prophylactic amount of the compound so that       |     |  |
| CC  | CC  | expression of TGF-beta 2 is inhibited; and screening an antisense         |     |  |
| CC  | CC  | compound. The antisense compound has cytostatic, nontropic,               |     |  |
| CC  | CC  | neuroprotective, and immunosuppressive activities. The compound,          |     |  |
| CC  | CC  | composition and methods are useful for treating a disease or condition    |     |  |
| CC  | CC  | associated with TGF-beta 2, such as a hyperproliferative disorder e.g.    |     |  |
| CC  | CC  | cancer, a neurodegenerative disorder, or a disease or condition involving |     |  |
| CC  | CC  | hyperactivation of an immune response. This polynucleotide sequence       |     |  |
| XX  | XX  | represents an antisense oligonucleotide of the invention.                 |     |  |
| XX  | XX  |   |     |  |
| XX  | XX  | Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;                         |     |  |
| Query Match 0.5%; Score 20; DB 1; Length 20;                |   |   |     |  |
| Best Local Similarity 100.0%; Pred. No. 54;                 |   |   |     |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |   |     |  |
| QY  | 914                                       | CCTCTCCCTTCCAGGAGAAA  | 933 |  |
| Db  | 20  | CCTCTCCCTTCCAGGAGAAA  | 1   |  |



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RESULT 32
ADI80105/c
ID ADI80105 standard; DNA; 20 BP.
XX AC ADI80105;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 106.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US200406030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX DR New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 106; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1314 ATCGCGAAGAGGATCGAGGC 1333
DB 20 ATGCGCAAGAGGATCGAGGC 1
RESULT 33
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ADI80119/c
ID ADI80119 standard; DNA; 20 BP.
XX AC ADI80119;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 120.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US200406030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX DR New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 120; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with:
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 5 A; 2 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1584 TACAGACCTACTTCAGAAAT 1603
DB 20 TACAGACCTACTTCAGAAAT 1
RESULT 34
ADI80139/c
ID ADI80139 standard; DNA; 20 BP.
XX
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AC ADI80139;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 140.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 140; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 2 A; 2 C; 8 G; 8 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2292 CAACACCAAGTCTCTAG 2311  
 DB 20 CAACACCAAGTCTCTAG 1  
 RESULT 35  
 ADI80140/C  
 ID ADI80140 standard; DNA; 20 BP.  
 XX  
 AC ADI80140;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX

XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 141.  
 DE  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 141; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2349 CCTTCTGTGTCTCCAGCA 2368  
 DB 20 CCTTCTGTGTCTCCAGCA 1  
 RESULT 36  
 ADI80141/C  
 ID ADI80141 standard; DNA; 20 BP.  
 XX  
 AC ADI80141;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 142.  
 XX

KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 OS Mus musculus.  
 PN US2004006030-A1.  
 XX 08-JAN-2004.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 DR New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX Example 16; SEQ ID NO 142; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;  
 SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2444 GTCTGTGAATGACGCTAAA 2463  
 DB 20 GTCTGTGAATGACGCTAAA 1  
 RESULT 37  
 ADI80152/c  
 ID ADI80152 standard; DNA; 20 BP.  
 XX ADI80152;  
 XX 22-APR-2004 (first entry)  
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 153.  
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.

KW immune; ss; mouse; murine.  
 OS Mus musculus.  
 PN US2004006030-A1.  
 XX 08-JAN-2004.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 DR New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX Example 16; SEQ ID NO 153; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX Sequence 20 BP; 9 A; 4 C; 2 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3279 AATTGTAATGGTCTTTGTC 3298  
 DB 20 AATTGTAATGGTCTTTGTC 1  
 RESULT 38  
 ADI80159/c  
 ID ADI80159 standard; DNA; 20 BP.  
 XX ADI80159;  
 XX 22-APR-2004 (first entry)  
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 160.  
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 OS Mus musculus.

XX US2004006030-A1.  
 PN  
 XX  
 XX 08-JAN-2004.  
 PD  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PF  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PR  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX  
 XX Monia BP, Freier SM, Dobie KW;  
 PI  
 XX WPI; 2004-081742/08.  
 DR  
 XX  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 PT  
 XX  
 XX Example 16; SEQ ID NO 160; 135pp; English.  
 PS  
 XX  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 XX Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3737 ATTGCCATTATGACATG 3756  
 Db  
 20 ATTGCCATTATGACATG 1  
 RESULT 39  
 ADI80162/c  
 ID ADI80162 standard; DNA; 20 BP.  
 XX  
 XX ADI80162;  
 AC  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX  
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 163.  
 DE  
 XX  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX US2004006030-A1.  
 PN  
 XX  
 XX 08-JAN-2004.  
 PD  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PF  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX  
 XX Monia BP, Freier SM, Dobie KW;  
 PI  
 XX WPI; 2004-081742/08.  
 DR  
 XX  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 PT  
 XX  
 XX Example 16; SEQ ID NO 160; 135pp; English.  
 PS  
 XX  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 XX Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PD 08-JAN-2004.  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PF  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PR  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX  
 XX Monia BP, Freier SM, Dobie KW;  
 PI  
 XX WPI; 2004-081742/08.  
 DR  
 XX  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 PT  
 XX  
 XX Example 16; SEQ ID NO 163; 135pp; English.  
 PS  
 XX  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 XX Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4245 CTTTCAGGCTGATTAAAAA 4264  
 Db  
 20 CTTTCAGGCTGATTAAAAA 1  
 RESULT 40  
 ADI80259  
 ID ADI80259 standard; DNA; 20 BP.  
 XX  
 XX ADI80259;  
 AC  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX  
 XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 260.  
 DE  
 XX  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX US2004006030-A1.  
 PN  
 XX  
 XX 08-JAN-2004.  
 PD  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PF

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XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 260; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2226 GAACCCAAAGGGTACAATGC 2245
DB 1 GAACCCAAAGGGTACAATGC 20
RESULT 41
ADI80269
ID ADI80269 standard; DNA; 20 BP.
XX AC ADI80269;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 270.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
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PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 270; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3049 AAACATCATGGATGGCTTAAG 3068
DB 1 AAACATCATGGATGGCTTAAG 20
RESULT 42
ADI80100/c.
ID ADI80100 standard; DNA; 20 BP.
XX AC ADI80100;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 101.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
```

XX WPI; 2004-081742/08.

PT New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX Example 16; SEQ ID NO 101; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 7 A; 1 C; 5 G; 7 T; 0 U; 0 Other;

XX Query Match 0.5%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 54;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1205 TCCTTTTAAAAACATGCAC 1224

DB 20 TCCTTTTAAAAACATGCAC 1

RESULT 43

ADI80106/c

ID ADI80106 standard; DNA; 20 BP.

XX AC ADI80106;

XX 22-APR-2004 (first entry)

XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 107.

DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

XX cytostatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; mouse; murine.

XX Mus musculus.

XX US2004006030-A1.

PN 08-JAN-2004.

XX 02-JUL-2002; 2002US-00189267.

XX 02-JUL-2002; 2002US-00189267.

PR (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

PT New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX Example 16; SEQ ID NO 107; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 0.5%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 54;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1321 ACAGGATCGAGGCCATCCGC 1340

DB 20 ACAGGATCGAGGCCATCCGC 1

RESULT 44

ADI80107/c

ID ADI80107 standard; DNA; 20 BP.

XX AC ADI80107;

XX 22-APR-2004 (first entry)

XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 108.

DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytostatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; mouse; murine.

XX Mus musculus.

XX US2004006030-A1.

PN 08-JAN-2004.

XX 02-JUL-2002; 2002US-00189267.

XX 02-JUL-2002; 2002US-00189267.

PR (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a

XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a

XX neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX Example 16; SEQ ID NO 108; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.

XX SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1335 ATCCGGGGCAGATCCTGAG 1354  
DB 20 ATCCGGGGCAGATCCTGAG 1

RESULT 45  
AD180117/c  
ID AD180117 standard; DNA; 20 BP.  
XX  
AC AD180117;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 118.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.  
XX  
PS Example 16; SEQ ID NO 118; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.

XX SQ Sequence 20 BP; 5 A; 1 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 CCACCTTCTACAGACCTTAC 1595  
DB 20 CCACCTTCTACAGACCTTAC 1

RESULT 46  
AD180134/c  
ID AD180134 standard; DNA; 20 BP.  
XX  
AC AD180134;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 135.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.  
XX  
PS Example 16; SEQ ID NO 135; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic



CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 9 A; 3 C; 2 G; 6 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2181 CTTTACATTCGATTTTAAGAG 2200  
Db 20 CTTTACATTCGATTTTAAGAG 1  
RESULT 47  
AD180143/c  
ID AD180143 standard; DNA; 20 BP.  
AC  
XX AD180143;  
XX  
DT 22-APR-2004 (first entry)  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 144.  
DE  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 144; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX

CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 3 A; 4 C; 4 G; 9 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2487 AAAATCAGCGTGCAATGAC 2506  
Db 20 AAAATCAGCGTGCAATGAC 1  
RESULT 48  
AD180231  
ID AD180231 standard; DNA; 20 BP.  
AC  
XX AD180231;  
XX  
DT 22-APR-2004 (first entry)  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 232.  
DE  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 232; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX



CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX  
 SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1269 GCGCTCAGTCTGTCTACCTG 1288  
 Db 1 GCGCTCAGTCTGTCTACCTG 20  
 RESULT 49  
 ADI80240  
 ID ADI80240 standard; DNA; 20 BP.  
 AC ADI80240;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 241.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 241; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX  
 SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1507 AGTACTACGCCAAGGAGTT 1526  
 Db 1 AGTACTACGCCAAGGAGTT 20  
 RESULT 50  
 ADI80094/C  
 ID ADI80094 standard; DNA; 20 BP.  
 AC ADI80094;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 95.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 95; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 7 A; 1 C; 7 G; 5 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 860 ACACTGAACCTCCATTCTTC 879  
Db 20 ACACTGAACCTCCATTCTTC 1  
RESULT 51  
AD180129/c  
ID AD180129 standard; DNA; 20 BP.  
XX  
AC AD180129;  
XX  
DT 22-APR-2004 (first entry)  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 130.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PS New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.  
XX  
PS Example 16; SEQ ID NO 130; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2060 CCTGCTAATGTTGTGCCCT 2079  
Db 20 CCTGCTAATGTTGTGCCCT 1  
RESULT 52  
AD180132/c  
ID AD180132 standard; DNA; 20 BP.  
XX  
AC AD180132;  
XX  
DT 22-APR-2004 (first entry)  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 133.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PS New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.  
XX  
PS Example 16; SEQ ID NO 133; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.

```
XX SQ Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2151 AATGTGCAGGATTAATGCTG 2170
|||||
Db 20 AATGTGCAGGATTAATGCTG 1

RESULT 53
ADI80144/c
ID ADI80144 standard; DNA; 20 BP.
XX AC ADI80144;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 145.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosatic; nontropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 145; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 9 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2635 GTTCTGTTGTTAAACTGG 2654
|||||
Db 20 GTTCTGTTGTTAAACTGG 1

RESULT 54
ADI80241
ID ADI80241 standard; DNA; 20 BP.
XX AC ADI80241;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 242.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosatic; nontropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 242; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 8 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1515 GCCAAGGAGGTTTATATAAT 1534  
 DB |||||  
 1 GCCAAGGAGGTTTATATAAT 20

RESULT 55  
 ADI80257  
 ID ADI80257 standard; DNA; 20 BP.  
 AC  
 XX  
 AC ADI80257;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 258.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytotatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 258; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX  
 SQ Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 GATTTTAAGAGGATCTTGG 2209  
 DB |||||

DB 1 GATTTTAAGAGGATCTTGG 20

RESULT 56  
 ADI80268  
 ID ADI80268 standard; DNA; 20 BP.  
 XX  
 AC ADI80268;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 269.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytotatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 269; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX  
 SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2988 ACCTTTTCATTACCTTGAA 3007  
 DB |||||  
 1 ACCTTTTCATTACCTTGAA 20

```
RESULT 57
ADI80011
XX ADI80011 standard; DNA; 20 BP.
XX AC
XX ADI80011;
XX DT
XX 22-APR-2004 (first entry)
XX DE
XX Mouse transforming growth factor-beta 2 forward PCR primer.
XX antisenase; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosatic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; mouse; murine; primer; ss.
XX OS
XX Mus musculus.
XX PN
XX US2004006030-A1.
XX PD
XX 08-JAN-2004.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX 02-JUL-2002; 2002US-00189267.
XX PA
XX (ISIS-) ISIS PHARM INC.
XX PI
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 13; SEQ ID NO 12; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a primer used in the exemplification of the invention.
XX SQ
XX Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1757 CACCAGCGCTACATCGATA 1776
XX 1 CACCAGCGCTACATCGATA 20
XX
XX RESULT 58
ADI80099/c
XX ADI80099 standard; DNA; 20 BP.
XX ID
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```
XX
XX ADI80099;
XX 22-APR-2004 (first entry)
XX DE
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 100.
XX antisenase; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosatic; nontropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX OS
XX Mus musculus.
XX PN
XX US2004006030-A1.
XX PD
XX 08-JAN-2004.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX 02-JUL-2002; 2002US-00189267.
XX PA
XX (ISIS-) ISIS PHARM INC.
XX PI
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 100; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nontropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX SQ
XX Sequence 20 BP; 9 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1138 CTGAGAACTACTAGTTTCTT 1157
XX 20 CTGAGAACTACTAGTTTCTT 1
XX
XX RESULT 59
ADI80136/c
XX ADI80136 standard; DNA; 20 BP.
XX ID
XX ADI80136;
XX AC
XX
```

DT 22-APR-2004 (first entry)  
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 137.  
 DE  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 DR WPI; 2004-081742/08.  
 XX  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 137; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;  
 XX  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2217 TGGATCCATGAACCCAAAGG 2236  
 DB 20 TGGATCCATGAACCCAAAGG 1  
 RESULT 60  
 ADI80147/c  
 ID ADI80147 standard; DNA; 20 BP.  
 XX  
 AC ADI80147;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 148.  
 DE

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 DR WPI; 2004-081742/08.  
 XX  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 148; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 8 A; 1 C; 4 G; 7 T; 0 U; 0 Other;  
 XX  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2977 CTATATATGAACCTTTTCAT 2996  
 DB 20 CTATATATGAACCTTTTCAT 1  
 RESULT 61  
 ADI80148/c  
 ID ADI80148 standard; DNA; 20 BP.  
 XX  
 AC ADI80148;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 149.  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
 KW

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
OS Mus musculus.  
XX US2004006030-A1.  
XX 08-JAN-2004.  
XX 02-JUL-2002; 2002US-00189267.  
XX 02-JUL-2002; 2002US-00189267.  
XX 02-JUL-2002; 2002US-00189267.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.  
XX Example 16; SEQ ID NO 149; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
XX in length targeted to, and which specifically hybridizes with, a nucleic  
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX inhibits the expression of TGF-beta 2. The invention further relates to:  
XX a compound 8-80 nucleobases in length that specifically hybridizes with  
XX at least an 8-nucleobase portion of an active site on a nucleic acid  
XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX tissues by contacting the cells or tissues with the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; and screening an antisense  
XX compound. The antisense compound has cytostatic, neurotropic,  
XX neuroprotective, and immunosuppressive activities. The compound,  
XX composition and methods are useful for treating a disease or condition  
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
XX cancer, a neurodegenerative disorder, or a disease or condition involving  
XX hyperactivation of an immune response. This polynucleotide sequence  
XX represents an antisense oligonucleotide of the invention.  
XX Sequence 20 BP; 7 A; 2 C; 6 G; 5 T; 0 U; 0 Other;  
SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2988 ACCTTTCATTACCTTGGAA 3007  
Db 20 ACCTTTCATTACCTTGGAA 1  
RESULT 62  
ADI80230  
ID ADI80230 standard; DNA; 20 BP.  
XX AC ADI80230;  
XX AC ADI80230;  
XX 22-APR-2004 (first entry)  
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 231.  
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX US2004006030-A1.

OS Mus musculus.  
XX US2004006030-A1.  
XX 08-JAN-2004.  
XX 02-JUL-2002; 2002US-00189267.  
XX 02-JUL-2002; 2002US-00189267.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.  
XX Example 16; SEQ ID NO 231; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
XX in length targeted to, and which specifically hybridizes with, a nucleic  
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX inhibits the expression of TGF-beta 2. The invention further relates to:  
XX a compound 8-80 nucleobases in length that specifically hybridizes with  
XX at least an 8-nucleobase portion of an active site on a nucleic acid  
XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX tissues by contacting the cells or tissues with the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; and screening an antisense  
XX compound. The antisense compound has cytostatic, neurotropic,  
XX neuroprotective, and immunosuppressive activities. The compound,  
XX composition and methods are useful for treating a disease or condition  
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
XX cancer, a neurodegenerative disorder, or a disease or condition involving  
XX hyperactivation of an immune response. This polynucleotide sequence  
XX represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;  
SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1218 ATGCACTACTGTGTCTGAG 1237  
Db 1 ATGCACTACTGTGTCTGAG 20  
RESULT 63  
ADI80234  
ID ADI80234 standard; DNA; 20 BP.  
XX AC ADI80234;  
XX AC ADI80234;  
XX 22-APR-2004 (first entry)  
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 235.  
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX US2004006030-A1.



XX 08-JAN-2004.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 XX neurodegenerative disorder, or a disease involving hyperactivation of  
 XX immune response.  
 XX Example 16; SEQ ID NO 235; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 XX in length targeted to, and which specifically hybridizes with, a nucleic  
 XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 XX inhibits the expression of TGF-beta 2. The invention further relates to:  
 XX a compound 8-80 nucleobases in length that specifically hybridizes with  
 XX at least an 8-nucleobase portion of an active site on a nucleic acid  
 XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
 XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 XX tissues by contacting the cells or tissues with the compound so that  
 XX expression of TGF-beta 2 is inhibited; treating an animal having a  
 XX disease or condition associated with TGF-beta 2 by administering to the  
 XX animal a therapeutic or prophylactic amount of the compound so that  
 XX expression of TGF-beta 2 is inhibited; and screening an antisense  
 XX compound. The antisense compound has cytostatic, neurotropic,  
 XX neuroprotective, and immunosuppressive activities. The compound,  
 XX composition and methods are useful for treating a disease or condition  
 XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 XX cancer, a neurodegenerative disorder, or a disease or condition involving  
 XX hyperactivation of an immune response. This polynucleotide sequence  
 XX represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1335 ATCCGGCGGCAGATCTCTGAG 1354  
 DB 1 ATCCGGCGGCAGATCTCTGAG 20  
 RESULT 64  
 ADI80239  
 ID ADI80239 standard; DNA; 20 BP.  
 XX  
 XX ADI80239;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 240.  
 DE  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 XX Mus musculus.  
 OS  
 XX US2004006030-A1.  
 PN  
 XX 08-JAN-2004.  
 XX

PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 DR  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 XX neurodegenerative disorder, or a disease involving hyperactivation of  
 XX immune response.  
 XX Example 16; SEQ ID NO 240; 135pp; English.  
 PS  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 XX in length targeted to, and which specifically hybridizes with, a nucleic  
 XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 XX inhibits the expression of TGF-beta 2. The invention further relates to:  
 XX a compound 8-80 nucleobases in length that specifically hybridizes with  
 XX at least an 8-nucleobase portion of an active site on a nucleic acid  
 XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
 XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 XX tissues by contacting the cells or tissues with the compound so that  
 XX expression of TGF-beta 2 is inhibited; treating an animal having a  
 XX disease or condition associated with TGF-beta 2 by administering to the  
 XX animal a therapeutic or prophylactic amount of the compound so that  
 XX expression of TGF-beta 2 is inhibited; and screening an antisense  
 XX compound. The antisense compound has cytostatic, neurotropic,  
 XX neuroprotective, and immunosuppressive activities. The compound,  
 XX composition and methods are useful for treating a disease or condition  
 XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 XX cancer, a neurodegenerative disorder, or a disease or condition involving  
 XX hyperactivation of an immune response. This polynucleotide sequence  
 XX represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1463 AAGCCGGAGGCGAGCGCCT 1482  
 DB 1 AAGCCGGAGGCGAGCGCCT 20  
 RESULT 65  
 ADI80245  
 ID ADI80245 standard; DNA; 20 BP.  
 XX  
 XX ADI80245;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 246.  
 DE  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 XX Mus musculus.  
 OS  
 XX US2004006030-A1.  
 PN  
 XX 08-JAN-2004.  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PF  
 XX 02-JUL-2002; 2002US-00189267.  
 PR





XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PS neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 271; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3279 AATTGAAATGGTCTTTGC 3298  
Db 1 AATTGAAATGGTCTTTGC 20

RESULT 68  
ADI80098/c  
ID ADI80098 standard; DNA; 20 BP.  
XX AC ADI80098;  
XX DT 22-APR-2004 (first entry)  
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 99.  
XX antisen; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX Mus musculus.  
XX OS US2004006030-A1.  
XX PN 08-JAN-2004.  
XX PD 02-JUL-2002; 2002US-00189267.  
XX PF 02-JUL-2002; 2002US-00189267.  
XX PR 02-JUL-2002; 2002US-00189267.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 99; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1133 CCGCTCTGAGAATTACTAGT 1152  
Db 20 CCGCTCTGAGAATTACTAGT 1

RESULT 69  
ADI80133/c  
ID ADI80133 standard; DNA; 20 BP.  
XX AC ADI80133;  
XX DT 22-APR-2004 (first entry)  
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 134.  
XX antisen; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX Mus musculus.  
XX OS US2004006030-A1.  
XX PN 08-JAN-2004.  
XX PD 02-JUL-2002; 2002US-00189267.  
XX PF 02-JUL-2002; 2002US-00189267.  
XX PR 02-JUL-2002; 2002US-00189267.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.

```
PS Example 16; SEQ ID NO 134; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 8 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TGCCTTCGCCCTCTTACAT 2188
Db 20 TGCCTTCGCCCTCTTACAT 1

RESULT 70
AD180142/C
ID AD180142 standard; DNA; 20 BP.
XX
AC AD180142;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 143.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 143; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 8 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2451 AAATGCAGCTAAAGTCTTG 2470
Db 20 AAATGCAGCTAAAGTCTTG 1

RESULT 71
AD180224
ID AD180224 standard; DNA; 20 BP.
XX
AC AD180224;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 225.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 225; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
```

CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX  
 SQ Sequence 20 BP; 5 A; 7 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 ACACGAACTCCATTTCTTC 879  
 |||||  
 Db 1 ACACGAACTCCATTTCTTC 20

RESULT 72  
 ADI80225  
 ID ADI80225 standard; DNA; 20 BP.  
 XX  
 AC ADI80225;  
 XX  
 DT 22-APR-2004 (first entry)  
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 226.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 226; 135pp; English.  
 XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX  
 SQ Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 914 CCTCTCCCTTCCAGGAGAAA 933  
 |||||  
 Db 1 CCTCTCCCTTCCAGGAGAAA 20

RESULT 73  
 ADI80243  
 ID ADI80243 standard; DNA; 20 BP.  
 XX  
 AC ADI80243;  
 XX  
 DT 22-APR-2004 (first entry)  
 DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 244.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 244; 135pp; English.  
 XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1555 CCTCCGAAAATGCCATCCCG 1574  
DB 1 CCTCCGAAAATGCCATCCCG 20

RESULT 74  
AD180037/c  
ID AD180037 standard; DNA; 20 BP.  
XX  
AC AD180037;  
DT 22-APR-2004 (first entry)  
XX  
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 38.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; human.

XX Homo sapiens.  
XX  
XX US2004006030-A1.  
XX  
XX 08-JAN-2004.  
XX  
XX 02-JUL-2002; 2002US-00189267.  
XX  
XX 02-JUL-2002; 2002US-00189267.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.

XX Example 15; SEQ ID NO 38; 135pp; English.  
XX  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
XX in length targeted to, and which specifically hybridizes with, a nucleic  
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX inhibits the expression of TGF-beta 2. The invention further relates to:  
XX a compound 8-80 nucleobases in length that specifically hybridizes with  
XX at least an 8-nucleobase portion of an active site on a nucleic acid  
XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX tissues by contacting the cells or tissues with the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
XX represents an antisense oligonucleotide of the invention.

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1337 CCGCGGCGAGATCCTGAGCA 1356  
DB 20 CCGCGGCGAGATCCTGAGCA 1

RESULT 75  
AD180096/c  
ID AD180096 standard; DNA; 20 BP.  
XX  
AC AD180096;  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 97.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.

XX Mus musculus.  
XX  
XX US2004006030-A1.  
XX  
XX 08-JAN-2004.  
XX  
XX 02-JUL-2002; 2002US-00189267.  
XX  
XX 02-JUL-2002; 2002US-00189267.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.

XX Example 16; SEQ ID NO 97; 135pp; English.  
XX  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
XX in length targeted to, and which specifically hybridizes with, a nucleic  
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX inhibits the expression of TGF-beta 2. The invention further relates to:  
XX a compound 8-80 nucleobases in length that specifically hybridizes with  
XX at least an 8-nucleobase portion of an active site on a nucleic acid  
XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX tissues by contacting the cells or tissues with the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; and screening an antisense  
XX compound. The antisense compound has cytostatic, nontropic,  
XX neuroprotective, and immunosuppressive activities. The compound,  
XX composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1015 GTTGGGACGCGTTGCATT 1034  
DB 20 GTTGGGACGCGTTGCATT 1  
RESULT 76  
ADI80128/c  
ID ADI80128 standard; DNA; 20 BP.  
XX  
AC ADI80128;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 129.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PS New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 129; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence

CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2051 CCCACATCTCTGCTAATGT 2070  
DB 20 CCCACATCTCTGCTAATGT 1  
RESULT 77  
ADI80153/c  
ID ADI80153 standard; DNA; 20 BP.  
XX  
AC ADI80153;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 154.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PS New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 154; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
XX  
SQ Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |      |                      |      |
|----|------|----------------------|------|
| QY | 3292 | TCTTTGCCAGTTTAAGCAAG | 3311 |
|    |      |                      |      |
| Db | 20   | TCTTTGCCAGTTTAAGCAAG | 1    |

|                                |   |
|--------------------------------|---|
| RESULT 78                      |   |
| ADI80253                       |   |
| ADI80253 standard; DNA; 20 BP. |   |
| XX                             |   |
| XX                             |   |
| AC                             | ADI80253;   |
| XX                             |   |
| XX                             |   |
| 22-APR-2004                    | (first entry)   |
| XX                             |   |
| DT                             |   |
| XX                             |   |
| DE                             | Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 254. |
| XX                             |   |
| XX                             | antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;           |
| KW                             | cytostatic; nontropic; neuroprotective; immunosuppressive;                |
| KW                             | hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  |
| KW                             | immune; ss; mouse; murine.  |

SQ Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;

|    |         |                    |              |    |            |    |        |    |      |    |
|----|---------|--------------------|--------------|----|------------|----|--------|----|------|----|
|    | Matches | 20;                | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| Qy | 2060    | CCTGCTAATGTGGTGCCT | 2079         |    |            |    |        |    |      |    |
| Dd | 1       | CCTGCTAATGTGGTGCCT | 20           |    |            |    |        |    |      |    |

|           |  |
|-----------|--|
| RESULT 79 |  |
| AD180255  |  |
| ID        | AD180255 standard; DNA; 20 BP.   |
| XX        |  |
| XX        |  |
| XX        | AD180255;  |
| XX        |  |
| DT        | 22-APR-2004 (first entry)  |
| XX        |  |
| DE        | Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 256 |
| XX        |  |
| KW        | antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;          |
| KW        | cytostatic; nontropic; neuroprotective; immunosuppressive;               |
| KW        | hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; |
| KW        | immune; ss; mouse; murine.   |

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels

QY 2142 TGCTTTAGAAATGTCAGGA 2161



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Db      1  TGCTTTAGAAATGTCAGGA 20
|||||
RESULT 81
ADI80109/c
ID      ADI80109 standard; DNA; 20 BP.
XX
AC      ADI80109;
XX
DT      22-APR-2004 (first entry)
XX
DE      Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 110.
XX
KW      antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW      cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW      hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW      immune; ss; mouse; murine.
XX
OS      Mus musculus.
XX
PN      US2004006030-A1.
XX
PD      08-JAN-2004.
XX
PF      02-JUL-2002; 2002US-00189267.
XX
PR      02-JUL-2002; 2002US-00189267.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Monia BP, Freier SM, Dobie KW;
XX
DR      WPI; 2004-081742/08.
XX
PT      New compounds, particularly antisense oligonucleotides targeted to a
PT      nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT      neurodegenerative disorder, or a disease involving hyperactivation of
PT      immune response.
XX
PS      Example 16; SEQ ID NO 110; 135pp; English.
XX
CC      The invention relates to a novel antisense compound of 8-80 nucleobases
CC      in length targeted to, and which specifically hybridizes with, a nucleic
CC      acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC      inhibits the expression of TGF-beta 2. The invention further relates to:
CC      a compound 8-80 nucleobases in length that specifically hybridizes with
CC      at least an 8-nucleobase portion of an active site on a nucleic acid
CC      molecule encoding TGF-beta 2; a composition comprising the compound and a
CC      carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC      tissues by contacting the cells or tissues with the compound so that
CC      expression of TGF-beta 2 is inhibited; treating an animal having a
CC      disease or condition associated with TGF-beta 2 by administering to the
CC      animal a therapeutic or prophylactic amount of the compound so that
CC      expression of TGF-beta 2 is inhibited; and screening an antisense
CC      compound. The antisense compound has cytostatic, neurotropic,
CC      neuroprotective, and immunosuppressive activities. The compound,
CC      composition and methods are useful for treating a disease or condition
CC      associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC      cancer, a neurodegenerative disorder, or a disease or condition involving
CC      hyperactivation of an immune response. This polynucleotide sequence
CC      represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ      Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2451 AAATGAGCTAAAGTCCTTG 2470
|||||
Db      1  AAATGAGCTAAAGTCCTTG 20
|||||
RESULT 82
ADI80111/c

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ID ADI80111 standard; DNA; 20 BP.
XX
AC ADI80111;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 112.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 112; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 4 A; 2 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1422 TCCATCTACACAGTACCAG 1441
Db ||||||||||||||||
20 TCCATCTACACAGTACCAG 1

RESULT 83
ADI80122/c
ID ADI80122 standard; DNA; 20 BP.
XX
AC ADI80122;
XX

ID ADI80111 standard; DNA; 20 BP.
XX
AC ADI80111;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 123.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosolic; nontropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
OS Mus musculus.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 123; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, nontropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1877 TAAATAAGTTTACACTGCC 1896
Db ||||||||||||||||
20 TAAATAAGTTTACACTGCC 1

RESULT 84
ADI80135/c
ID ADI80135 standard; DNA; 20 BP.
XX
AC ADI80135;
XX
DT 22-APR-2004 (first entry)
XX

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DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 136.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX  
 DR New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 PT  
 XX  
 PS Example 16; SEQ ID NO 136; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2190 GATTTTAAAGGGGATCTTG 2209  
 DB 20 GATTTTAAAGGGGATCTTG 1  
 RESULT 85  
 AD180150/c  
 ID AD180150 standard; DNA; 20 BP.  
 XX  
 AC AD180150;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 151.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW

KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX  
 DR New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 PT  
 XX  
 PS Example 16; SEQ ID NO 151; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 4 A; 4 C; 4 G; 8 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3073 TTGAACCTCAATAAGCCAGG 3092  
 DB 20 TTGAACCTCAATAAGCCAGG 1  
 RESULT 86  
 AD180171  
 ID AD180171 standard; DNA; 20 BP.  
 XX  
 AC AD180171;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 172.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.

```
XX OS Homo sapiens.
XX PD US2004006030-A1.
XX PN 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PP 02-JUL-2002; 2002US-00189267.
XX PS Example 16; SEQ ID NO 172; 135pp; English.
XX PT The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, nototropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 4 A; 3 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1965 TTTGCAGGTATTGTCAC 1984
DB 1 TTTGCAGGTATTGTCAC 20
RESULT 87
ADI80238
ID ADI80238 standard; DNA; 20 BP.
XX AC ADI80238;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 239.
XX antisenase; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytotatic; notropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
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PN US2004006030-A1.
XX 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PP (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX PS Example 16; SEQ ID NO 239; 135pp; English.
XX PT The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, notropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1422 TCCATCTACAACAGTACCAG 1441
DB 1 TCCATCTACAACAGTACCAG 20
RESULT 88
ADI80242
ID ADI80242 standard; DNA; 20 BP.
XX AC ADI80242;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 243.
XX antisenase; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytotatic; notropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
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XX PF 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
PR 02-JUL-2002; 2002US-00189267.
XX PI Monia BP, Freier SM, Dobie KW;
XX PA (ISIS-) ISIS PHARM INC.
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 243; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1525 TTTATAAATCGACATGCCG 1544
DB 1 TTTATAAATCGACATGCCG 20
XX
RESULT 89
AD180246
ID AD180246 standard; DNA; 20 BP.
XX AC AD180246;
XX AC AD180246;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 247.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.

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PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX PA WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 16; SEQ ID NO 247; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX SQ Sequence 20 BP; 7 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1584 TACAGACCCCTACTTCAGAAAT 1603
DB 1 TACAGACCCCTACTTCAGAAAT 20
XX
RESULT 90
AD180252
ID AD180252 standard; DNA; 20 BP.
XX AC AD180252;
XX AC AD180252;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 253.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.

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XX Monia BP, Freier SM, Dobie KW;  
PI WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 253; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX Sequence 20 BP; 9 A; 2 C; 4 G; 5 T; 0 U; 0 Other;  
SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2000 TGGTGATCAGAAACTATAA 2019  
DB 1 TGGTGATCAGAAACTATAA 20  
RESULT 91  
AD180264  
ID AD180264 standard; DNA; 20 BP.  
XX AC  
XX AD180264;  
XX AC  
XX 22-APR-2004 (first entry)  
XX DE  
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 265.  
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX OS  
XX Mus musculus.  
XX OS  
XX US2004006030-A1.  
XX PN  
XX 08-JAN-2004.  
XX PD  
XX 02-JUL-2002; 2002US-00189267.  
XX PF  
XX 02-JUL-2002; 2002US-00189267.  
XX PR  
XX (ISIS-) ISIS PHARM INC.  
XX PA  
XX Monia BP, Freier SM, Dobie KW;  
PI WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a

DR WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 265; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX Sequence 20 BP; 9 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2487 AAAATCACGGTGACATGAC 2506  
DB 1 AAAATCACGGTGACATGAC 20  
RESULT 92  
AD180020/c  
ID AD180020 standard; DNA; 20 BP.  
XX AC  
XX AD180020;  
XX AC  
XX 22-APR-2004 (first entry)  
XX DT  
XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 21.  
XX DE  
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; human.  
XX OS  
XX Homo sapiens.  
XX OS  
XX US2004006030-A1.  
XX PN  
XX 08-JAN-2004.  
XX PD  
XX 02-JUL-2002; 2002US-00189267.  
XX PF  
XX 02-JUL-2002; 2002US-00189267.  
XX PR  
XX (ISIS-) ISIS PHARM INC.  
XX PA  
XX Monia BP, Freier SM, Dobie KW;  
PI WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
XX  
PS Example 15; SEQ ID NO 21; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 7 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1965 TTTCAGGATTGATGGCAC 1984  
Db 20 TTTCAGGATTGATGGCAC 1  
  
RESULT 93  
AD180101/c  
ID AD180101 standard; DNA; 20 BP.  
XX  
AC AD180101;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 102.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.

XX  
PS Example 16; SEQ ID NO 102; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 6 A; 2 C; 4 G; 8 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1209 TTTAAAAACATGCACCTACTG 1228  
Db 20 TTTAAAAACATGCACCTACTG 1  
  
RESULT 94  
AD180126/c  
ID AD180126 standard; DNA; 20 BP.  
XX  
AC AD180126;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 127.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
XX Example 16; SEQ ID NO 127; 135pp; English.  
XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2000 TGGTGATCAGAAACTATAA 2019  
Db 20 TGGTGATCAGAAACTATAA 1  
|||||

RESULT 95  
AD180146/c  
ID AD180146 standard; DNA; 20 BP.  
XX AC AD180146;  
XX DT 22-APR-2004 (first entry)  
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 147.  
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytosolic; neurotropic; neuroprotective; immunosuppressive;  
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX immune; ss; mouse; murine.  
XX OS Mus musculus.  
XX PN US2004006030-A1.  
XX PD 08-JAN-2004.  
XX PF 02-JUL-2002; 2002US-00189267.  
XX PR 02-JUL-2002; 2002US-00189267.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.

XX Example 16; SEQ ID NO 147; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX

SQ Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2970 TGTGTTACTATATATGAAC 2989  
Db 20 TGTGTTACTATATATGAAC 1  
|||||

RESULT 96  
AD180244  
ID AD180244 standard; DNA; 20 BP.  
XX AC AD180244;  
XX DT 22-APR-2004 (first entry)  
XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 245.  
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytosolic; neurotropic; neuroprotective; immunosuppressive;  
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX immune; ss; mouse; murine.  
XX OS Mus musculus.  
XX PN US2004006030-A1.  
XX PD 08-JAN-2004.  
XX PF 02-JUL-2002; 2002US-00189267.  
XX PR 02-JUL-2002; 2002US-00189267.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.

XX Example 16; SEQ ID NO 245; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid







CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX Sequence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3292 TCCTTCCAGTTTAAGCAAG 3311  
 Db 1 TCCTTCCAGTTTAAGCAAG 20

RESULT 99  
 ADI80112/c  
 ID ADI80112 standard; DNA; 20 BP.  
 XX  
 AC ADI80112;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID NO 113.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 113; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; screening an antisense  
 CC compound, The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX Sequence 20 BP; 1 A; 8 C; 7 G; 4 T; 0 U; 0 Other;  
 SQ

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1463 AAGCCGGAGGCGAGCGCCT 1482  
 Db 20 AAGCCGGAGGCGAGCGCCT 1

RESULT 100  
 ADI80127/c  
 ID ADI80127 standard; DNA; 20 BP.  
 XX  
 AC ADI80127;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID NO 128.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 128; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; screening an antisense  
 CC compound, The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 4 A; 3 C; 4 G; 9 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2011 AAACATATAAGTCCACTAGG 2030  
 DB 20 AAACATATAAGTCCACTAGG 1  
 RESULT 101  
 ADI80130/C  
 ID ADI80130 standard; DNA; 20 BP.  
 XX  
 AC ADI80130;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 131.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 131; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX

SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2075 GCCCTCCTACAGCTGGAGT 2094  
 DB 20 GCCCTCCTACAGCTGGAGT 1  
 RESULT 102  
 ADI80156/C  
 ID ADI80156 standard; DNA; 20 BP.  
 XX  
 AC ADI80156;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 157.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 157; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;

|  |   |  |
|--|---|--|
| Best Local Similarity 100.0%; Pred. No. 54;<br>Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |  |
| QY   | 3520 CATGTAATCTGTAGATCTTA 3539<br>  |  |
| Db   | 20 CATGTAATCTGTAGATCTTA 1<br>   |  |
| RESULT 103   |   |  |
| AD180226   |   |  |
| ID   | AD180226 standard; DNA; 20 BP.  |  |
| AC   |   |  |
| XX   | AD180226;   |  |
| DT   | 22-APR-2004 (first entry)   |  |
| DE   | Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 227. |  |
| XX   | antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;           |  |
| XX   | cytostatic; neurotropic; neuroprotective; immunosuppressive;              |  |
| KW   | hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  |  |
| KW   | immune; ss; mouse; murine.  |  |
| XX   |   |  |
| OS   | Mus musculus.   |  |
| XX   |   |  |
| PN   | US2004006030-A1.  |  |
| XX   |   |  |
| PD   | 08-JAN-2004.  |  |
| XX   |   |  |
| PF   | 02-JUL-2002; 2002US-00189267.   |  |
| XX   |   |  |
| PR   | 02-JUL-2002; 2002US-00189267.   |  |
| XX   |   |  |
| PA   | (ISIS-) ISIS PHARM INC.   |  |
| XX   |   |  |
| PI   | Monia BP, Freier SM, Dobie KW;  |  |
| XX   |   |  |
| DR   | WPI; 2004-081742/08.  |  |
| XX   |   |  |
| PT   | New compounds, particularly antisense oligonucleotides targeted to a      |  |
| PT   | nucleic acid encoding TGF-beta 2, useful for treating cancer, a           |  |
| PT   | neurodegenerative disorder, or a disease involving hyperactivation of     |  |
| PT   | immune response.  |  |
| XX   |   |  |
| PS   | Example 16; SEQ ID NO 227; 135pp; English.                                |  |
| XX   |   |  |
| CC   | The invention relates to a novel antisense compound of 8-80 nucleobases   |  |
| CC   | in length targeted to, and which specifically hybridizes with, a nucleic  |  |
| CC   | acid molecule encoding transforming growth factor (TGF)-beta 2, and       |  |
| CC   | inhibits the expression of TGF-beta 2. The invention further relates to:  |  |
| CC   | a compound 8-80 nucleobases in length that specifically hybridizes with   |  |
| CC   | at least an 8-nucleobase portion of an active site on a nucleic acid      |  |
| CC   | molecule encoding TGF-beta 2; a composition comprising the compound and a |  |
| CC   | carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or   |  |
| CC   | tissues by contacting the cells or tissues with the compound so that      |  |
| CC   | expression of TGF-beta 2 is inhibited; treating an animal having a        |  |
| CC   | disease or condition associated with TGF-beta 2 by administering to the   |  |
| CC   | animal a therapeutic or prophylactic amount of the compound so that       |  |
| CC   | expression of TGF-beta 2 is inhibited; and screening an antisense         |  |
| CC   | compound. The antisense compound has cytostatic, neurotropic,             |  |
| CC   | neuroprotective, and immunosuppressive activities. The compound,          |  |
| CC   | composition and methods are useful for treating a disease or condition    |  |
| CC   | associated with TGF-beta 2, such as a hyperproliferative disorder e.g.    |  |
| CC   | cancer, a neurodegenerative disorder, or a disease or condition involving |  |
| CC   | hyperactivation of an immune response. This polynucleotide sequence       |  |
| CC   | represents a preferred target DNA region of TGF-beta 2 of the invention.  |  |
| XX   |   |  |
| SQ   | Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;                         |  |
| Query Match 0.5%; Score 20; DB 1; Length 20;   |   |  |
| Best Local Similarity 100.0%; Pred. No. 54;  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |   |  |

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|--|---|--|
| Best Local Similarity 100.0%; Pred. No. 54;<br>Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |  |
| QY   | 1015 GTTGGGAACGCGTTCGATTT 1034<br>  |  |
| Db   | 1 GTTGGGAACGCGTTCGATTT 20<br>   |  |
| RESULT 104   |   |  |
| AD180228   |   |  |
| ID   | AD180228 standard; DNA; 20 BP.  |  |
| AC   |   |  |
| XX   | AD180228;   |  |
| DT   | 22-APR-2004 (first entry)   |  |
| DE   | Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 229. |  |
| XX   | antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;           |  |
| KW   | cytostatic; neurotropic; neuroprotective; immunosuppressive;              |  |
| KW   | hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  |  |
| KW   | immune; ss; mouse; murine.  |  |
| XX   |   |  |
| OS   | Mus musculus.   |  |
| XX   |   |  |
| PN   | US2004006030-A1.  |  |
| XX   |   |  |
| PD   | 08-JAN-2004.  |  |
| XX   |   |  |
| PF   | 02-JUL-2002; 2002US-00189267.   |  |
| XX   |   |  |
| PR   | 02-JUL-2002; 2002US-00189267.   |  |
| XX   |   |  |
| PA   | (ISIS-) ISIS PHARM INC.   |  |
| XX   |   |  |
| PI   | Monia BP, Freier SM, Dobie KW;  |  |
| XX   |   |  |
| DR   | WPI; 2004-081742/08.  |  |
| XX   |   |  |
| PT   | New compounds, particularly antisense oligonucleotides targeted to a      |  |
| PT   | nucleic acid encoding TGF-beta 2, useful for treating cancer, a           |  |
| PT   | neurodegenerative disorder, or a disease involving hyperactivation of     |  |
| PT   | immune response.  |  |
| XX   |   |  |
| PS   | Example 16; SEQ ID NO 229; 135pp; English.                                |  |
| XX   |   |  |
| CC   | The invention relates to a novel antisense compound of 8-80 nucleobases   |  |
| CC   | in length targeted to, and which specifically hybridizes with, a nucleic  |  |
| CC   | acid molecule encoding transforming growth factor (TGF)-beta 2, and       |  |
| CC   | inhibits the expression of TGF-beta 2. The invention further relates to:  |  |
| CC   | a compound 8-80 nucleobases in length that specifically hybridizes with   |  |
| CC   | at least an 8-nucleobase portion of an active site on a nucleic acid      |  |
| CC   | molecule encoding TGF-beta 2; a composition comprising the compound and a |  |
| CC   | carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or   |  |
| CC   | tissues by contacting the cells or tissues with the compound so that      |  |
| CC   | expression of TGF-beta 2 is inhibited; treating an animal having a        |  |
| CC   | disease or condition associated with TGF-beta 2 by administering to the   |  |
| CC   | animal a therapeutic or prophylactic amount of the compound so that       |  |
| CC   | expression of TGF-beta 2 is inhibited; and screening an antisense         |  |
| CC   | compound. The antisense compound has cytostatic, neurotropic,             |  |
| CC   | neuroprotective, and immunosuppressive activities. The compound,          |  |
| CC   | composition and methods are useful for treating a disease or condition    |  |
| CC   | associated with TGF-beta 2, such as a hyperproliferative disorder e.g.    |  |
| CC   | cancer, a neurodegenerative disorder, or a disease or condition involving |  |
| CC   | hyperactivation of an immune response. This polynucleotide sequence       |  |
| CC   | represents a preferred target DNA region of TGF-beta 2 of the invention.  |  |
| XX   |   |  |
| SQ   | Sequence 20 BP; 5 A; 3 C; 3 G; 9 T; 0 U; 0 Other;                         |  |
| Query Match 0.5%; Score 20; DB 1; Length 20;   |   |  |
| Best Local Similarity 100.0%; Pred. No. 54;  |   |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |   |  |

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|--|-------------------------------------|--|
| Best Local Similarity 100.0%; Pred. No. 54;<br>Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                     |  |
| QY   | 1138 CTGAGAAATTACTAGTTTCTT 1157<br> |  |
| Db   | 1 CTGAGAAATTACTAGTTTCTT 20<br>      |  |
| Query Match 0.5%; Score 20; DB 1; Length 20;   |                                     |  |
| Best Local Similarity 100.0%; Pred. No. 54;  |                                     |  |
| Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |                                     |  |

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|----|--------------------------------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|

```
RESULT 105
ADI80118/c
ID ADI80118 standard; DNA; 20 BP.
XX AC
XX ADI80118;
XX AC
XX 22-APR-2004 (first entry)
XX DE
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 119.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS
XX Mus musculus.
XX PN
XX US2004006030-A1.
XX PD
XX 08-JAN-2004.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS
XX Example 16; SEQ ID NO 119; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ
XX Sequence 20 BP; 7 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1580 TTCTACAGACCCCTACTTCA 1599
XX Db
XX 20 TTCTACAGACCCCTACTTCA 1
XX RESULT 106
```

```
ADI80131/c
ID ADI80131 standard; DNA; 20 BP.
XX AC
XX ADI80131;
XX AC
XX 22-APR-2004 (first entry)
XX DE
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 132.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS
XX Mus musculus.
XX PN
XX US2004006030-A1.
XX PD
XX 08-JAN-2004.
XX PF
XX 02-JUL-2002; 2002US-00189267.
XX PR
XX 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX DR
XX New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS
XX Example 16; SEQ ID NO 132; 135pp; English.
XX CC
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ
XX Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 2142 TGCCTTAGAATGTCAGGA 2161
XX Db
XX 20 TGCCTTAGAATGTCAGGA 1
XX RESULT 107
ADI80137/c
ID ADI80137 standard; DNA; 20 BP.
XX
```

AC ADI80137;  
 XX 22-APR-2004 (first entry)  
 XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 138.  
 DE  
 XX  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 DE cytotatic; neurotropic; neuroprotective; immunosuppressive;  
 XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 KW  
 XX Mus musculus.  
 OS  
 XX US2004006030-A1.  
 XX  
 XX 08-JAN-2004.  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PF  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 DR  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 XX neurodegenerative disorder, or a disease involving hyperactivation of  
 XX immune response.  
 XX  
 XX Example 16; SEQ ID NO 138; 135pp; English.  
 PS  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 XX in length targeted to, and which specifically hybridizes with, a nucleic  
 XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 XX inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 XX Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2226 GAACCCCAAGGGTACAATGC 2245  
 DB 20 GAACCCCAAGGGTACAATGC 1  
 RESULT 108  
 ADI80157/c  
 ID ADI80157 standard; DNA; 20 BP.  
 XX  
 XX ADI80157;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT

XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 158.  
 DE  
 XX  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytotatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 XX Mus musculus.  
 OS  
 XX US2004006030-A1.  
 XX  
 XX 08-JAN-2004.  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 XX  
 XX 02-JUL-2002; 2002US-00189267.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 DR  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 XX neurodegenerative disorder, or a disease involving hyperactivation of  
 XX immune response.  
 XX  
 XX Example 16; SEQ ID NO 158; 135pp; English.  
 PS  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 XX in length targeted to, and which specifically hybridizes with, a nucleic  
 XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 XX inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3642 GCTGGCCAGTACCTTTGAAT 3661  
 DB 20 GCTGGCCAGTACCTTTGAAT 1  
 RESULT 109  
 ADI80274  
 ID ADI80274 standard; DNA; 20 BP.  
 XX  
 XX ADI80274;  
 AC  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 275.  
 DE  
 XX

KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PP 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PS (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 275; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 6 A; 2 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3520 CATGTAATGCTAGATCTTA 3539  
DB 1 CATGTAATGCTAGATCTTA 20  
RESULT 110  
AD180114/c  
ID AD180114 standard; DNA; 20 BP.  
XX  
AC AD180114;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 115.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.

KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PP 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PS (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 115; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1515 GCCAAGGAGGTTTATAAAT 1534  
DB 20 GCCAAGGAGGTTTATAAAT 1  
RESULT 111  
AD180116/c  
ID AD180116 standard; DNA; 20 BP.  
XX  
AC AD180116;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 117.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.

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XX US2004006030-A1.
PN
XX
XX
PD 08-JAN-2004.
XX
XX
XX 02-JUL-2002; 2002US-00189267.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Freier SM, Dobie KW;
PI
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 117; 135pp; English.
PS
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and
CC a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 3 A; 3 C; 9 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CCTCCGAAATGCCATCCCG 1574
DB 20 CCTCCGAAATGCCATCCCG 1

RESULT 112
ADI80124/c
ID ADI80124 standard; DNA; 20 BP.
XX
XX AC ADI80124;
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 125.
DE
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
PN
XX
XX 02-JUL-2002; 2002US-00189267.
PD
XX
XX

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PD 08-JAN-2004.
XX
XX 02-JUL-2002; 2002US-00189267.
PF
XX
XX 02-JUL-2002; 2002US-00189267.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Monia BP, Freier SM, Dobie KW;
PI
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 125; 135pp; English.
PS
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1967 TGCAGGTATTGATGGCACCT 1986
DB 20 TGCAGGTATTGATGGCACCT 1

RESULT 113
ADI80149/c
ID ADI80149 standard; DNA; 20 BP.
XX
XX AC ADI80149;
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 150.
DE
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
PN
XX
XX 08-JAN-2004.
PD
XX
XX 02-JUL-2002; 2002US-00189267.
PF

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XX 02-JUL-2002; 2002US-00189267.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 150; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
XX represents an antisense oligonucleotide of the invention.  
XX Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 U; 0 Other;  
SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3049 AAATCATGGATGGCTTAAG 3068  
DB 20 AAATCATGGATGGCTTAAG 1  
RESULT 114  
ADI80158/c  
ID ADI80158 standard; DNA; 20 BP.  
XX AC ADI80158;  
XX 22-APR-2004 (first entry)  
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 159.  
DE antisenase; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytosstatic; nontropic; neuroprotective; immunosuppressive;  
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX immune; ss; mouse; murine.  
XX Mus musculus.  
XX US2004006030-A1.  
XX 08-JAN-2004.  
XX 02-JUL-2002; 2002US-00189267.  
XX 02-JUL-2002; 2002US-00189267.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM, Dobie KW;  
XX

PA (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 159; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
XX represents an antisense oligonucleotide of the invention.  
XX Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;  
SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3673 ATTTGACTTGCACTACAAA 3692  
DB 20 ATTTGACTTGCACTACAAA 1  
RESULT 115  
ADI80160/c  
ID ADI80160 standard; DNA; 20 BP.  
XX AC ADI80160;  
XX 22-APR-2004 (first entry)  
XX Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 161.  
DE antisenase; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytosstatic; nontropic; neuroprotective; immunosuppressive;  
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX immune; ss; mouse; murine.  
XX Mus musculus.  
XX US2004006030-A1.  
XX 08-JAN-2004.  
XX 02-JUL-2002; 2002US-00189267.  
XX 02-JUL-2002; 2002US-00189267.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM, Dobie KW;  
XX



XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX Example 16; SEQ ID NO 161; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

XX Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3935 GAAGTTGCGCACAATGTAGG 3954

DB 20 GAAGTTGCGCACAATGTAGG 1

RESULT 116

AD180232

ID AD180232 standard; DNA; 20 BP.

XX AC AD180232;

XX DT 22-APR-2004 (first entry)

XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 233.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytostatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; mouse; murine.

XX Mus musculus.

XX US2004006030-A1.

XX 08-JAN-2004.

XX 02-JUL-2002; 2002US-00189267.

XX 02-JUL-2002; 2002US-00189267.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

PT New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX Example 16; SEQ ID NO 233; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

XX Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1314 ATCGCAAGAGGATCGAGGC 1333

DB 1 ATCGCAAGAGGATCGAGGC 20

RESULT 117

AD180233

ID AD180233 standard; DNA; 20 BP.

XX AC AD180233;

XX DT 22-APR-2004 (first entry)

XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 234.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytostatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; mouse; murine.

XX Mus musculus.

XX US2004006030-A1.

XX 08-JAN-2004.

XX 02-JUL-2002; 2002US-00189267.

XX 02-JUL-2002; 2002US-00189267.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.  
XX Example 16; SEQ ID NO 234; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1321 AGAGGATCGAGGCCATCCGC 1340  
DB 1 AGAGGATCGAGGCCATCCGC 20  
RESULT 118  
ADI80247  
ID ADI80247 standard; DNA; 20 BP.  
XX  
AC ADI80247;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 248.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 248; 135pp; English.

XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1593 TACTTCAGAAATCGTCGGCTT 1612  
DB 1 TACTTCAGAAATCGTCGGCTT 20  
RESULT 119  
ADI80103/c  
ID ADI80103 standard; DNA; 20 BP.  
XX  
AC ADI80103;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID NO 104.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 104; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1239 ACCTTTTGTCTGTCATCT 1258  
 DB 20 ACCTTTTGTCTGTCATCT 1

RESULT 120  
 ADI80104/C  
 ID ADI80104 standard; DNA; 20 BP.  
 XX  
 AC ADI80104;  
 XX  
 DT 22-APR-2004 (first entry)  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 105.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX

PS Example 16; SEQ ID NO 105; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1269 GCGCTCAGTCTGCTACCTG 1288  
 DB 20 GCGCTCAGTCTGCTACCTG 1

RESULT 121  
 ADI80110/C  
 ID ADI80110 standard; DNA; 20 BP.  
 XX  
 AC ADI80110;  
 XX  
 DT 22-APR-2004 (first entry)  
 DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 111.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 111; 135pp; English.  
 XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;  
 SQ

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCATCTACAAC 1433  
 DB 20 AGGTGATTTCCATCTACAAC 1

RESULT 122  
 ADI80120/c  
 ID ADI80120 standard; DNA; 20 BP.

XX  
 AC ADI80120;  
 DT 22-APR-2004 (first entry)

DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 121.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.

XX Mus musculus.  
 XX US2004006030-A1.

XX 08-JAN-2004.  
 PF 02-JUL-2002; 2002US-00189267.

XX 02-JUL-2002; 2002US-00189267.  
 PR (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;  
 PI WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.

XX Example 16; SEQ ID NO 121; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1593 TACTTCAGAAATCGTCGCTT 1612  
 DB 20 TACTTCAGAAATCGTCGCTT 1

RESULT 123  
 ADI80154/c  
 ID ADI80154 standard; DNA; 20 BP.

XX  
 AC ADI80154;  
 DT 22-APR-2004 (first entry)

DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 155.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.

XX Mus musculus.  
 XX US2004006030-A1.

XX 08-JAN-2004.  
 PF 02-JUL-2002; 2002US-00189267.

XX 02-JUL-2002; 2002US-00189267.  
 PR (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;  
 PI WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.

XX Example 16; SEQ ID NO 155; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.

XX  
SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3505 ACAGTAACACTTACATGT 3524  
|||||  
Db 20 ACAGTAACACTTACATGT 1

RESULT 124  
ADI80189  
ID ADI80189 standard; DNA; 20 BP.  
XX  
XX  
AC ADI80189;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 190.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; human.  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
XX  
DR WPI; 2004-081742/08.  
XX  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
XX  
PS Example 16; SEQ ID NO 190; 135pp; English.

XX  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX  
SQ Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GGAGGTGATTCCTCTACA 1431  
|||||  
Db 1 GGAGGTGATTCCTCTACA 20

RESULT 125  
ADI80229  
ID ADI80229 standard; DNA; 20 BP.  
XX  
XX  
AC ADI80229;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 230.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
XX  
DR WPI; 2004-081742/08.  
XX  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
XX  
PS Example 16; SEQ ID NO 230; 135pp; English.

XX  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.

```

XX SQ Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1209 TTTAAACATGCTACTG 1228
DB 1 TTTAAACATGCTACTG 20

RESULT 126
ADI80235
ID ADI80235 standard; DNA; 20 BP.
AC ADI80235;
XX
XX 22-APR-2004 (first entry)
DT
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 236.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
XX
XX 08-JAN-2004.
PD
XX 02-JUL-2002; 2002US-00189267.
PF
XX 02-JUL-2002; 2002US-00189267.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Freier SM, Dobie KW;
PI WPI; 2004-081742/08.
DR
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 236; 135pp; English.
PS
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1376 CCCGGAAGACTATCCGAGC 1395
DB 1 CCCGGAAGACTATCCGAGC 20

RESULT 127
ADI80261
ID ADI80261 standard; DNA; 20 BP.
XX
XX ADI80261;
AC
XX 22-APR-2004 (first entry)
DT
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 262.
XX
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX
XX Mus musculus.
OS
XX US2004006030-A1.
XX
XX 08-JAN-2004.
PD
XX 02-JUL-2002; 2002US-00189267.
PF
XX 02-JUL-2002; 2002US-00189267.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Freier SM, Dobie KW;
PI WPI; 2004-081742/08.
DR
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
XX Example 16; SEQ ID NO 262; 135pp; English.
PS
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
XX Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 22-APR-2004 (first entry)
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 238.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytotatic; neutropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KM;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 238; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neutropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1414 AGGTGATTTCCATCTCAAC 1433
DB 1 AGGTGATTTCCATCTCAAC 20
RESULT 133
ADI80248
ID ADI80248 standard; DNA; 20 BP.
XX AC ADI80248;
XX AC ADI80248;
XX 22-APR-2004 (first entry)
DT Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 249.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytotatic; neutropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KM;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 238; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neutropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
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XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytotatic; neutropic; neuroprotective; immunosuppressive;
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; mouse; murine.
XX Mus musculus.
XX US2004006030-A1.
XX 08-JAN-2004.
XX 02-JUL-2002; 2002US-00189267.
XX 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Dobie KM;
XX WPI; 2004-081742/08.
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX Example 16; SEQ ID NO 249; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neutropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents a preferred target DNA region of TGF-beta 2 of the invention.
XX Sequence 20 BP; 8 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1854 CACAAAGACAGAACCTCTGG 1873
DB 1 CACAAAGACAGAACCTCTGG 20
RESULT 134
ADI80256
ID ADI80256 standard; DNA; 20 BP.
XX AC ADI80256;
XX AC ADI80256;
XX 22-APR-2004 (first entry)
DT Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 257.
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytotatic; neutropic; neuroprotective; immunosuppressive;
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KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX immune; ss; mouse; murine.  
OS Mus musculus.  
XX US2004006030-A1.  
XX 08-JAN-2004.  
XX 02-JUL-2002; 2002US-00189267.  
XX 02-JUL-2002; 2002US-00189267.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM, Dobie KW;  
PI WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 257; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX Sequence 20 BP; 2 A; 8 C; 2 G; 8 T; 0 U; 0 Other;  
SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2169 TGCCTTCGCCCTCTTACAT 2188  
DB 1 TGCCTTCGCCCTCTTACAT 20  
RESULT 135  
AD180260  
ID AD180260 standard; DNA; 20 BP.  
XX AC AD180260;  
XX 22-APR-2004 (first entry)  
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 261.  
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX

OS Mus musculus.  
XX US2004006030-A1.  
XX 08-JAN-2004.  
XX 02-JUL-2002; 2002US-00189267.  
XX 02-JUL-2002; 2002US-00189267.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM, Dobie KW;  
PI WPI; 2004-081742/08.  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 261; 135pp; English.  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 U; 0 Other;  
SQ Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2238 TACAATGCTTAACCTCTGTGC 2257  
DB 1 TACAATGCTTAACCTCTGTGC 20  
RESULT 136  
AD180262  
ID AD180262 standard; DNA; 20 BP.  
XX AC AD180262;  
XX 22-APR-2004 (first entry)  
XX Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 263.  
DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX Mus musculus.  
XX US2004006030-A1.

XX PD 08-JAN-2004.  
 XX PR 02-JUL-2002; 2002US-00189267.  
 XX PF 02-JUL-2002; 2002US-00189267.  
 XX PR 02-JUL-2002; 2002US-00189267.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Freier SM, Dobie KW;  
 XX DR WPI; 2004-081742/08.  
 XX PT New compounds, particularly antisense oligonucleotides targeted to a  
 XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 XX PT neurodegenerative disorder, or a disease involving hyperactivation of  
 XX PT immune response.  
 XX PS Example 16; SEQ ID NO 263; 135pp; English.  
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX SQ Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2444 GTCTGTAATGAGCTAAA 2463  
 DB 1 GTCTGTAATGAGCTAAA 20  
 RESULT 137  
 ADI80265  
 ID ADI80265 standard; DNA; 20 BP.  
 XX AC ADI80265;  
 XX DT 22-APR-2004 (first entry).  
 XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 266.  
 XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX OS Mus musculus.  
 XX PN US2004006030-A1.  
 XX PD 08-JAN-2004.  
 XX PF 02-JUL-2002; 2002US-00189267.  
 XX PR 02-JUL-2002; 2002US-00189267.

PF 02-JUL-2002; 2002US-00189267.  
 XX PR 02-JUL-2002; 2002US-00189267.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Freier SM, Dobie KW;  
 XX DR WPI; 2004-081742/08.  
 XX PT New compounds, particularly antisense oligonucleotides targeted to a  
 XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 XX PT neurodegenerative disorder, or a disease involving hyperactivation of  
 XX PT immune response.  
 XX PS Example 16; SEQ ID NO 266; 135pp; English.  
 XX CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX SQ Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2635 GTTCTGTTTGTAAACTGG 2654  
 DB 1 GTTCTGTTTGTAAACTGG 20  
 RESULT 138  
 ADI80272  
 ID ADI80272 standard; DNA; 20 BP.  
 XX AC ADI80272;  
 XX DT 22-APR-2004 (first entry)  
 XX DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 273.  
 XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.  
 XX OS Mus musculus.  
 XX PN US2004006030-A1.  
 XX PD 08-JAN-2004.  
 XX PF 02-JUL-2002; 2002US-00189267.  
 XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM, Dobie KW;  
XX DR WPI; 2004-081742/08.  
XX PT New compounds, particularly antisense oligonucleotides targeted to a  
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX PT neurodegenerative disorder, or a disease involving hyperactivation of  
XX PT immune response.  
XX PS Example 16; SEQ ID NO 273; 135pp; English.  
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases  
XX CC in length targeted to, and which specifically hybridizes with, a nucleic  
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:  
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with  
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid  
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX CC tissues by contacting the cells or tissues with the compound so that  
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a  
XX CC disease or condition associated with TGF-beta 2 by administering to the  
XX CC animal a therapeutic or prophylactic amount of the compound so that  
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense  
XX CC compound. The antisense compound has cytostatic, neurotropic,  
XX CC neuroprotective, and immunosuppressive activities. The compound,  
XX CC composition and methods are useful for treating a disease or condition  
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving  
XX CC hyperactivation of an immune response. This polynucleotide sequence  
XX CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX SQ Sequence 20 BP; 7 A; 4 C; 2 G; 7 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3505 ACAGTAACACTTACATGT 3524  
Db 1 ACAGTAACACTTACATGT 20  
RESULT 139  
ADI80097/c  
ID ADI80097 standard; DNA; 20 BP.  
XX AC ADI80097;  
XX AC ADI80097;  
XX DT 22-APR-2004 (first entry)  
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 98.  
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 98.  
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX KW immune; ss; mouse; murine.  
XX OS Mus musculus.  
XX OS US2004006030-A1.  
XX PN 08-JAN-2004.  
XX PD 02-JUL-2002; 2002US-00189267.  
XX PF 02-JUL-2002; 2002US-00189267.  
XX PR 02-JUL-2002; 2002US-00189267.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM, Dobie KW;  
XX PA WPI; 2004-081742/08.

PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX PT New compounds, particularly antisense oligonucleotides targeted to a  
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX PT neurodegenerative disorder, or a disease involving hyperactivation of  
XX PT immune response.  
XX PS Example 16; SEQ ID NO 98; 135pp; English.  
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases  
XX CC in length targeted to, and which specifically hybridizes with, a nucleic  
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:  
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with  
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid  
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX CC tissues by contacting the cells or tissues with the compound so that  
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a  
XX CC disease or condition associated with TGF-beta 2 by administering to the  
XX CC animal a therapeutic or prophylactic amount of the compound so that  
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense  
XX CC compound. The antisense compound has cytostatic, neurotropic,  
XX CC neuroprotective, and immunosuppressive activities. The compound,  
XX CC composition and methods are useful for treating a disease or condition  
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving  
XX CC hyperactivation of an immune response. This polynucleotide sequence  
XX CC represents an antisense oligonucleotide of the invention.  
XX SQ Sequence 20 BP; 9 A; 3 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1094 CTTTCGAAAAGTTTCGTATT 1113  
Db 20 CTTTCGAAAAGTTTCGTATT 1  
RESULT 140  
ADI80102/c  
ID ADI80102 standard; DNA; 20 BP.  
XX AC ADI80102;  
XX AC ADI80102;  
XX DT 22-APR-2004 (first entry)  
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 103.  
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 103.  
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX KW immune; ss; mouse; murine.  
XX OS Mus musculus.  
XX OS US2004006030-A1.  
XX PN 08-JAN-2004.  
XX PD 02-JUL-2002; 2002US-00189267.  
XX PF 02-JUL-2002; 2002US-00189267.  
XX PR 02-JUL-2002; 2002US-00189267.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM, Dobie KW;  
XX PA WPI; 2004-081742/08.

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XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 103; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1218 ATGCACTACTGTGCTGTGAG 1237
DB 20 ATGCACTACTGTGCTGTGAG 1

RESULT 141
ADI80115/c
ID ADI80115 standard; DNA; 20 BP.
XX AC ADI80115;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 116.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosstatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX Example 16; SEQ ID NO 116; 135pp; English.
XX The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 TTTATAAAATCGACATGCCG 1544
DB 20 TTTATAAAATCGACATGCCG 1

RESULT 142
ADI80123/c
ID ADI80123 standard; DNA; 20 BP.
XX AC ADI80123;
XX DT 22-APR-2004 (first entry)
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 124.
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX cytosstatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS Mus musculus.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.

```

Example 16; SEQ ID NO 124; 135pp; English.

The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.

Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1962 AGATTTCAGGTATTGATCG 1981  
|||||  
DB 20 AGATTTCAGGTATTGATCG 1

RESULT 143  
ADI80145/c  
ID ADI80145 standard; DNA; 20 BP.  
AC ADI80145;  
XX  
XX  
DT 22-APR-2004 (first entry)  
XX  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID NO 146.  
XX  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
XX  
PD 08-JAN-2004.  
XX  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PA (ISIS-) ISIS PHARM INC.  
PI Monia BP, Freier SM, Dobie KW;  
XX  
XX  
DR WPI; 2004-081742/08.  
XX  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.  
XX  
XX  
PS Example 16; SEQ ID NO 146; 135pp; English.  
XX  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.

Sequence 20 BP; 7 A; 7 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1962 AGATTTCAGGTATTGATCG 1981  
|||||  
DB 20 AGATTTCAGGTATTGATCG 1

RESULT 143  
ADI80145/c  
ID ADI80145 standard; DNA; 20 BP.  
AC ADI80145;  
XX  
XX  
DT 22-APR-2004 (first entry)  
XX  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID NO 146.  
XX  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
XX  
PD 08-JAN-2004.  
XX  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PA (ISIS-) ISIS PHARM INC.  
PI Monia BP, Freier SM, Dobie KW;  
XX  
XX  
DR WPI; 2004-081742/08.  
XX  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.  
XX  
XX  
PS Example 16; SEQ ID NO 146; 135pp; English.  
XX  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.

Sequence 20 BP; 8 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2640 GTTTGTTAAACTGGCATCT 2659  
|||||  
DB 20 GTTTGTTAAACTGGCATCT 1

RESULT 144  
ADI80161/c  
ID ADI80161 standard; DNA; 20 BP.  
AC ADI80161;  
XX  
XX  
DT 22-APR-2004 (first entry)  
XX  
XX  
DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID NO 162.  
XX  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
XX  
PD 08-JAN-2004.  
XX  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
XX  
PA (ISIS-) ISIS PHARM INC.  
PI Monia BP, Freier SM, Dobie KW;  
XX  
XX  
DR WPI; 2004-081742/08.  
XX  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.  
XX  
XX  
PS Example 16; SEQ ID NO 162; 135pp; English.  
XX  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, neurotropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.

Sequence 20 BP; 8 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2640 GTTTGTTAAACTGGCATCT 2659  
|||||  
DB 20 GTTTGTTAAACTGGCATCT 1

CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 7 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4138 TGAGTTTTCAAAGGGGAA 4157  
 |||||  
 Db 20 TCAGTTTTCAAAGGGGAA 1

RESULT 145  
 ADI80249  
 ID ADI80249 standard; DNA; 20 BP.

AC ADI80249;

DT 22-APR-2004 (first entry)

DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 250.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.

XX Mus musculus.

XX US2004006030-A1.

PN 08-JAN-2004.

PF 02-JUL-2002; 2002US-00189267.

PR 02-JUL-2002; 2002US-00189267.

PA (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.

XX Example 16; SEQ ID NO 250; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with:  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1877 TAAATAAGTTTACACTGCC 1896  
 |||||  
 Db 1 TAAATAAGTTTACACTGCC 20

RESULT 146  
 ADI80258  
 ID ADI80258 standard; DNA; 20 BP.

AC ADI80258;

DT 22-APR-2004 (first entry)

DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 259.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; mouse; murine.

XX Mus musculus.

XX US2004006030-A1.

XX 08-JAN-2004.

PF 02-JUL-2002; 2002US-00189267.

PR 02-JUL-2002; 2002US-00189267.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.

XX Example 16; SEQ ID NO 259; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with:  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a



CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX  
SQ Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2217 TGGATCCATGAACCCAAAGG 2236

DB 1 TGGATCCATGAACCCAAAGG 20  
|||||

#### RESULT 147

ADI80121/C  
ID ADI80121 standard; DNA; 20 BP.

XX AC ADI80121;

XX DT 22-APR-2004 (first entry)

XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 122.

XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX KW immune; ss; mouse; murine.

XX OS Mus musculus.

XX PN US2004006030-A1.

XX PD 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX DR WPI; 2004-081742/08.

XX PT New compounds, particularly antisense oligonucleotides targeted to a  
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX PT neurodegenerative disorder, or a disease involving hyperactivation of  
XX PT immune response.

XX PS Example 16; SEQ ID NO 122; 135pp; English.

XX CC The invention relates to a novel antisense compound of 8-80 nucleobases  
XX CC in length targeted to, and which specifically hybridizes with, a nucleic  
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:  
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with  
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid  
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX CC tissues by contacting the cells or tissues with the compound so that  
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a  
XX CC disease or condition associated with TGF-beta 2 by administering to the  
XX CC animal a therapeutic or prophylactic amount of the compound so that  
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
XX represents an antisense oligonucleotide of the invention.

XX SQ Sequence 20 BP; 1 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1854 CACAAAGACAGGAACCTGGG 1873

DB 20 CACAAAGACAGGAACCTGGG 1  
|||||

#### RESULT 148

ADI80183  
ID ADI80183 standard; DNA; 20 BP.

XX AC ADI80183;

XX DT 22-APR-2004 (first entry)

XX DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 184.

XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;

XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

XX KW immune; ss; human.

XX OS Homo sapiens.

XX PN US2004006030-A1.

XX PD 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX DR WPI; 2004-081742/08.

XX PT New compounds, particularly antisense oligonucleotides targeted to a  
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX PT neurodegenerative disorder, or a disease involving hyperactivation of  
XX PT immune response.

XX PS Example 16; SEQ ID NO 184; 135pp; English.

XX CC The invention relates to a novel antisense compound of 8-80 nucleobases  
XX CC in length targeted to, and which specifically hybridizes with, a nucleic  
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:  
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with  
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid  
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX CC tissues by contacting the cells or tissues with the compound so that  
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a  
XX CC disease or condition associated with TGF-beta 2 by administering to the  
XX CC animal a therapeutic or prophylactic amount of the compound so that  
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense  
XX CC compound. The antisense compound has cytostatic, neurotropic,  
XX CC neuroprotective, and immunosuppressive activities. The compound,  
XX CC composition and methods are useful for treating a disease or condition



CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX  
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 CCGCGGCGAGATCTGAGCA 1356  
|||||  
Db 1 CCGCGGCGAGATCTGAGCA 20

RESULT 149  
ADI80236  
ID ADI80236 standard; DNA; 20 BP.  
XX  
AC ADI80236;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 237.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 237; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence

CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX  
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CCGGAGGTGATTCCATCT 1428  
|||||  
Db 1 CCGGAGGTGATTCCATCT 20

RESULT 150  
ADI80250  
ID ADI80250 standard; DNA; 20 BP.  
XX  
AC ADI80250;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 251.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 251; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX  
SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1967 TGCAGGTATTGATGGCACCT 1986  
DB 1 TGCAGGTATTGATGGCACCT 20

RESULT 151  
ADI80266  
ID ADI80266 standard; DNA; 20 BP.  
XX AC  
XX AC  
XX ADI80266;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 267.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytosatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
XX WPI; 2004-081742/08.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
XX Example 16; SEQ ID NO 267; 135pp; English.  
XX  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3512 CTACTTACATGTAATGTGT 3531

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2640 GTTTGTTAAACTGGCATCT 2659  
DB 1 GTTTGTTAAACTGGCATCT 20

RESULT 152  
ADI80273  
ID ADI80273 standard; DNA; 20 BP.  
XX AC  
XX AC  
XX ADI80273;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 274.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytosatic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
XX WPI; 2004-081742/08.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
XX Example 16; SEQ ID NO 274; 135pp; English.  
XX  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 3 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db      1 CTACTTTACATGTAATGTGT 20
|||||
RESULT 153
ADI80275
ID      ADI80275 standard; DNA; 20 BP.
XX
AC      ADI80275;
XX
DT      22-APR-2004 (first entry)
XX
DE      Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 276.
XX
KW      antisense; transforming growth factor; TGF-beta 2; TGF-beta 2;
KW      cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW      hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW      immune; ss; mouse; murine.
XX
OS      Mus musculus.
XX
PN      US2004006030-A1.
XX
PD      08-JAN-2004.
XX
PF      02-JUL-2002; 2002US-00189267.
XX
PR      02-JUL-2002; 2002US-00189267.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Monia BP, Freier SM, Dobie KW;
XX
DR      WPI; 2004-081742/08.
XX
PT      New compounds, particularly antisense oligonucleotides targeted to a
PT      nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT      neurodegenerative disorder, or a disease involving hyperactivation of
PT      immune response.
XX
PS      Example 16; SEQ ID NO 276; 135pp; English.
XX
CC      The invention relates to a novel antisense compound of 8-80 nucleobases
CC      in length targeted to, and which specifically hybridizes with, a nucleic
CC      acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC      inhibits the expression of TGF-beta 2. The invention further relates to:
CC      a compound 8-80 nucleobases in length that specifically hybridizes with
CC      at least an 8-nucleobase portion of an active site on a nucleic acid
CC      molecule encoding TGF-beta 2; a composition comprising the compound and a
CC      carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC      tissues by contacting the cells or tissues with the compound so that
CC      expression of TGF-beta 2 is inhibited; treating an animal having a
CC      disease or condition associated with TGF-beta 2 by administering to the
CC      animal a therapeutic or prophylactic amount of the compound so that
CC      expression of TGF-beta 2 is inhibited; and screening an antisense
CC      compound. The antisense compound has cytostatic, neurotropic,
CC      neuroprotective, and immunosuppressive activities. The compound,
CC      composition and methods are useful for treating a disease or condition
CC      associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC      cancer, a neurodegenerative disorder, or a disease or condition involving
CC      hyperactivation of an immune response. This polynucleotide sequence
CC      represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ      Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3642 GCTGGCCAGTACTTTGAAT 3661
|||||
Db      1 GCTGGCCAGTACTTTGAAT 20
|||||
RESULT 154
ADI80276
ID      ADI80276 standard; DNA; 20 BP.
XX
AC      ADI80276;
XX
DT      22-APR-2004 (first entry)
XX
DE      Mouse transforming growth factor-beta 2 target DNA region, SEQ ID NO 277.
XX
KW      antisense; transforming growth factor; TGF-beta 2; TGF-beta 2;
KW      cytostatic; neurotropic; neuroprotective; immunosuppressive;
KW      hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW      immune; ss; mouse; murine.
XX
OS      Mus musculus.
XX
PN      US2004006030-A1.
XX
PD      08-JAN-2004.
XX
PF      02-JUL-2002; 2002US-00189267.
XX
PR      02-JUL-2002; 2002US-00189267.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Monia BP, Freier SM, Dobie KW;
XX
DR      WPI; 2004-081742/08.
XX
PT      New compounds, particularly antisense oligonucleotides targeted to a
PT      nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT      neurodegenerative disorder, or a disease involving hyperactivation of
PT      immune response.
XX
PS      Example 16; SEQ ID NO 277; 135pp; English.
XX
CC      The invention relates to a novel antisense compound of 8-80 nucleobases
CC      in length targeted to, and which specifically hybridizes with, a nucleic
CC      acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC      inhibits the expression of TGF-beta 2. The invention further relates to:
CC      a compound 8-80 nucleobases in length that specifically hybridizes with
CC      at least an 8-nucleobase portion of an active site on a nucleic acid
CC      molecule encoding TGF-beta 2; a composition comprising the compound and a
CC      carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC      tissues by contacting the cells or tissues with the compound so that
CC      expression of TGF-beta 2 is inhibited; treating an animal having a
CC      disease or condition associated with TGF-beta 2 by administering to the
CC      animal a therapeutic or prophylactic amount of the compound so that
CC      expression of TGF-beta 2 is inhibited; and screening an antisense
CC      compound. The antisense compound has cytostatic, neurotropic,
CC      neuroprotective, and immunosuppressive activities. The compound,
CC      composition and methods are useful for treating a disease or condition
CC      associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC      cancer, a neurodegenerative disorder, or a disease or condition involving
CC      hyperactivation of an immune response. This polynucleotide sequence
CC      represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ      Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4245 CTTTGAGGCTGATTAAAAA 4264
|||||
Db      1 CTTTGAGGCTGATTAAAAA 20
|||||
RESULT 155
ADI80108/c
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ID ADI80108 standard; DNA; 20 BP.
XX AC ADI80108;
XX DT
XX DE
XX DT 22-APR-2004 (first entry)
XX XX
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 109.
XX XX
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; nontropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS
XX OS Mus musculus.
XX PN
XX PN US2004006030-A1.
XX PD
XX PD 08-JAN-2004.
XX PF
XX PF 02-JUL-2002; 2002US-00189267.
XX PR
XX PR 02-JUL-2002; 2002US-00189267.
XX PA
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX PI Monia BP, Freier SM, Dobie KW;
XX DR
XX DR WPI; 2004-081742/08.
XX PT
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS
XX PS Example 16; SEQ ID NO 109; 135pp; English.
XX CC
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, nontropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ
XX SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1376 CCCGGAAGACTATCCGGAGC 1395
Db 20 CCCGGAAGACTATCCGGAGC 1
RESULT 156
ADI80113/c
ID ADI80113 standard; DNA; 20 BP.
XX AC ADI80113;
XX DT
XX DE
XX DT 22-APR-2004 (first entry)
XX XX
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 109.
XX XX
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; nontropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS
XX OS Mus musculus.
XX PN
XX PN US2004006030-A1.
XX PD
XX PD 08-JAN-2004.
XX PF
XX PF 02-JUL-2002; 2002US-00189267.
XX PR
XX PR 02-JUL-2002; 2002US-00189267.
XX PA
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX PI Monia BP, Freier SM, Dobie KW;
XX DR
XX DR WPI; 2004-081742/08.
XX PT
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS
XX PS Example 16; SEQ ID NO 109; 135pp; English.
XX CC
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, nontropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ
XX SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1376 CCCGGAAGACTATCCGGAGC 1395
Db 20 CCCGGAAGACTATCCGGAGC 1
RESULT 156
ADI80113/c
ID ADI80113 standard; DNA; 20 BP.
XX AC ADI80113;
XX DT
XX DE
XX DT 22-APR-2004 (first entry)
XX XX
XX DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 109.
XX XX
XX KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytosolic; nontropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; mouse; murine.
XX OS
XX OS Mus musculus.
XX PN
XX PN US2004006030-A1.
XX PD
XX PD 08-JAN-2004.
XX PF
XX PF 02-JUL-2002; 2002US-00189267.
XX PR
XX PR 02-JUL-2002; 2002US-00189267.
XX PA
XX PA (ISIS-) ISIS PHARM INC.
XX PI
XX PI Monia BP, Freier SM, Dobie KW;
XX DR
XX DR WPI; 2004-081742/08.
XX PT
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS
XX PS Example 16; SEQ ID NO 114; 135pp; English.
XX CC
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, nontropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ
XX SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1507 AGTACTACGCCAAGAGGTT 1526
Db 20 AGTACTACGCCAAGAGGTT 1
RESULT 157
ADI80155/c
ID ADI80155 standard; DNA; 20 BP.
XX AC ADI80155;
XX DT
XX DT 22-APR-2004 (first entry)
XX XX
```

DE Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 156.  
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 156; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 9 A; 3 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3512 CTACTTTACATGTAATGTGT 3531  
DB 20 CTACTTTACATGTAATGTGT 1  
  
RESULT 158  
AD180227  
ID AD180227 standard; DNA; 20 BP.  
XX  
AC AD180227;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 228.  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.

KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.  
XX  
OS Mus musculus.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 228; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1133 CCGCTCTGAGAATTACTAGT 1152  
DB 1 CCGCTCTGAGAATTACTAGT 20  
  
RESULT 159  
AD180267  
ID AD180267 standard; DNA; 20 BP.  
XX  
AC AD180267;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 268.  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; mouse; murine.

XX OS Mus musculus.  
 XX PN US2004006030-A1.  
 XX PD 08-JAN-2004.  
 XX PF 02-JUL-2002; 2002US-00189267.  
 XX PR 02-JUL-2002; 2002US-00189267.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX Example 16; SEQ ID NO 268; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX SQ Sequence 20 BP; 7 A; 2 C; 3 G; 8 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2970 TGTGTTACTATATAATGAAC 2989  
 Db 1 TGTGTTACTATATAATGAAC 20  
 RESULT 160  
 AAQ41618  
 ID AAQ41618 standard; cDNA; 21 BP.  
 AC AAQ41618;  
 XX 25-MAR-2003 (revised)  
 DT 26-AUG-1993 (first entry)  
 XX TGF-beta2 sense strand (nucleotides 111-131) PCR primer.  
 XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;  
 KW cancer treatment; bone repair; growth regulation;  
 KW polymerase chain reaction; ss.  
 XX OS Synthetic.  
 XX

PN EP542679-A1.  
 XX 19-MAY-1993.  
 XX PF 03-NOV-1992; 92EP-00810845.  
 XX PR 11-NOV-1991; 91EP-00810870.  
 XX PA (CIBA ) CIBA GEIGY AG.  
 XX McMaster GK, Cox D, Cerletti N, Kuhla J;  
 XX WPI; 1993-161126/20.  
 XX PT New hybrid transforming growth factor-beta molecules - comprise portions  
 PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
 PT antiinflammatory and immunosuppressive agents etc.  
 XX Example 1; Page 36; 48pp; English.  
 XX The invention covers hybrid TGF-beta molecules consisting of parts of the  
 CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
 CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-  
 CC beta polypeptides were constructed from the appropriate, PCR-amplified  
 CC segments of the wild-type isoforms. For the construction of hybrid DNA  
 CC molecules encoding TGF-beta hybrids all having the hinge points between  
 CC amino acids 44 and 45, the primers AAQ41614-Q41619 (corresp. to the hinge  
 CC regions) were used with the appropriate primers (see AAQ41608-Q41613)  
 CC which flank the regions coding for each of the three full-length mature  
 CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.5%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 78;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2234 AGGGTACAAATGCTAACTTCTG 2254  
 Db 1 AGGGTACAAATGCTAACTTCTG 21  
 RESULT 161  
 AAQ41619/c  
 ID AAQ41619 standard; cDNA; 21 BP.  
 AC AAQ41619;  
 XX 25-MAR-2003 (revised)  
 DT 26-AUG-1993 (first entry)  
 XX TGF-beta2 antisense strand (nucleotides 111-131) PCR primer.  
 XX hTGF-beta2; Transforming Growth Factor; hybrid protein; wound healing;  
 KW cancer treatment; bone repair; growth regulation;  
 KW polymerase chain reaction; ss.  
 XX OS Synthetic.  
 XX EP542679-A1.  
 XX 19-MAY-1993.  
 XX PF 03-NOV-1992; 92EP-00810845.  
 XX PR 11-NOV-1991; 91EP-00810870.  
 XX PA (CIBA ) CIBA GEIGY AG.  
 XX McMaster GK, Cox D, Cerletti N, Kuhla J;  
 XX WPI; 1993-161126/20.

XX New hybrid transforming growth factor-beta molecules - comprise portions  
PT of mature TGF-beta isoforms; useful as wound healants, cardioprotective,  
PT antiinflammatory and immunosuppressive agents etc.  
XX  
PS Example 1; Page 37; 48pp; English.  
XX  
CC The invention covers hybrid TGF-beta molecules consisting of parts of the  
CC human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600  
CC and AAQ41601, respectively). Hybrid cDNAs coding for these hybrid TGF-  
CC beta polypeptides were constructed from the appropriate, PCR-amplified  
CC segments of the wild-type isoforms. For the construction of hybrid DNA  
CC molecules encoding TGF-beta hybrids all having the hinge points between  
CC amino acids 44 and 45, the primers AAQ41614-Q41619 (corresp. to the hinge  
CC regions) were used with the appropriate primers (see AAQ41608-Q41613)  
CC which flank the regions coding for each of the three full-length mature  
CC TGF-beta isoforms. See also AAQ41602-Q41643. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 78;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2234 AGGTACAATGCTAACTTCTG 2254  
|||||  
DB 21 AGGTACAATGCCAATCTCTG 1  
  
RESULT 162  
ADM92728/C  
ID ADM92728 standard; DNA; 21 BP.  
XX  
AC ADM92728;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE SNP-containing cardiovascular associated gene primer #58.  
XX  
XX SNP; single nucleotide polymorphism; cardiovascular associated gene;  
KW allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;  
KW restenosis; arterial inflammation; myocardial infarction; stroke; primer;  
KW ss.  
XX Homo sapiens.  
OS  
XX WO2003057911-A2.  
PN  
XX 17-JUL-2003.  
PD  
XX 07-JAN-2003; 2003WO-EP000060.  
PF  
XX 08-JAN-2002; 2002EP-00000153.  
PR  
XX (FARB ) BAYER AG.  
PA  
XX Stropp U, Schwes S, Kallabis H;  
PI  
XX WPI; 2003-577532/54.  
DR  
XX  
XX New isolated polynucleotides comprising single nucleotide polymorphisms  
PT of the cardiovascular gene, useful for assessing predisposition or  
PT susceptibility to a cardiovascular disease, e.g. atherosclerosis,  
PT restenosis or stroke.  
XX  
XX Disclosure; Page 68; 187pp; English.  
PS  
XX The invention relates an isolated polynucleotide (I) encoded by a  
CC cardiovascular associated (CA) gene, having allelic variation contained  
CC in a functional surrounding like full length cDNA for CA gene  
CC polypeptide, and with or without the CA gene promoter sequence. (I) is a  
CC polynucleotide comprising single nucleotide polymorphisms predicting

CC cardiovascular disease. The polynucleotides are useful for assessing  
CC predisposition or susceptibility to a cardiovascular disease, e.g.  
CC atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial  
CC inflammation, myocardial infarction, and stroke. These may also be used  
CC to predict personal medication schemes omitting adverse drug reactions,  
CC or as probes for detecting genetic polymorphisms and as templates for the  
CC recombinant production of normal or variant peptides/polypeptides encoded  
CC by the genes. This sequence corresponds to a PCR primer to amplify one of  
CC the genes of the invention.  
XX  
SQ Sequence 21 BP; 10 A; 5 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 78;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3283 GTAAATGGTCTTTCGCAGTT 3303  
|||||  
DB 21 GTAAATGGTCTTTCGCAGTT 1  
  
RESULT 163  
AAX59725  
ID AAX59725 standard; DNA; 24 BP.  
XX  
AC AAX59725;  
XX  
DT 22-JUL-1999 (first entry)  
XX  
DE DNA target used for the modified oligodeoxyribonucleotides.  
XX  
XX Oligodeoxyribonucleotide; intersubunit linkage;  
KW phosphoramidate intersubunit; antisense activity; nuclease resistant;  
KW in-vitro cell growth inhibition assay; infection;  
KW smooth muscle cell proliferation disorder; inflammatory process;  
KW genetic disorder; cancer; ss.  
XX  
XX Synthetic.  
OS  
XX WO9525814-A1.  
PN  
XX 28-SEP-1995.  
PD  
XX 20-MAR-1995; 95WO-US003575.  
PF  
XX 18-MAR-1994; 94US-00210505.  
PR  
XX 18-MAR-1994; 94US-00214599.  
XX  
XX (LYNX-) LYNX THERAPEUTICS INC.  
PA  
XX Gryaznov SM, Schultz RG, Chen J;  
PI  
XX WPI; 1995-344627/44.  
DR  
XX  
XX Oligo:nucleotide N3'-P5' phosphoramidate(s) - have improved resistance  
PT toward phosphodiesterase digestion, and form stable duplexes with DNA and  
PT RNA strands.  
XX  
XX Disclosure; Page 61; 101pp; English.  
PS  
XX The specification describes oligodeoxyribonucleotides having contiguous  
CC nucleoside subunits joined by intersubunit linkages, where at least 3  
CC contiguous subunits are joined by phosphoramidate intersubunits. The  
CC oligodeoxyribonucleotides has a sequence of nucleoside subunits effective  
CC to form a duplex with a target nucleic acid molecule. The  
CC oligodeoxyribonucleotides are more resistant to nuclease digestion and  
CC have improved RNA and dsDNA hybridisation characteristics, relative to  
CC oligonucleotides not containing N3'-P5' phosphoramidate linkages. They  
CC also have excellent antisense activity against complementary mRNA targets  
CC in in-vitro cell growth inhibition assays. They also exhibit low  
CC cytotoxicity. They may be used in diagnostic and therapeutic  
CC applications, e.g., in combatting infections agents such as bacteria,  
CC viruses, etc. or in treatment of smooth muscle cell proliferation



This sequence represents a synthetic polyguanosine tract PCR primer #22, used with primer #21 (AAZ19841) to generate a vector to the substitute a polyguanosine tract for the plastid atpB gene 3' untranslated region (3' UTR). This vector was then used in the generation of transgenic plants which can inducibly express a trehalose biosynthetic enzyme in a plastid. Trehalose is a disaccharide (a-D-glucopyranosyl-[1,1]-a-D-glucopyranoside) commonly found in organisms such as bacteria, fungi and insects which acts as a protectant against the deleterious effects of various stresses such as heat, desiccation and the deleterious effects of biosynthesis requires two enzymic activities; a trehalose-6-phosphate synthase catalyses the condensation of UDP-glucose and glucose-6-phosphate to trehalose-6-phosphate; and a trehalase-6-phosphate phosphatase phosphorylates trehalose-6-phosphate to trehalose. Previous attempts have been made to express trehalase biosynthetic enzymes in plants; however, certain deleterious effects appear to be associated with constitutive trehalase production in the cytosol, particularly when expression occurs in root tissue or during early development. These adverse effects include stunted growth, abnormal leaves and undeveloped roots. The use of an inducible promoter prevents these effects. Transformation with constructs containing trehalase biosynthetic enzymes under the control of an inducible promoter can provide plants protected against drought, high salinity, osmotic stress and temperature extremes. They can also be used for increasing the storage properties of plants.

QY 968 AGATTCCCCCCCCACCCGCCCA 99  
|||  
Db 1 AGCTTCCCCCCCCCCCCCCCCCA 24



RESULT 166  
AAD21596  
ID AAD21596 standard; DNA; 24 BP.  
XX  
AC AAD21596;  
XX  
DT 28-JAN-2002 (first entry)  
XX  
DE Kinase oligo #2 to construct pAT222 vector using polyguanosine tract.  
XX  
KW Transgenic plant; antibacterial; immunosuppressive; virucide; therapy;  
KW antiparasitic; allergy; autoimmune disease; immune response; PCR primer;  
KW transplantation; ss.  
XX  
OS Unidentified.  
XX  
FN WO200177353-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-BP003788.  
XX  
PR 05-APR-2000; 2000US-00543619.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Heifetz PB, Goff SA, Tuttle AB, Griot-Wenk ME;  
XX  
DR WPI; 2001-657175/75.  
XX  
PT Novel plant useful for treating or preventing allergy, comprising a DNA  
PT molecule encoding a mature ragweed pollen allergen in its plasmid genome  
PT and capable of expressing the pollen allergen.  
XX  
PS Example 10; Page 47; 99pp; English.  
XX  
CC The invention relates to a transgenic plant comprising in its plasmid  
CC genome a DNA molecule encoding a mature ragweed pollen allergen, which is  
CC capable of expressing the pollen allergen. The plant or plant matter  
CC derived from the transgenic plant such as tobacco, tomato, soybean, rice  
CC or maize is useful for treating or preventing an allergy. The plant is  
CC also useful as a pharmaceutical and as a medical food. The plant is  
CC useful for suppressing and reducing undesired immune response, and  
CC production of an antigen for determination of immunological activity. The  
CC plant is useful for treating and preventing bacterial, parasitic and  
CC viral diseases, allergies, autoimmune diseases and transplantations. The  
CC present sequence is an oligonucleotide used for constructing pAT222  
CC vector using polyguanosine tract as a substitute for 3' UTR  
XX  
SQ Sequence 24 BP; 2 A; 19 C; 1 G; 2 T; 0 U; 0 Other;  
Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 968 AGATTCCCCCCCCACCCGCCCA 991  
DB 1 AGCTTCCCCCCCCCCCCCCCCCA 24  
RESULT 167  
ADD29304  
ID ADD29304 standard; DNA; 24 BP.  
XX  
AC ADD29304;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Molecular and biological process inhibiting oligonucleotide seq id 67.  
XX  
KW molecular process inhibition; monomeric unit;

KW oligonucleotide interaction; polynucleotide interaction;  
KW enzyme interaction; local interaction; ss.  
XX  
OS Synthetic.  
XX  
FN US6548251-B1.  
XX  
PD 15-APR-2003.  
XX  
PF 05-SEP-2000; 2000US-00655804.  
XX  
PR 05-SEP-2000; 2000US-00655804.  
XX  
PA (FIDE-) FIDELITY SYSTEMS INC.  
XX  
PI Kozyavkin SA, Malykh AG, Polouchine NN, Slesarev AI;  
XX  
DR WPI; 2003-786284/74.  
XX  
PT Inhibiting nucleic acid hybridization and/or extension in a sample  
PT comprises administering to the sample a modified oligonucleotide or  
PT polynucleotide that contains at least one monomeric unit.  
XX  
PS Disclosure; SEQ ID NO 67; 38pp; English.  
XX  
CC The invention describes a method of inhibiting a molecular process  
CC involving the interaction between nucleic acids in a sample capable of  
CC undergoing the molecular process. The method comprises administering to  
CC the sample an oligonucleotide or polynucleotide that contains at least  
CC one monomeric unit having a specific formula. The method is useful in  
CC inhibiting undesired molecular interaction between oligonucleotides and  
CC their complexes with polynucleotides and enzymes, including local  
CC interactions between their chemical units (nucleotides or amino acids).  
CC This sequence represents an oligonucleotide used to inhibit undesired  
CC molecular interaction between oligonucleotides and their complexes with  
CC polynucleotides and enzymes.  
XX  
SQ Sequence 24 BP; 11 A; 3 C; 0 G; 10 T; 0 U; 0 Other;  
Query Match 0.4%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2730 CAAAAGAAAACATCTTTTTTTT 2753  
DB 1 CAAAAGAAAACATCTTTTTTTT 24  
RESULT 168  
ADH34300  
ID ADH34300 standard; DNA; 24 BP.  
XX  
AC ADH34300;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Hairpin oligonucleotide.  
XX  
KW Nucleoside analogue; oligonucleotide synthesis; antisense therapy;  
KW antigene method; hairpin oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT stem\_loop 1..24  
FT /\*tag= a  
XX  
PN WO2003068795-A1.  
XX  
PD 21-AUG-2003.  
XX  
PF 13-FEB-2003; 2003WO-JF001485.  
XX

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PR 13-FEB-2002; 2002JP-00035706.
XX (IMAN//) IMANISHI T.
XX Imanishi T, Obika S;
XX WPI; 2003-689651/65.
XX New nucleoside analogs for producing oligonucleotide analogs useful e.g.
PT as antisense compounds.
XX Example 2; Page 48; 74pp; Japanese.
XX The invention relates to nucleoside analogues and their salts. The
CC invention also encompasses oligonucleotides and their salts comprising at
CC least one nucleoside analogue of the invention. The nucleoside analogues
CC are produced by reducing an nucleoside azide derivative and optionally
CC further interconverting, or by reacting a nucleoside derivative with
CC formaldehyde and optionally deprotecting and/or interconverting. The
CC nucleoside analogues can be used for producing oligonucleotides useful as
CC antisense compounds and in antigenic methods. The present sequence
CC represents a hairpin oligonucleotide used in an example of the invention.
XX
XX Sequence 24 BP; 10 A; 4 C; 0 G; 10 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 AAAAAGAAACATCTTTTTTTT 2754
DB 1 AAAAAAAAAACCCCTTTTTTTTTT 24

RESULT 169
ADH63059
ID ADH63059 standard; DNA; 24 BP.
XX AC
XX ADH63059;
XX 25-MAR-2004 (first entry)
XX Murine fibroblast growth factor receptor 2 probe, SEQ ID 13.
XX Cytostatic; Vulnary; Gene Therapy; Antisense;
XX fibroblast growth factor receptor 2; FGF receptor 2;
XX hyperproliferative disorder; cancer; developmental disorder;
XX wound healing; murine; probe; ss.
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Labelled with FAM"
FT modified_base 24
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Labelled with FAM"
XX
XX WO2003024987-A1.
XX
XX 27-MAR-2003.
XX
XX 12-SEP-2002; 2002WO-US029149.
XX
XX 14-SEP-2001; 2001US-00954556.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Freier SM, Cooper SR;
XX
WPI; 2003-354582/33.
XX New antisense oligonucleotides for modulating expression of genes
PT encoding fibroblast growth factor receptor 2, useful for treating
PT hyperproliferative (e.g. cancer of the colon, lung, breast or skin) or
PT developmental disorders.
XX Example 13; SEQ ID NO 13; 200pp; English.
XX The present invention relates to antisense oligonucleotides (ADH63077-
CC ADH63154) targeted to fibroblast growth factor (FGF) receptor 2 coding
CC sequences (ADH63049 and ADH63056), which specifically hybridize with and
CC inhibit FGF receptor 2 expression. The antisense oligonucleotides are
CC useful for treating or preventing diseases or conditions associated with
CC FGF receptor 2 in an animal, e.g. hyperproliferative disorders
CC (particularly cancer of the colon, lung, breast or skin), or
CC developmental disorders. The antisense compound may also be used in wound
CC healing. The antisense compounds are useful for diagnostics,
CC therapeutics, prophylaxis, or as research reagents or kits. ADH63059 is a
CC probe for FGF receptor 2 coding sequence.
XX
XX Sequence 24 BP; 5 A; 13 C; 2 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2927 CTCCTCCGTCCTTCTCTCAAGCT 2950
DB 1 CCACACCGTCCTCATCTCCAAGCT 24

RESULT 170
AAC88273
ID AAC88273 standard; DNA; 25 BP.
XX AC
XX AAC88273;
XX 02-MAR-2001 (first entry)
XX SCDNA102 DNA sequence.
XX Drug binding site; viscosity; biomolecule interaction; drug target;
XX electronic transducer; primer; ds.
XX Synthetic.
XX WO200068419-A2.
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-CA000504.
XX
XX 05-MAY-1999; 99CA-02271179.
XX (SENS-) SENSORCHEM INT CORP.
XX McGovern M, Thompson M;
XX WPI; 2001-024875/03.
XX
XX Monitoring/detecting small molecule-biomolecule interactions for drug
PT screening involves contacting a solution of small molecules with
PT immobilized biomolecules and measuring the frequency generated with an
PT acoustic wave device.
XX Example 4; Fig 5; 44pp; English.
XX The present invention describes a device and method for monitoring small
CC molecule-biomolecule interactions. These involve the measurement of the
CC oscillation of a liquid when in contact with the biomolecule only
CC compared with the small molecule-biomolecule complex. This uses a
CC piezoelectric device and can be used with biomolecules such as DNA. The

```

CC present sequence was used as an example. The device can be used to screen  
 CC for drug candidates, to determine the conditions in which small molecules  
 CC will not bind to given biomolecules and to obtain information on the  
 CC tertiary structure of biomolecules

XX Sequence 25 BP; 0 A; 13 C; 12 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 19.2; DB 1; Length 25;  
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCGCGCGCGCGCGCGAC 638  
 DB 1 GCGCGCGCGCGCGCGCGCGCGCGCGC 24

RESULT 171  
 AAV48956/c  
 ID AAV48956 standard; DNA; 19 BP.  
 XX AC AAV48956;  
 XX DT 15-OCT-1998 (first entry)  
 XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-27.  
 DE Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 KW Synthetic.  
 OS Homo sapiens.  
 XX EP856579-A1.  
 XX OS-AUG-1998.  
 XX 31-JAN-1997; 97EP-00101531.  
 XX 31-JAN-1997; 97EP-00101531.  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PI Schlingensiepen K, Brysch W;  
 DR WPI; 1998-400910/35.  
 XX Preparation of antisense oligo:nucleotide(s) which lack long runs of  
 PT consecutive guanosine or inosine - and have specific ratio of residues  
 PT able to form two or three hydrogen bonds, have greater activity and  
 PT reduced toxicity, used therapeutically or to modulate growth of cells in  
 PT culture.  
 XX Claim 10; Fig 8a; 286pp; English.

CC AAV4930-49007 represent antisense oligonucleotides directed against  
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only  
 CC oligonucleotides AAV4930-67 resulted in significant reduction in TGF-  
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
 CC little effect. The oligonucleotides exemplify the invention. The  
 CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 CC which contain at most 8 nucleotides that can each form three hydrogen  
 CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 CC form three H-bonds each to four consecutive cytosines; do not contain two  
 CC sequences of three consecutive nucleotides each able to form three H-  
 CC bonds to three consecutive cytosines, and the ratio between residues able  
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 CC genes, particularly the genes for p53, Erb-2, junB, jund, TGF-beta 1 or  
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 CC keratinocytes). The oligonucleotides can also be used to analyse function  
 CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for

CC stimulating the immune system  
 XX Sequence 19 BP; 5 A; 6 C; 1 G; 7 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2149 GAAATGTGCAGGATAATTG 2167  
 DB 19 GAAATGTGCAGGATAATTG 1

RESULT 172  
 AAZ65459/c  
 ID AAZ65459 standard; DNA; 19 BP.  
 XX AC AAZ65459;  
 XX DT 30-MAR-2000 (first entry)  
 XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-19.  
 XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; ss;  
 KW atherosclerosis.  
 XX Unidentified.  
 OS WO9963975-A2.  
 XX 16-DEC-1999.  
 XX 10-JUN-1999; 99WO-EP004013.  
 XX 10-JUN-1998; 98EP-00110709.  
 PR 25-JUL-1998; 98EP-00113974.  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;  
 DR WPI; 2000-097470/08.  
 XX Composition containing immune stimulant and inhibitor of agent that  
 PT adversely affects the immune response, for treating cancers and  
 PT infections.  
 XX Claim 5; Fig 1; 30pp; English.

CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
 CC used in the invention. The invention relates to a composition which  
 CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor  
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes  
 CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukaemia; (non-Hodgkin's lymphoma; carcinoma of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
 CC syndrome and the formation of atherosclerotic plaque  
 XX

|            |   |   |   |
|------------|---|---|---|
| SQ         | Sequence 19 BP; 5 A; 6 C; 1 G; 7 T; 0 U; 0 Other;   | Best Local Similarity 100.0%; Pred. NO. 68; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |
|            | Query Match 0.4%; Score 19; DB 1; Length 19;  |   |   |
|            | Best Local Similarity 100.0%; Pred. NO. 68; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |   |   |
| QY         | 2149 GAAATGTGCAGGATAATTG 2167<br>   | 1816 CTTTCGACGTGACAGACGC 1834<br>   |   |
| DB         | 19 GAAATGTGCAGGATAATTG 1  | 19 CTTTCGACGTGACAGACGC 1  |   |
| RESULT 173 |   | RESULT 174  |   |
| ADI80012/C |   | ADO23058  |   |
| ID         | ADI80012 standard; DNA; 19 BP.  | ID  | ADO23058 standard; cDNA; 19 BP.   |
| XX         |   | XX  |   |
| AC         | ADI80012;   | AC  | ADO23058;   |
| XX         |   | XX  |   |
| DT         | 22-APR-2004 (first entry)   | DT  | 01-JUL-2004 (first entry)   |
| XX         |   | XX  |   |
| DE         | Mouse transforming growth factor-beta 2 reverse PCR primer.   | DE  | Human transforming growth factor beta 2 SDO target region #5.             |
| XX         |   | XX  |   |
| KW         | antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;   | KW  | Human; ss; SDO; short double stranded oligonucleotide; cleavage site;     |
| XX         |   | KW  | viral infection; malignant tumour; genetic disease; metabolic disease;    |
| KW         | cytostatic; neurotropic; neuroprotective; immunosuppressive;  | KW  | gene chip; protein chip; microarray; gene drug; Dermogene; Lungene;       |
| XX         |   | KW  | Hepatogene; Leukogene; Lymphogene; Prostogene; Breastogene;               |
| KW         | hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;                                | KW  | Brainumogene; Skin-whitogene; short interfering RNA; siRNA; cancer;       |
| XX         |   | KW  | RNA interference.   |
| XX         | immune; mouse; murine; primer; ss.  | XX  |   |
| OS         | Mus musculus.   | OS  | Homo sapiens.   |
| XX         |   | XX  |   |
| PN         | US2004006030-A1.  | PN  | US2004072769-A1.  |
| XX         |   | XX  |   |
| PD         | 08-JAN-2004.  | PD  | 15-APR-2004.  |
| XX         |   | XX  |   |
| PF         | 02-JUL-2002; 2002US-00189267.   | PF  | 16-SEP-2002; 2002US-00016490.   |
| XX         |   | XX  |   |
| PR         | 02-JUL-2002; 2002US-00189267.   | PR  | 16-SEP-2002; 2002US-00016490.   |
| XX         |   | XX  |   |
| PA         | (ISIS-) ISIS PHARM INC.   | PA  | (YINJ/) YIN J Q.  |
| XX         |   | XX  |   |
| PI         | Monia BP, Freier SM, Dobie KW;  | PI  | Yin JQ;   |
| XX         |   | XX  |   |
| DR         | WPI; 2004-081742/08.  | DR  | WPI; 2004-355427/33.  |
| XX         |   | XX  |   |
| PT         | New compounds, particularly antisense oligonucleotides targeted to a                                    | PT  | Designing and selecting short double-stranded oligonucleotides for        |
| XX         |   | PT  | treating viral infections, cancer and genetic or metabolic diseases,      |
| PT         | nucleic acid encoding TGF-beta 2, useful for treating cancer, a   | PT  | comprises using gene chip and protein chip microarrays to identify        |
| XX         |   | PT  | neurodegenerative disorder, or a disease involving hyperactivation of     |
| PT         | immune response.  | PT  | specific DNA sequences.   |
| XX         |   | XX  |   |
| PS         | Example 13; SEQ ID NO 13; 135pp; English.   | PS  | Example 1; Page 18; 58pp; English.  |
| XX         |   | XX  |   |
| CC         | The invention relates to a novel antisense compound of 8-80 nucleobases                                 | CC  | The invention relates to screening, identifying or predicting, and        |
| XX         |   | CC  | assembling 19-25 nt double-stranded oligonucleotides (termed short double |
| CC         | in length targeted to, and which specifically hybridizes with, a nucleic                                | CC  | stranded oligonucleotides, SDO) as active pharmaceutical compositions     |
| XX         |   | CC  | for the treatment of viral infections, malignant tumours, and genetic and |
| CC         | acid molecule encoding transforming growth factor (TGF)-beta 2, and                                     | CC  | metabolic diseases, comprising screening and identifying a specific DNA   |
| XX         |   | CC  | sequence in an abnormal gene encoding a protein with gene chip and        |
| CC         | inhibits the expression of TGF-beta 2. The invention further relates to:                                | CC  | protein chip microarrays. The above method comprises screening the        |
| XX         |   | CC  | sequence in an abnormal gene encoding a protein with gene chip and        |
| CC         | a compound 8-80 nucleobases in length that specifically hybridizes with                                 | CC  | gene chip and protein chip microarrays, identifying a specific DNA        |
| XX         |   | CC  | disease-causing genes, over-expressing in cells and/or tissues, with the  |
| CC         | at least an 8-nucleobase portion of an active site on a nucleic acid                                    | CC  | gene chip and protein chip microarrays, identifying a specific DNA        |
| XX         |   | CC  | sequence within the abnormal gene encoding a protein or playing other     |
| CC         | molecule encoding TGF-beta 2; a composition comprising the compound and a                               | CC  | biological roles with the assistance of computer and specific software,   |
| XX         |   | CC  | predicting efficacious 19-25 nt double-stranded oligonucleotides with a   |
| CC         | carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or                                 | CC  | 5'-AU(T)CCG-3' or 5'-U(T)CCG-3' special pattern complementary to at       |
| XX         |   | CC  | least a portion of an RNA molecule and making sure that selected sequence |
| CC         | tissues by contacting the cells or tissues with the compound so that                                    | CC  | is not localised within the stem-loop of target mRNA with any related     |
| XX         |   | CC  | software. Also included are pharmaceutical compositions of gene drugs     |
| CC         | expression of TGF-beta 2 is inhibited; treating an animal having a                                      | CC  | (such as Dermogene, Lungene, Hepatogene, Leukogene, Lymphogene,           |
| XX         |   | CC  | Prostogene, Breastogene, Brainumogene and Skin-whitogene including but    |
| CC         | disease or condition associated with TGF-beta 2 by administering to the                                 | CC  | being not limited to part or all of the following components: single or a |
| XX         |   | CC  | group of specific 19-25 nt dsRNA, 19-25 nt srRNA-cDNA, 19-25 nt dsRNA     |
| CC         | animal a therapeutic or prophylactic amount of the compound so that                                     | CC  | and/or single-stranded RNA and/or DNA with the special pattern, 5'-       |
| XX         |   | CC  | CGGAT(U)-3' or its derivatives, one or more nucleic acid condensation     |
| CC         | expression of TGF-beta 2 is inhibited; and screening an antisense                                       | CC  | agents (or none), one or more pharmaceutical carriers, one or more        |
| XX         |   | CC  | specific cell-targeting proteins and other active agents and additional   |
| CC         | compound. The antisense compound has cytostatic, neurotropic,   | CC  | materials) and a simplified method for predicting and selecting a         |
| XX         |   | CC  |   |
| CC         | neuroprotective, and immunosuppressive activities. The compound,  |   |   |
| XX         |   |   |   |
| CC         | composition and methods are useful for treating a disease or condition                                  |   |   |
| XX         |   |   |   |
| CC         | associated with TGF-beta 2, such as a hyperproliferative disorder e.g.                                  |   |   |
| XX         |   |   |   |
| CC         | cancer, a neurodegenerative disorder, or a disease or condition involving                               |   |   |
| XX         |   |   |   |
| CC         | hyperactivation of an immune response. This polynucleotide sequence                                     |   |   |
| XX         |   |   |   |
| CC         | represents a primer used in the exemplification of the invention.                                       |   |   |
| XX         |   |   |   |
| SQ         | Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;   | SQ  | Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;                         |
|            | Query Match 0.4%; Score 19; DB 1; Length 19;  |   | Query Match 0.4%; Score 19; DB 1; Length 19;                              |

CC specific and efficacious small double-stranded oligonucleotides (SDSO),  
CC antisense oligonucleotide molecules or short interfering RNA (siRNA)  
CC (comprising identifying a special pattern that can be localised in any  
CC position of an oligonucleotide sequence evaluating the specificity of a  
CC selected sequence). The short interfering RNA (siRNA) are targeted  
CC against genes involved in viral infection, malignant tumours, genetic and  
CC metabolic diseases. The methods are useful for designing and selecting  
CC short double-stranded oligonucleotides as a gene drug that can  
CC specifically inactivate a group of corresponding genes. The composition  
CC may be used for treating diseases or disorders associated with abnormal  
CC expression of genes in cells or tissues of humans or animals, such as  
CC viral infections, cancer, or genetic or metabolic diseases. The present  
CC sequence is a target region for an SDSO from an human cDNA.  
XX  
SQ Sequence 19 BP; 4 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1338 CGCGGCGAGATCTCTGAGCA 1356  
Db 1 CGCGGCGAGATCTCTGAGCA 19

RESULT 175  
ADI80213  
ID ADI80213 standard; DNA; 20 BP.  
XX  
AC ADI80213;  
DT 22-APR-2004 (first entry)  
XX  
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID NO 214.  
DE  
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytosolic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; human.  
XX  
OS Homo sapiens.  
XX  
PN US2004006030-A1.  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 214; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, nontropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 GCAAGCTGAAGCTCACCAG 1372  
Db 1 GCAAGCTGAAGCTCACCAG 19

RESULT 176  
ADI80073/C  
ID ADI80073 standard; DNA; 20 BP.  
XX  
AC ADI80073;  
DT 22-APR-2004 (first entry)  
XX  
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID NO 74.  
DE  
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytosolic; nontropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; human.  
XX  
OS Homo sapiens.  
XX  
PN US2004006030-A1.  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 15; SEQ ID NO 74; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1354 GCAAGCTGAGCTCACCAG 1372  
|||||  
DB 20 GCAAGCTGAGCTCACCAG 2  
  
RESULT 177  
AAV48947/c  
ID AAV48947 standard; DNA; 20 BP.  
XX  
AC AAV48947;  
XX  
DT 15-OCT-1998 (first entry)  
XX  
DE TGF-beta2 antisense oligonucleotide TGF-beta2-18.  
XX  
KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
KW modulate; gene expression; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN EP856579-A1.  
XX  
PD 05-AUG-1998.  
XX  
PF 31-JAN-1997; 97EP-00101531.  
XX  
PR 31-JAN-1997; 97EP-00101531.  
XX  
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
PI Schlingensiepen K, Brysch W;  
XX  
DR WPI; 1998-400910/35.  
XX  
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of  
PT consecutive guanosine or inosine - and have specific ratio of residues  
PT able to form two or three hydrogen bonds, have greater activity and  
PT reduced toxicity, used therapeutically or to modulate growth of cells in  
PT culture.  
XX  
PS Claim 10; Fig 8a; 286pp; English.  
XX  
CC AAV48930-49007 represent antisense oligonucleotides directed against  
CC transforming growth factor-beta2 (TGF-beta2). Of these, only  
CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
CC little effect. The oligonucleotides exemplify the invention. The  
CC specification describes oligonucleotides that contain 8-30 nucleotides,  
CC which contain at most 8 nucleotides that can each form three hydrogen  
CC bonds to cytosine; do not contain four consecutive nucleotides able to  
CC form three H-bonds each to four consecutive cytosines; do not contain two  
CC sequences of three consecutive nucleotides each able to form three H-  
CC bonds to three consecutive cytosines, and the ratio between residues able  
CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or  
CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or

CC keratinocytes). The oligonucleotides can also be used to analyse function  
CC of proteins (by altering their expression or activity) and  
CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
CC stimulating the immune system  
XX  
SQ Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 98;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1853 CCACAAAGACAGGAACTGG 1872  
|||||  
DB 20 CCATAAAGACAGGAACTGG 1  
  
RESULT 178  
ABA91534  
ID ABA91534 standard; DNA; 20 BP.  
XX  
AC ABA91534;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE DNA oligonucleotide AGT02022 used to test RNase H cleavage.  
XX  
KW Nucleic acid detection; probe; mismatch; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 12 /tag= a  
FT /note= "mismatch to target DNA"  
FT misc\_feature 13 /tag= b  
FT /note= "mismatch to target DNA"  
XX  
PN WO200206531-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 12-JUL-2001; 2001WO-US022166.  
XX  
PR 14-JUL-2000; 2000US-00616761.  
PR 30-MAR-2001; 2001US-00823647.  
XX  
PA (GENE-) APPLIED GENE TECHNOLOGIES INC.  
XX  
PI Dattagupta N;  
XX  
DR WPI; 2002-171819/22.  
XX  
PT Probes for detecting target nucleotide sequence in sample, has sequence  
PT that forms hairpin structure having a double-stranded segment and single-  
PT stranded loop collectively forming region complementary to target  
PT sequence.  
XX  
XX Example 5; Page 50; 72pp; English.  
XX  
PS The present sequence is that of oligonucleotide AGT02022, which contains  
CC a single mismatch with a target DNA oligonucleotide (see ABA91531). It is  
CC one of a set of oligonucleotides (see ABA91532-37) containing  
CC mismatch(es) to the target DNA that were tested in a hybridisation/RNase  
CC H cleavage assay. The results showed that 2 mismatches between the target  
CC and the probe ablated RNase H cleavage. The invention provides probes for  
CC nucleic acid hybridisation. The probes form a hairpin structure  
CC comprising a double-stranded stem and a single-stranded loop, and are  
CC capable of both intra-molecular and intermolecular hybridisation. The  
CC double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that  
CC is resistant to RNase H cleavage. When the probe hybridises with a target  
CC DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H  
CC treatment and can be removed. Arrays and methods for nucleic acid

CC hybridisation using the probes are provided

XX Sequence 20 BP; 16 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

SQ Query Match 0.4%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 98;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAAA 2599

DB 1 AAAAAAAAAATTGGAGAAAAA 20

RESULT 179

ADI80077/C

ID ADI80077 standard; DNA; 20 BP.

XX AC ADI80077;

XX DT 22-APR-2004 (first entry)

DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 78.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytosatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; human.

XX OS Homo sapiens.

XX US2004006030-A1.

XX PN 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX Example 15; SEQ ID NO 78; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, neurotropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 98;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2240 CAATGCTAACTTCTGTGCTG 2259

DB 20 CAATGCCAACTTCTGTGCTG 1

RESULT 180

ADI80049/C

ID ADI80049 standard; DNA; 20 BP.

XX AC ADI80049;

XX DT 22-APR-2004 (first entry)

DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 50.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytosatic; neurotropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; human.

XX OS Homo sapiens.

XX US2004006030-A1.

XX PN 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 15; SEQ ID NO 50; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; and screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 7 A; 5 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 98;



```
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2187 ATTGATTTTAAAGGATCT 2206
    ||||| ||||| |||||
Db 20 ATTGATTTTCAAGGATCT 1
    ||||| ||||| |||||

RESULT 181
ADI80199
ID ADI80199 standard; DNA; 20 BP.
XX
AC ADI80199;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID NO 200.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 200; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
    Query Match 0.4%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 98;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1310 GTTATGCGCAGAGGATCG 1329
    ||||| ||||| |||||
```

```
Db 1 GTTCATGCCGACAGGATCG 20
    ||||| ||||| ||||| |||||

RESULT 182
ADI80075/c
ID ADI80075 standard; DNA; 20 BP.
XX
AC ADI80075;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID NO 76.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; neurotropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 15; SEQ ID NO 76; 135pp; English.
XX
CC The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, neurotropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents an antisense oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 2 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
    Query Match 0.4%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 98;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1851 CACCACAAAGACAGGAACCT 1870
    ||||| ||||| ||||| |||||
Db 20 CACCATAAAGACAGGAACCT 1
    ||||| ||||| ||||| |||||
```





XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 42.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX cytotatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; human.  
XX  
OS Homo sapiens.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PS (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.  
XX  
XX Example 15; SEQ ID NO 42; 135pp; English.  
XX  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
XX in length targeted to, and which specifically hybridizes with, a nucleic  
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX inhibits the expression of TGF-beta 2. The invention further relates to:  
XX a compound 8-80 nucleobases in length that specifically hybridizes with  
XX at least an 8-nucleobase portion of an active site on a nucleic acid  
XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX carrier or diluent; inhibiting the cells or tissues with the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; and screening an antisense  
XX compound. The antisense compound has cytostatic, neurotropic,  
XX neuroprotective, and immunosuppressive activities. The compound,  
XX composition and methods are useful for treating a disease or condition  
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
XX cancer, a neurodegenerative disorder, or a disease or condition involving  
XX hyperactivation of an immune response. This polynucleotide sequence  
XX represents an antisense oligonucleotide of the invention.  
XX  
XX Sequence 20 BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 0.4%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 98;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 2442 AGCTCTTGAATGCAGCTA 2461  
DB 20 AGCTCTTGAATGCAGCTA 1  
XX  
RESULT 186  
ADI80179  
ID ADI80179 standard; DNA; 20 BP.  
XX  
AC ADI80179;  
XX  
DT 22-APR-2004 (first entry)  
XX

DE  
XX  
XX Human transforming growth factor-beta 2 target DNA region, SEQ ID No 180.  
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytotatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; human.  
XX  
OS Homo sapiens.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PS (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
XX neurodegenerative disorder, or a disease involving hyperactivation of  
XX immune response.  
XX  
XX Example 16; SEQ ID NO 180; 135pp; English.  
XX  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
XX in length targeted to, and which specifically hybridizes with, a nucleic  
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX inhibits the expression of TGF-beta 2. The invention further relates to:  
XX a compound 8-80 nucleobases in length that specifically hybridizes with  
XX at least an 8-nucleobase portion of an active site on a nucleic acid  
XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX carrier or diluent; inhibiting the cells or tissues with the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; and screening an antisense  
XX compound. The antisense compound has cytostatic, neurotropic,  
XX neuroprotective, and immunosuppressive activities. The compound,  
XX composition and methods are useful for treating a disease or condition  
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
XX cancer, a neurodegenerative disorder, or a disease or condition involving  
XX hyperactivation of an immune response. This polynucleotide sequence  
XX represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 0.4%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 98;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1281 TCTACTCTGCAGCACCCTCGA 1300  
DB 1 TCTACTCTGCAGCACCCTCGA 20  
XX  
RESULT 187  
ADI80030/c  
ID ADI80030 standard; DNA; 20 BP.  
XX  
AC ADI80030;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 31.  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytotatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 OS Homo sapiens.  
 XX US2004006030-A1.  
 PN 08-JAN-2004.  
 PD 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 PF 02-JUL-2002; 2002US-00189267.  
 PR (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 PI WPI; 2004-081742/08.  
 DR New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX Example 15; SEQ ID NO 31; 135pp; English.  
 PS The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 98;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1281 TCTACTCTGCAGCACCTCGA 1300  
 DB 20 TCTACTCTGCAGCACCTCGA 1  
 RESULT 188  
 ADI80056/C  
 ID ADI80056 standard; DNA; 20 BP.  
 XX ADI80056;  
 AC ADI80056;  
 XX 22-APR-2004 (first entry)  
 DT Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 57.  
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytotatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.

XX Homo sapiens.  
 OS US2004006030-A1.  
 PN 08-JAN-2004.  
 PD 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 PF 02-JUL-2002; 2002US-00189267.  
 PR (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 PI WPI; 2004-081742/08.  
 DR New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX Example 15; SEQ ID NO 57; 135pp; English.  
 PS The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 98;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1310 GTTTATGCGCAAGAGGATCG 1329  
 DB 20 GTTATGCGCAAGAGGATCG 1  
 RESULT 189  
 ADI80192  
 ID ADI80192 standard; DNA; 20 BP.  
 XX ADI80192;  
 AC ADI80192;  
 XX 22-APR-2004 (first entry)  
 DT Human transforming growth factor-beta 2 target DNA region, SEQ ID No 193.  
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytotatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 XX Homo sapiens.  
 OS



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PR 02-JUL-2002; 2002US-00189267.
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM, Dobie KW;
XX WPI; 2004-081742/08.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX neurodegenerative disorder, or a disease involving hyperactivation of
XX immune response.
XX
XX Example 15; SEQ ID NO 49; 135pp; English.
XX
XX The invention relates to a novel antisense compound of 8-80 nucleobases
XX in length targeted to, and which specifically hybridizes with, a nucleic
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX inhibits the expression of TGF-beta 2. The invention further relates to:
XX a compound 8-80 nucleobases in length that specifically hybridizes with
XX at least an 8-nucleobase portion of an active site on a nucleic acid
XX molecule encoding TGF-beta 2; a composition comprising the compound and a
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX tissues by contacting the cells or tissues with the compound so that
XX expression of TGF-beta 2 is inhibited; treating an animal having a
XX disease or condition associated with TGF-beta 2 by administering to the
XX animal a therapeutic or prophylactic amount of the compound so that
XX expression of TGF-beta 2 is inhibited; and screening an antisense
XX compound. The antisense compound has cytostatic, neurotropic,
XX neuroprotective, and immunosuppressive activities. The compound,
XX composition and methods are useful for treating a disease or condition
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX cancer, a neurodegenerative disorder, or a disease or condition involving
XX hyperactivation of an immune response. This polynucleotide sequence
XX represents an antisense oligonucleotide of the invention.
XX
XX Sequence 20 BP; 2 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 98;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 2224 ATGAACCCAAAGGTTCAAT 2243
Db | | | | | | | | | |
20 ACGAACCCAAAGGTTCAAT 1
XX
RESULT 192
AD023091
ID AD023091 standard; cDNA; 20 BP.
XX
XX AC AD023091,
XX
XX 01-JUL-2004 (first entry)
XX
XX Human transforming growth factor beta 2 SDO target region #2.
XX
XX Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
XX viral infection; malignant tumour; genetic disease; metabolic disease;
XX gene chip; protein chip; microarray; gene drug; Dermogene; Lungene;
XX Hepatogene; Leukogene; Lymphogene; Prostagene; Breastogene;
XX Brainumogene; Skin-whitogene; short interfering RNA; siRNA; cancer;
XX RNA interference.
XX
XX Homo sapiens.
XX
XX US2004072769-A1.
XX
XX 15-APR-2004.
XX
XX 16-SEP-2002; 2002US-00016490.
XX
XX 16-SEP-2002; 2002US-00016490.
XX

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XX (YINJ/) YIN J Q.
XX
XX Yin JQ;
XX
XX WPI; 2004-355427/33.
XX
XX Designing and selecting short double-stranded oligonucleotides for
XX treating viral infections, cancer and genetic or metabolic diseases,
XX comprises using gene chip and protein chip microarrays to identify
XX specific DNA sequences.
XX
XX Example 1; Page 18; 58pp; English.
XX
XX The invention relates to screening, identifying or predicting, and
XX assembling 19-25 nt double-stranded oligonucleotides (termed short double
XX stranded oligonucleotides, SDO) as active pharmaceutical compositions
XX for the treatment of viral infections, malignant tumours, and genetic and
XX metabolic diseases, comprising screening and identifying a specific DNA
XX sequence in an abnormal gene encoding a protein with gene chip and
XX protein chip microarrays. The above method comprises screening the
XX disease-causing genes over-expressing in cells and/or tissues, with the
XX gene chip and protein chip microarrays, identifying a specific DNA
XX sequence within the abnormal gene encoding a protein or playing other
XX biological roles with the assistance of computer and specific software,
XX predicting efficacious 19-25 nt double-stranded oligonucleotides with a
XX 5'-AU(T)CCG-3' or 5'-U(T)CCG-3' special pattern complementary to at
XX least a portion of an RNA molecule and making sure that selected sequence
XX is not localised within the stem-loop of target mRNA with any related
XX software. Also included are pharmaceutical compositions of gene drugs
XX (such as Dermogene, Lungene, Hepatogene, Leukogene, Lymphogene,
XX Prostagene, Breastogene, Brainumogene and Skin-whitogene including but
XX being not limited to part or all of the following components: single or a
XX group of specific 19-25 nt dsRNA, 19-25 nt sRNA-cDNA, 19-25 nt dsRNA
XX and/or single-stranded RNA and/or DNA with the special pattern, 5'-
XX CCGAT(U)-3' or its derivatives, one or more nucleic acid condensation
XX agents (or none), one or more pharmaceutical carriers, one or more
XX specific cell-targeting proteins and other active agents and selecting a
XX material) and a simplified method for predicting and selecting a
XX specific and efficacious small double-stranded oligonucleotides (SDSO),
XX antisense oligonucleotide molecules or short interfering RNA (siRNA)
XX (comprising identifying a special pattern that can be localised in any
XX position of an oligonucleotide sequence evaluating the specificity of a
XX selected sequence). The short interfering RNA (siRNA) are targeted
XX against genes involved in viral infection, malignant tumours, genetic and
XX metabolic diseases. The methods are useful for designing and selecting
XX short double-stranded oligonucleotides as a gene drug that can
XX specifically inactivate a group of corresponding genes. The composition
XX may be used for treating diseases or disorders associated with abnormal
XX expression of genes in cells or tissues of humans or animals, such as
XX viral infections, cancer, or genetic or metabolic diseases. The present
XX sequence is a target region for an SDO from an human cDNA.
XX
XX Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 98;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 2418 GAACAGCTTTCCAAATATGAT 2437
Db | | | | | | | | | |
1 GAACAGCTTTCCAAATATGAT 20
XX
RESULT 193
AAA80353
ID AAA80353 standard; DNA; 21 BP.
XX
XX AC AAA80353;
XX
XX 22-NOV-2000 (first entry)
XX
XX Human ASTH11 5' region polymorphic site, SEQ ID NO:100 (a).
XX

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RESULT 195
AAQ78455/c
ID AAQ78455 standard; DNA; 18 BP.
AC AAQ78455;
XX
XX
XX 25-MAR-2003 (revised)
DT 27-JUN-1995 (first entry)
DE
DE TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.
XX
XX Synthetic.
OS
XX WO9425588-A2.
PN
XX
XX 10-NOV-1994.
PD
XX
XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.
XX
XX Synthetic.
OS
XX WO9425588-A2.
PN
XX
XX 10-NOV-1994.
PD
XX
XX 29-APR-1994; 94WO-EP001362.
PF
XX
XX 30-APR-1993; 93EP-00107089.
PR
XX 13-MAY-1993; 93EP-00107849.
PR
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
PA
XX
XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI Bogdahn U;
PI
XX
XX WPI; 1994-358266/44.
DR
XX
XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
PT treating immunosuppression, tumours, etc.
PT
XX
XX Claim 6; Page 54; 74pp; English.
PS
XX
XX The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESSEQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESSEQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 4 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAAGTCCACTAGGA 2031
DB 18 CTATAAAGTCCACTAGGA 1

RESULT 196
AAQ78418/c
ID AAQ78418 standard; DNA; 18 BP.
XX
XX
XX AAQ78418;
AC
XX
XX 25-MAR-2003 (revised)
DT 27-JUN-1995 (first entry)
DE
DE Reverse PCR primer for human transforming growth factor-beta 2 cDNA.
XX
XX Human transforming growth factor-beta 2; TGF-beta3; oxygen tension;
KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW preeclampsia; pregnancy; choriocarcinoma; PCR primer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX

```

```

DE
XX TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.
XX
XX Synthetic.
OS
XX WO9425588-A2.
PN
XX
XX 10-NOV-1994.
PD
XX
XX 29-APR-1994; 94WO-EP001362.
PF
XX
XX 30-APR-1993; 93EP-00107089.
PR
XX 13-MAY-1993; 93EP-00107849.
PR
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
PA
XX
XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI Bogdahn U;
PI
XX
XX WPI; 1994-358266/44.
DR
XX
XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
PT treating immunosuppression, tumours, etc.
PT
XX
XX Claim 6; Page 43; 74pp; English.
PS
XX
XX The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESSEQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESSEQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 6 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1414 AGGTGATTTCCATCTACA 1431
DB 18 AGGTGATTTCCATCTACA 1

RESULT 197
AAV63218/c
ID AAV63218 standard; DNA; 18 BP.
XX
XX
XX AAV63218;
AC
XX
XX 14-JAN-1999 (first entry)
DT
XX
XX Reverse PCR primer for human transforming growth factor-beta 2 cDNA.
DE
XX
XX Human transforming growth factor-beta 2; TGF-beta3; oxygen tension;
KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW preeclampsia; pregnancy; choriocarcinoma; PCR primer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX

```



PN WO9840747-A1.  
 XX 17-SEP-1998.  
 PD  
 XX  
 PF 05-MAR-1998; 98WO-CA000180.  
 XX  
 PR 07-MAR-1997; 97US-0039919P.  
 XX  
 PA (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
 XX  
 PI Caniggia I, Post M, Iye S;  
 XX  
 DR WPI; 1998-520837/44.  
 XX  
 PT Regulation of trophoblast invasion - by, e.g. transforming growth factor-  
 PT beta3 inhibitor, useful for detecting or treating preeclampsia in  
 PT pregnant women.  
 XX  
 PS Example 4; Page 21; 59pp; English.  
 XX  
 CC PCR primers AAV63217-18 were used to amplify cDNA encoding human  
 CC transforming growth factor-beta 2 (TGF-beta2). The specification  
 CC describes a composition for regulating trophoblast invasion which  
 CC comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors,  
 CC hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The  
 CC composition is used in methods of diagnosing, monitoring, preventing or  
 CC treating conditions requiring regulation of trophoblast invasion,  
 CC especially preeclampsia in pregnant women or choriocarcinomas  
 XX  
 SQ Sequence 18 BP; 5 A; 2 C; 7 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1590 CCTACTTCAGATCGTC 1607  
 DB 18 CCTACTTCAGATCGTC 1  
 RESULT 198  
 AAV48953/c  
 ID AAV48953 standard; DNA; 18 BP.  
 XX  
 AC AAV48953;  
 XX  
 DT 15-OCT-1998 (first entry)  
 XX  
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-24.  
 XX  
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN EP856579-A1.  
 XX  
 XX 05-AUG-1998.  
 PD  
 XX 31-JAN-1997; 97EP-00101531.  
 PF  
 XX 31-JAN-1997; 97EP-00101531.  
 PR  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA Schlingensiepen K, Brysch W;  
 XX  
 PI WPI; 1998-400910/35.  
 XX  
 DR Preparation of antisense oligo:nucleotide(s) which lack long runs of  
 PT consecutive guanosine or inosine - and have specific ratio of residues  
 PT

PT able to form two or three hydrogen bonds, have greater activity and  
 PT reduced toxicity, used therapeutically or to modulate growth of cells in  
 PT culture.  
 XX  
 XX Claim 10; Fig 8a; 286pp; English.  
 PS  
 CC AAV48930-49007 represent antisense oligonucleotides directed against  
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only  
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
 CC little effect. The oligonucleotides exemplify the invention. The  
 CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 CC which contain at most 8 nucleotides that can each form three hydrogen  
 CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 CC form three H-bonds each to four consecutive cytosines; do not contain two  
 CC sequences of three consecutive nucleotides each able to form three H-  
 CC bonds to three consecutive cytosines, and the ratio between residues able  
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 CC genes, particularly the genes for p53, Erb-2, JunB, JunD, TGF-beta 1 or  
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 CC keratinocytes). The oligonucleotides can also be used to analyse function  
 CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 CC stimulating the immune system  
 XX  
 SQ Sequence 18 BP; 3 A; 2 C; 4 G; 9 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2007 CAGAAACTATAAGTCC 2024  
 DB 18 CAGAAACTATAAGTCC 1  
 RESULT 199  
 AAZ65457/c  
 ID AAZ65457 standard; DNA; 18 BP.  
 XX  
 AC AAZ65457;  
 XX  
 DT 30-MAR-2000 (first entry)  
 XX  
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-17.  
 XX  
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; ss;  
 KW atherosclerosis.  
 XX  
 OS Unidentified.  
 OS  
 XX WO9963975-A2.  
 PN  
 XX 16-DEC-1999.  
 PD  
 XX 10-JUN-1999; 99WO-EP004013.  
 PF  
 XX 10-JUN-1998; 98EP-00110709.  
 PR  
 XX 25-JUL-1998; 98EP-00113974.  
 PR  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA Schlingensiepen K, Schlingensiepen R, Brysch W;  
 XX  
 PI WPI; 2000-097470/08.  
 XX  
 DR Composition containing immune stimulant and inhibitor of agent that  
 PT



PT adversely affects the immune response, for treating cancers and  
 XX infections.

PS Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
 CC used in the invention. The invention relates to a composition which  
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor  
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes  
 CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
 CC syndrome and the formation of atherosclerotic plaque  
 XX

SQ Sequence 18 BP; 4 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 18; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2014 CTATAAGTCCACTAGGA 2031

DB 18 CTATAAGTCCACTAGGA 1

RESULT 200

AAQ05124/C

ID AAQ05124 standard; DNA; 20 BP.

AC AAQ05124;

XX 25-MAR-2003 (revised)

DT 02-NOV-1990 (first entry)

DE Probe used to screen cDNA library for human TGF-Beta2 precursor.

XX Human TGF-Beta2 precursor; cancer; tumorigenic; ss.

XX Synthetic.

XX EP376785-A.

XX 04-JUL-1990.

XX 14-DEC-1989; 89EP-00403480.

XX 16-DEC-1988; 88US-00285140.

PR 05-DEC-1989; 89US-00446020.

XX (ONCO ) ONCOGEN LP.

XX Purchio AF, Madisen L, Webb N;

XX WPI; 1990-203127/27.

XX Cloning and expression of transforming growth factor beta 2 - used for  
 PT treatment of tumours or for augmenting wound healing.

XX Example 6; Page 13; 58pp; English.

XX TGF-Beta2 may be used in treatment of tumors at effective doses, and may  
 CC also be useful in augmenting wound healing by stimulating cell

CC proliferation. The growth factor can be produced at high levels from a  
 CC CHO expression system. (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 20 BP; 3 A; 5 C; 3 G; 5 T; 0 U; 4 Other;

Query Match 0.4%; Score 18; DB 1; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2211 TGGAAATGGATCCATGAAC 2230

DB 20 TGGAAATGGATCCATGAAC 1

RESULT 201

AAF97183/C

ID AAF97183 standard; DNA; 21 BP.

XX AAF97183;

XX 18-NOV-2004 (revised)

DT 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #1944.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
 KW polymorphism; vascular disease; coronary artery disease; forensics;  
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
 KW pulmonary embolism; paternity test; ds.

OS Homo sapiens.

OS Unidentified.

PH Key Location/Qualifiers

FT Variation 11

FT /\*tag= a

FT /standard\_name= "Single nucleotide polymorphism"

XX WO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000WO-US024503.

XX 10-SEP-1999; 99US-0153357P.

PR 26-JUL-2000; 2000US-0220947P.

PR 16-AUG-2000; 2000US-0225724P.

XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
 XX WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in  
 PT applications such as forensics, paternity testing, medicine, genetic  
 PT analysis and phenotype correlations to diseases such as diabetes and  
 PT atherosclerosis.

XX Example; Page 180; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided  
 CC in the specification. In particular, the method can be used in the  
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and  
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
 CC useful in forensics, paternity testing, genetic analysis and phenotype  
 CC correlations to diseases. The present sequence is an example of one of  
 CC the human gene SNPs shown in the specification

CC Revised record issued on 18-NOV-2004 : The variantion feature was  
CC incorrectly given a capital V  
XX  
SQ Sequence 21 BP; 2 A; 7 C; 11 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 588 CCGCGCGCTCGCAGGCTCG 608  
DB 21 CCGCGGGCTCCCGAGGCTCG 1

RESULT 202  
AAS17230  
ID AAS17230 standard; DNA; 21 BP.  
XX AC  
AC AAS17230;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE DNA sequence #3 from reusable P-chip streptavidin-ds-DNA construct.  
XX  
KW Reusable protein chip microarray; P-chip; streptavidin-ds-DNA construct;  
KW Ab1-P-Ab2 sandwich; thermally decoupled linker; ss.  
XX  
OS Synthetic.  
XX

Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /\*mod\_base= OTHER  
FT /\*note= "Biotinylayted"

PN WO200181924-A2.

XX 01-NOV-2001.

XX 23-APR-2001; 2001WO-US013025.

XX 23-APR-2001; 2001WO-US013025.

XX (BIOT-) BIOTRACES INC.

XX Drukier AK;

XX WPI; 2002-041425/05.

XX Novel reusable protein chip useful for protein extraction, and protein  
PT quantification, can quantitate proteins with very high sensitivity.

XX Example; Page 52; 68pp; English.

XX The present invention relates to a new reusable protein chip (P-chip)  
CC microarray which can quantitate at least a few hundred proteins with a  
CC sensitivity not less than 10 pg/ml. The invention is useful for  
CC quantitating low abundance proteins and the P-chip is suitable for Ab1-P-  
CC Ab2 sandwich format with sensitivity better than 100 fg/ml for a majority  
CC of targets. The P-chip microarray of the invention is capable of  
CC detecting low abundance proteins from physiologic fluids that exist in  
CC concentrations smaller than 0.1 pg/ml. This superior sensitivity of P-  
CC chips allows them to be low cost, reliable and reusable. The present  
CC nucleic acid sequence forms a streptavidin-ds-DNA construct along with  
CC DNA sequence #4 (AAS17231). This construct was used in the invention to  
CC produce a reusable P-chip with a thermally decoupled linker

XX Sequence 21 BP; 0 A; 11 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CCGCGCGCACGACGCGCGGC 636  
DB 1 CCGCGCGCGCGCGCGCGGC 21

RESULT 203  
AAS17230/c  
ID AAS17230 standard; DNA; 21 BP.

XX AC

AC AAS17230;

XX 12-MAR-2002 (first entry)

XX DNA sequence #3 from reusable P-chip streptavidin-ds-DNA construct.

KW Reusable protein chip microarray; P-chip; streptavidin-ds-DNA construct;

KW Ab1-P-Ab2 sandwich; thermally decoupled linker; ss.

XX OS Synthetic.

XX Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /\*mod\_base= OTHER  
FT /\*note= "Biotinylayted"

XX PN WO200181924-A2.

XX 01-NOV-2001.

XX 23-APR-2001; 2001WO-US013025.

XX 23-APR-2001; 2001WO-US013025.

XX (BIOT-) BIOTRACES INC.

XX Drukier AK;

XX WPI; 2002-041425/05.

XX Novel reusable protein chip useful for protein extraction, and protein  
PT quantification, can quantitate proteins with very high sensitivity.

XX Example; Page 52; 68pp; English.

XX The present invention relates to a new reusable protein chip (P-chip)  
CC microarray which can quantitate at least a few hundred proteins with a  
CC sensitivity not less than 10 pg/ml. The invention is useful for  
CC quantitating low abundance proteins and the P-chip is suitable for Ab1-P-  
CC Ab2 sandwich format with sensitivity better than 100 fg/ml for a majority  
CC of targets. The P-chip microarray of the invention is capable of  
CC detecting low abundance proteins from physiologic fluids that exist in  
CC concentrations smaller than 0.1 pg/ml. This superior sensitivity of P-  
CC chips allows them to be low cost, reliable and reusable. The present  
CC nucleic acid sequence forms a streptavidin-ds-DNA construct along with  
CC DNA sequence #4 (AAS17231). This construct was used in the invention to  
CC produce a reusable P-chip with a thermally decoupled linker

XX Sequence 21 BP; 0 A; 11 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 CCGCGCGCGCACGACGCGGC 635

DB 21 CCGCGCGCGCGCGCGGC 1

RESULT 204  
AAV48945/c  
ID AAV48945 standard; DNA; 19 BP.

```

XX AAV48945;
XX
XX 15-OCT-1998 (first entry)
XX
XX TGF-beta2 antisense oligonucleotide TGF-beta2-16.
XX
XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
XX modulate; gene expression; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX EP856579-A1.
XX
XX 05-AUG-1998.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Brysch W;
XX
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX
XX Claim 10; Fig 8a; 286pp; English.
XX
XX AAV48930-49007 represent antisense oligonucleotides directed against
XX transforming growth factor-beta2 (TGF-beta2). Of these, only
XX oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
XX beta 2 protein expression, while oligonucleotides AAV48968-49007 had
XX little effect. The oligonucleotides exemplify the invention. The
XX specification describes oligonucleotides that contain 8-30 nucleotides,
XX which contain at most 8 nucleotides that can each form three hydrogen
XX bonds to cytosine; do not contain four consecutive nucleotides able to
XX form three H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
XX = 0.33-0.72. The oligonucleotides are used to modulate expression of
XX genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
XX marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
XX keratinocytes). The oligonucleotides can also be used to analyse function
XX of proteins (by altering their expression or activity) and
XX therapeutically, e.g. in cases of cancer or (targeting TGF) for
XX stimulating the immune system
XX
XX Sequence 19 BP; 5 A; 1 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 17.4; DB 1; Length 19;
XX Best Local Similarity 94.7%; Pred. No. 1.2e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 CCAAAGACTTACATCTCC 1756
DB 19 CCAAAGATTACATCTCC 1

RESULT 205
AAV48966/c
ID AAV48966 standard; DNA; 19 BP.
XX
XX AAV48966;
XX

```

```

DT 15-OCT-1998 (first entry)
XX
XX TGF-beta2 antisense oligonucleotide TGF-beta2-37.
XX
XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;
XX modulate; gene expression; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX EP856579-A1.
XX
XX 05-AUG-1998.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX 31-JAN-1997; 97EP-00101531.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Brysch W;
XX
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX
XX Claim 10; Fig 8a; 286pp; English.
XX
XX AAV48930-49007 represent antisense oligonucleotides directed against
XX transforming growth factor-beta2 (TGF-beta2). Of these, only
XX oligonucleotides AAV48930-67 resulted in significant reduction in TGF-
XX beta 2 protein expression, while oligonucleotides AAV48968-49007 had
XX little effect. The oligonucleotides exemplify the invention. The
XX specification describes oligonucleotides that contain 8-30 nucleotides,
XX which contain at most 8 nucleotides that can each form three hydrogen
XX bonds to cytosine; do not contain four consecutive nucleotides able to
XX form three H-bonds each (2R) or three such bonds (3R) is given by 2R/3R
XX = 0.33-0.72. The oligonucleotides are used to modulate expression of
XX genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or
XX marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or
XX keratinocytes). The oligonucleotides can also be used to analyse function
XX of proteins (by altering their expression or activity) and
XX therapeutically, e.g. in cases of cancer or (targeting TGF) for
XX stimulating the immune system
XX
XX Sequence 19 BP; 7 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 17.4; DB 1; Length 19;
XX Best Local Similarity 94.7%; Pred. No. 1.2e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2383 CCATTCCTCTATTACATTTGG 2401
DB 19 CCATTCCTCTACTACATTTGG 1

RESULT 206
ADO23060
ID ADO23060 standard; cDNA; 19 BP.
XX
XX ADO23060;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human transforming growth factor beta 2 SDO target region #7.
XX

```

XX Human; ss; SDSO; short double stranded oligonucleotide; cleavage site;  
KW viral infection; malignant tumour; genetic disease; metabolic disease;  
KW gene chip; protein chip; microarray; gene drug; Dermogene; Lungene;  
KW Hepatogene; Leukogene; Lymphogene; Prostogene; Breastogene;  
KW Braintumogene; Skin-whitogene; short interfering RNA; siRNA; cancer;  
KW RNA interference.  
XX  
XX Homo sapiens.  
XX  
XX US2004072769-A1.  
XX  
XX PD 15-APR-2004.  
XX  
XX PF 16-SEP-2002; 2002US-00016490.  
XX  
XX PR 16-SEP-2002; 2002US-00016490.  
XX  
XX PA (YIN/J) YIN J Q.  
XX  
XX PI Yin JQ;  
XX  
XX DR WPI; 2004-355427/33.  
XX  
XX PT Designing and selecting short double-stranded oligonucleotides for  
PT treating viral infections, cancer and genetic or metabolic diseases,  
PT comprises using gene chip and protein chip microarrays to identify  
PT specific DNA sequences.  
XX  
XX Example 1; Page 18; 59pp; English.  
XX  
XX The invention relates to screening, identifying or predicting, and  
XX assembling 19-25 nt double-stranded oligonucleotides (termed short double  
XX stranded oligonucleotides, SDSO) as active pharmaceutical compositions  
XX for the treatment of viral infections, malignant tumours, and genetic and  
XX metabolic diseases, comprising screening and identifying a specific DNA  
XX sequence in an abnormal gene encoding a protein with gene chip and  
XX protein chip microarrays. The above method comprises screening the  
XX disease-causing genes, over-expressing in cells and/or tissues, with the  
XX gene chip and protein chip microarrays, identifying a specific DNA  
XX sequence within the abnormal gene encoding a protein or playing other  
XX biological roles with the assistance of computer and specific software,  
XX predicting efficacious 19-25 nt double-stranded oligonucleotides with a  
XX 5'-AU(T)CCG-3' or 5'-U(T)CCC-3', special pattern complementary to at  
XX least a portion of an RNA molecule and making sure that selected sequence  
XX is not localised within the stem-loop of target mRNA with any related  
XX software. Also included are pharmaceutical compositions of gene drugs  
XX (such as Dermogene, Lungene, Hepatogene, Leukogene, Lymphogene,  
XX Prostogene, Breastogene, Braintumogene and Skin-whitogene including but  
XX being not limited to part or all of the following components: single or a  
XX group of specific 19-25 nt dsRNA, 19-25 nt srRNA-cDNA, 19-25 nt dsRNA  
XX and/or single-stranded RNA and/or DNA with the special pattern, 5'-  
XX CCGAT(U)-3' or its derivatives, one or more nucleic acid condensation  
XX agents (or none), one or more pharmaceutical carriers, one or more  
XX specific cell-targeting proteins and other active agents and additional  
XX materials) and a simplified method for predicting and selecting a  
XX specific and efficacious small double-stranded oligonucleotides (SDSO),  
XX antisense oligonucleotide molecules or short interfering RNA (siRNA)  
XX (comprising identifying a special pattern that can be localised in any  
XX position of an oligonucleotide sequence evaluating the specificity of a  
XX selected sequence). The short interfering RNA (siRNA) are targeted  
XX against genes involved in viral infection, malignant tumours, genetic and  
XX metabolic diseases. The methods are useful for designing and selecting  
XX short double-stranded oligonucleotides as a gene drug that can  
XX specifically inactivate a group of corresponding genes. The composition  
XX may be used for treating diseases or disorders associated with abnormal  
XX expression of genes in cells or tissues of humans or animals, such as  
XX viral infections, cancer, or genetic or metabolic diseases. The present  
XX sequence is a target region for an SDSO from an human cDNA.  
XX  
XX Sequence 19 BP; 8 A; 5 C; 5 G; 1 T; 0 U; 0 Other;  
SQ

Query Match 0.4%; Score 17.4; DB 1; Length 19;

Best Local Similarity 94.7%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2036 AACCACTGGGAGACCCCA 2054  
||| ||||| ||||| |||||  
DB 1 AAACACTGGGAGACCCCA 19  
RESULT 207  
AAA80354  
ID AAA80354 standard; DNA; 20 BP.  
XX  
XX AC AAA80354;  
XX  
XX DT 22-NOV-2000 (first entry)  
XX  
XX DE Human ASTH11 5' region polymorphic site, SEQ ID NO:100 (b).  
XX  
XX KW ASTH1 locus; ASTH11; ASTH1J; human; chromosome 11p; asthma;  
KW bronchial hyperreactivity; ets family; transcription factor;  
KW splice variant; genetic predisposition; polymorphism; antibody;  
KW drug screening; prophylaxis; therapy; diagnosis;  
KW single nucleotide polymorphism; SNP; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX FH Key Location/Qualifiers  
FT variation replace(10..11,TTA)  
FT /\*tag= a  
XX  
XX PN US6087485-A.  
XX  
XX PD 11-JUL-2000.  
XX  
XX PF 21-JAN-1998; 98US-00009913.  
XX  
XX PR 21-JAN-1997; 97US-0035663P.  
XX 01-JUL-1997; 97US-0051432P.  
XX (AXYS-) AXYS PHARM INC.  
XX  
XX PI Galvin M, Miller A, North M, Cardon L, Buckler A;  
PI Brooks-Wilson AR, Carey AH;  
XX WPI; 2000-505109/45.  
XX  
XX PT New nucleic acids other than naturally occurring chromosomes encoding  
PT ASTH1 protein, for e.g. screening compositions that modulate expression  
PT or function of ASTH1 proteins or as diagnostics for genetic  
PT predisposition to asthma.  
XX  
XX Example; Col 41-42; 131pp; English.  
XX  
XX The invention relates to the ASTH1 locus on the short arm of human  
XX chromosome (11p). This locus comprises the ASTH11 and ASTH1J genes, which  
XX are associated with a genetic predisposition to asthma and bronchial  
XX hyperreactivity. The ASTH11 and ASTH1J genes are oriented in opposite  
XX directions with the ASTH1 locus, and have similar patterns of expression  
XX and common sequence motifs. They are both expressed in trachea, lung and  
XX several other tissues. ASTH11 and ASTH1J are novel members of the ets  
XX family of transcription factors, which have been implicated in the  
XX activation of a variety of genes including the TCRA gene and cytokine  
XX genes known to be important in the aetiology of asthma. Both ASTH11 and  
XX ASTH1J mRNAs are alternatively spliced. Alternative splicing of  
XX transcripts has no effect on the open reading frame of ASTH1J, as the  
XX exons involved are all 5' to the start codon in exon b. In contrast,  
XX alternative splicing of ASTH11 transcripts results in 3 different ASTH11  
XX isoforms. The invention also encompasses mouse asth1j protein. The ASTH11  
XX nucleic acids are useful as diagnostics to identify a hereditary  
XX predisposition to asthma, as probes for identifying ASTH1 related genes,  
XX for identifying expression of the gene in a biological specimen, and for  
XX generating genetically modified non-human animals or site specific gene  
XX modifications in cell lines. The encoded ASTH1 proteins are useful as

CC immunogens to raise specific antibodies; in drug screening for  
 CC compositions that mimic or modulate activity or expression of ASTH11  
 CC and/or ASTH1J (including altered forms of these proteins); and as a  
 CC therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,  
 CC ASTH1 genomic regulatory regions, and anti-ASTH11 and anti-ASTH1J  
 CC antibodies are useful in the identification of individuals predisposed to  
 CC development of asthma, and for modulation of gene activity in vivo for  
 CC prophylactic and therapeutic purposes. The intact ASTH11 or ASTH1J  
 CC proteins or active fragments thereof may be used to modulate or reduce  
 CC bronchial hyperreactivity. Sequences AAA80260-A80261 and AAA80264-A80416  
 CC represent polymorphic sites within the ASTH1J or ASTH11 genes

XX Sequence 20 BP; 8 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2747 TTTTCTTTTAAAGGAAAAA 2765

Db 2 TTTTCTTTTAAAGGAAAAA 20

RESULT 208

AD180042/c

ID AD180042 standard; DNA; 20 BP.

XX AC AD180042;

XX AC AD180042;

XX DT 22-APR-2004 (first entry)

XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 43.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosolic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.

XX OS Homo sapiens.

XX PN US2004006030-A1.

XX PD 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX DR WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.

XX Example 15; SEQ ID NO 43; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC disease or condition associated with TGF-beta 2 by administering a  
 CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.

XX Sequence 20 BP; 3 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2084 CAGACTGGAGTCACACACAG 2102

Db 20 CAGACTTGAGTCACACACAG 2

RESULT 209

AD180069/c

ID AD180069 standard; DNA; 20 BP.

XX AC AD180069;

XX AC AD180069;

XX DT 22-APR-2004 (first entry)

XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 70.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosolic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.

XX OS Homo sapiens.

XX PN US2004006030-A1.

XX PD 08-JAN-2004.

XX PF 02-JUL-2002; 2002US-00189267.

XX PR 02-JUL-2002; 2002US-00189267.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Monia BP, Freier SM, Dobie KW;

XX DR WPI; 2004-081742/08.

XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.

XX Example 15; SEQ ID NO 70; 135pp; English.

XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC disease or condition associated with TGF-beta 2 by administering a  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX

Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3027 TCGAGACCAATACTTTGC 3045  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 19 TGGAGACCAATACTTTGC 1

RESULT 210  
 ADI80210  
 ID ADI80210 standard; DNA; 20 BP.  
 AC ADI80210;  
 XX  
 DT 22-APR-2004 (first entry)  
 DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 211.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 XX cytosstatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 XX

OS Homo sapiens.  
 XX  
 PN US2004006030-A1.  
 XX

PD 08-JAN-2004.  
 XX

PF 02-JUL-2002; 2002US-00189267.  
 XX

PR 02-JUL-2002; 2002US-00189267.  
 XX

PA (ISIS-) ISIS PHARM INC.  
 XX

PI Monia BP, Freier SM, Dobie KW;  
 XX

DR WPI; 2004-081742/08.  
 XX

PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX

PS Example 16; SEQ ID NO 211; 135pp; English.  
 XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX

Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3027 TCGAGACCAATACTTTGC 3045  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 2 TGGAGACCAATACTTTGC 20

RESULT 211  
 ADI80200  
 ID ADI80200 standard; DNA; 20 BP.  
 XX  
 AC ADI80200;  
 XX  
 DT 22-APR-2004 (first entry)  
 DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 201.

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosstatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 XX

OS Homo sapiens.  
 XX  
 PN US2004006030-A1.  
 XX

PD 08-JAN-2004.  
 XX

PF 02-JUL-2002; 2002US-00189267.  
 XX

PR 02-JUL-2002; 2002US-00189267.  
 XX

PA (ISIS-) ISIS PHARM INC.  
 XX

PI Monia BP, Freier SM, Dobie KW;  
 XX

DR WPI; 2004-081742/08.  
 XX

PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX

PS Example 16; SEQ ID NO 201; 135pp; English.  
 XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX

SQ Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 800 TCTGTCCTTTGGCCGG 818  
 |||||  
 Db 2 TCTTCTCCCTTTGGCCGG 20

RESULT 212  
 ADI80032/c  
 ID ADI80032 standard; DNA; 20 BP.  
 XX  
 AC ADI80032;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 33.  
 XX  
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosstatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 15; SEQ ID NO 33; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 5 A; 1 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1746 TTAACATCTCCACCAGC 1764  
 |||||  
 Db 19 TTAACATCTCCACCAGC 1

RESULT 213  
 ADI80057/c  
 ID ADI80057 standard; DNA; 20 BP.  
 XX  
 AC ADI80057;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 58.  
 XX  
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosstatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Freier SM, Dobie KW;  
 XX  
 DR WPI; 2004-081742/08.  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 15; SEQ ID NO 58; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



Qy 800 TCTGTCCTTTTGGCCG 818  
 Db 19 TCTCTTCCCTTTTGGCCG 1

## RESULT 214

AD180186

ID AD180186 standard; DNA; 20 BP.

XX

AC AD180186;

XX

DT 22-APR-2004 (first entry)

XX

DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 187.

XX

KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;

KW cytosatic; nontropic; neuroprotective; immunosuppressive;

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;

KW immune; ss; human.

XX

OS Homo sapiens.

XX

PN US2004006030-A1.

XX

PD 08-JAN-2004.

XX

PF 02-JUL-2002; 2002US-00189267.

XX

PR 02-JUN-2002; 2002US-00189267.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Monia BP, Freier SM, Dobie KW;

XX

DR WPI; 2004-081742/08.

XX

PT New compounds, particularly antisense oligonucleotides targeted to a

PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of

PT immune response.

XX

PS Example 16; SEQ ID NO 187; 135pp; English.

XX

CC The invention relates to a novel antisense compound of 8-80 nucleobases

CC in length targeted to, and which specifically hybridizes with, a nucleic

CC acid molecule encoding transforming growth factor (TGF)-beta 2, and

CC inhibits the expression of TGF-beta 2. The invention further relates to:

CC a compound 8-80 nucleobases in length that specifically hybridizes with

CC at least an 8-nucleobase portion of an active site on a nucleic acid

CC molecule encoding TGF-beta 2; a composition comprising the compound and a

CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

CC tissues by contacting the cells or tissues with the compound so that

CC expression of TGF-beta 2 is inhibited; treating an animal having a

CC disease or condition associated with TGF-beta 2 by administering to the

CC animal a therapeutic or prophylactic amount of the compound so that

CC expression of TGF-beta 2 is inhibited; and screening an antisense

CC compound. The antisense compound has cytostatic, nontropic,

CC neuroprotective, and immunosuppressive activities. The compound,

CC composition and methods are useful for treating a disease or condition

CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.

CC cancer, a neurodegenerative disorder, or a disease or condition involving

CC hyperactivation of an immune response. This polynucleotide sequence

CC represents a preferred target DNA region of TGF-beta 2 of the invention.

XX

SQ Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

XX

Query Match 0.4%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2084 CAGACTGGAGTCACACAG 2102

Db 1 CAGACTGGAGTCACACAG 19

## RESULT 215

AD158461/c

ID AD158461 standard; DNA; 20 BP.

XX

AC AD158461;

XX

DT 03-JUN-2004 (first entry)

XX

DE Human ESM-1 antisense oligonucleotide seqid 710.

XX

KW cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;

KW gene therapy; endothelial specific molecule-1; ESM-1;

KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;

KW angiogenic disorder; immunological disorder; cardiovascular disorder;

KW neurological disorder; antisense technology; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "OTHER= phosphorothioate backbone. All cytidine

FT residues are 5-methylcytidines"

FT modified\_base 1..5

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"

FT modified\_base 16..20

FT /\*tag= c

FT /mod\_base= OTHER

FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"

FT

XX WO2004021978-A2.

PN

XX

PD 18-MAR-2004.

XX

PF 19-AUG-2003; 2003WO-US025833.

XX

PR 19-AUG-2002; 2002US-0404495P.

XX

PA (PHAA ) PHARMACIA CORP.

XX

PI Weinstein EJ, Griggs DW;

XX

DR WPI; 2004-248358/23.

XX

PT New antisense compound, having a sequence targeted to a nucleic acid

PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a

PT composition for treating e.g., diabetes, cancer or cardiovascular

PT disorder.

XX

PS Claim 3; SEQ ID NO 710; 555pp; English.

XX

CC The invention describes a new antisense compound, having a sequence

CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial

CC specific molecule-1 (ESM-1), that specifically hybridises with the

CC nucleic acid ESM-1 and inhibits its expression. Also described are: a

CC composition; inhibiting the expression of ESM-1 in cells or tissues; and

CC treating an animal having a disease or condition associated with ESM-1.

CC The compound is useful for preparing a composition for treating diabetes,

CC cancer, ischaemia or reperfusion injury, or angiogenic, immunological,

CC cardiovascular or neurological disorder. This sequence represents an

CC antisense oligonucleotide that can be used to modulate expression of

CC endothelial specific molecule-1 (ESM-1).

XX

SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

XX

Query Match 0.4%; Score 17.4; DB 1;

Best Local Similarity 94.7%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 362 TGGCCGCTGGAGCAAGAA 380  
 Db 19 TGGCCGCTGGAGCAATAA 1

RESULT 216  
 ADL58256/c  
 ID ADL58256 standard; DNA; 20 BP.  
 XX AC ADL58256;  
 XX DT 03-JUN-2004 (first entry)  
 XX DE Human ESM-1 antisense oligonucleotide seqid 505.  
 XX KW cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;  
 KW gene therapy; endothelial specific molecule-1; ESM-1;  
 KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
 KW angiogenic disorder; immunological disorder; cardiovascular disorder;  
 KW neurological disorder; antisense technology; ss.  
 XX OS Homo sapiens.

FH Key Location/Qualifiers  
 modified\_base 1..20 /\*tag= b  
 /mod\_base= OTHER  
 /note= "OTHER= phosphorothioate backbone. All cytidine  
 residues are 5-methylcytidines"  
 modified\_base 1..5 /\*tag= a  
 /mod\_base= OTHER  
 /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 modified\_base 16..20 /\*tag= c  
 /mod\_base= OTHER  
 /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 WO2004021978-A2.  
 18-MAR-2004.

XX 19-AUG-2003; 2003WO-US025833.  
 XX 19-AUG-2002; 2002US-0404495P.  
 XX (PHAA ) PHARMACIA CORP.  
 XX Weinstein EJ, Griggs DW;  
 WPI; 2004-248358/23.

XX New antisense compound, having a sequence targeted to a nucleic acid  
 encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 composition for treating e.g., diabetes, cancer or cardiovascular  
 disorder.

XX Claim 3; SEQ ID NO 505; 555pp; English.

XX The invention describes a new antisense compound, having a sequence  
 comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 specific molecule-1 (ESM-1), that specifically hybridises with the  
 nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 treating an animal having a disease or condition associated with ESM-1.  
 The compound is useful for preparing a composition for treating diabetes,  
 cancer, ischaemia or reperfusion injury, or angiogenic, immunological,  
 cardiovascular or neurological disorder. This sequence represents an  
 antisense oligonucleotide that can be used to modulate expression of  
 endothelial specific molecule-1 (ESM-1).

XX Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 362 TGGCCGCTGGAGCAAGAA 380  
 Db 20 TGGCCGCTGGAGCAATAA 2

RESULT 217  
 ADQ90968  
 ID ADQ90968 standard; DNA; 20 BP.  
 XX AC ADQ90968;  
 XX DT 21-OCT-2004 (first entry)  
 XX DE Human fibrillin-like protein-specific cloning/sequencing primer #2.  
 XX KW human; fibrillin-like protein; skin damage; multiple sclerosis; cancer;  
 KW osteoarthritis; rheumatoid arthritis; osteoporosis;  
 KW cardiovascular disease; fibrosis; liver fibrosis; kidney fibrosis;  
 KW renal disorder; hepatitis; bone reconstruction; joint reconstruction;  
 KW ligament reconstruction; fracture; lesion; cloning; sequencing; primer;  
 KW ss.  
 XX OS Homo sapiens.  
 XX WO2004063226-A2.  
 XX 29-JUL-2004.  
 XX 22-DEC-2003; 2003WO-BP051089.  
 XX 27-DEC-2002; 2002US-0436835P.  
 XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
 XX Mcallister G, Bienkowska J;  
 WPI; 2004-544073/52.

XX New isolated polypeptide having fibrillin-like activity, useful for  
 manufacturing a medicament for treating e.g., skin damage, multiple  
 sclerosis, cancer, osteoarthritis, cardiovascular disease and hepatitis.

XX Example 3; Page 50; 150pp; English.

XX The invention comprises the amino acid and coding sequences of human  
 fibrillin-like proteins. The DNA and protein sequences of the invention  
 are useful for characterising ligands which bind to fibrillin-like  
 proteins. The DNA and protein sequences of the invention are useful for  
 the treatment of diseases and conditions in which fibrillin-like proteins  
 are implicated, such as: skin damage (e.g. through ageing, injuries or  
 sun exposure), multiple sclerosis, cancer, osteoarthritis, rheumatoid  
 arthritis, osteoporosis, cardiovascular diseases and fibrosis (e.g. liver  
 fibrosis or kidney fibrosis), renal disorders and hepatitis. The DNA and  
 protein sequences of the invention are also useful for bone, joint or  
 ligament reconstruction after fractures or lesions. The present DNA  
 sequence represents a primer that was used in an example of the  
 invention.

XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 17.4; DB 1; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4241 CATTCTTTGCAGGCTGATT 4259  
 Db 2 CATTCTCTCAGGCTGATT 20



XX EP676474-A1.  
 PN XX  
 PD 11-OCT-1995.  
 XX  
 PF 14-DEC-1989; 95EP-00104223.  
 XX  
 PR 16-DEC-1988; 88US-00285140.  
 PR 05-DEC-1989; 89US-0046020.  
 XX  
 PA (ONCO ) ONCOGEN LP.  
 XX  
 PI Purchio AF, Madsen L, Webb N;  
 DR WPI; 1995-346094/45.  
 XX  
 PT Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used to  
 PT produce biologically active, mature TGF-beta-2.  
 XX  
 PS Example 6; Page 13; 52pp; English.  
 XX  
 CC This probe is used during a procedure for the cloning of TGF-beta2  
 CC precursor from human prostate adenocarcinoma cell line PC-3. DS cDNA was  
 CC synthesized from polyadenylated RNACC isolated from PC-3 cells treated  
 CC with tamoxifen for 24 hr. cDNA fractions larger than 1000 bases were  
 CC cloned into phage lambda gt10. The library was first screened in duplicate  
 CC with this 32P-labelled 24-mer degenerate probe complementary to DNA  
 CC encoding AA WKVHEP which are conserved between TGF-beta1 and TGF-beta2.  
 CC Positive clones were then screened with a 2nd degenerate probe (AAT04119).  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 20 BP; 3 A; 5 C; 3 G; 5 T; 0 U; 4 Other;  
 Query Match 0.4%; Score 17.2; DB 1; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 2211 TGGAAATGGATCCATGAACC 2230  
 DB 20 TGGAAATGGATDCAYGARCC 1  
 RESULT 221  
 AAV48933/C  
 ID AAV48933 standard; DNA; 17 BP.  
 AC AAV48933;  
 XX  
 DT 15-OCT-1998 (first entry)  
 XX  
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-4.  
 XX  
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN EP856579-A1.  
 XX  
 PD 05-AUG-1998.  
 XX  
 PF 31-JAN-1997; 97EP-00101531.  
 XX  
 PR 31-JAN-1997; 97EP-00101531.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Brysch W;  
 XX WPI; 1998-400910/35.  
 DR  
 XX Preparation of antisense oligo:nucleotide(s) which lack long runs of

PT consecutive guanosine or inosine - and have specific ratio of residues  
 PT able to form two or three hydrogen bonds, have greater activity and  
 PT reduced toxicity, used therapeutically or to modulate growth of cells in  
 PT culture.  
 XX Claim 10; Fig 8a; 286pp; English.  
 PS  
 XX AAV48930-49007 represent antisense oligonucleotides directed against  
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only  
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
 CC little effect. The oligonucleotides exemplify the invention. The  
 CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 CC which contain at most 8 nucleotides that can each form three hydrogen  
 CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 CC form three H-bonds each to four consecutive cytosines; do not contain two  
 CC sequences of three consecutive nucleotides each able to form three H-  
 CC bonds to three consecutive cytosines, and the ratio between residues able  
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 CC genes, particularly the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or  
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 CC keratinocytes). The oligonucleotides can also be used to analyse function  
 CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 CC stimulating the immune system  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1343 GCAGATCCTGAGCAAGC 1359  
 DB 17 GCAGATCCTGAGCAAGC 1  
 RESULT 222  
 AA265508/C  
 ID AA265508 standard; DNA; 17 BP.  
 XX  
 AC AA265508;  
 XX  
 DT 30-MAR-2000 (first entry)  
 XX  
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta-17-c-2260.  
 XX  
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; ss;  
 XX  
 OS Unidentified.  
 OS  
 XX WO963975-A2.  
 PN  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 10-JUN-1999; 99WO-EP004013.  
 XX  
 PR 10-JUN-1998; 98EP-00110709.  
 PR 25-JUL-1998; 98EP-00113974.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;  
 XX WPI; 2000-097470/08.  
 DR  
 XX

```

PT Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
PT infections.
XX
XX Claim 10; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1509 TACTACGCCAAGGAGGT 1525
DB 17 TACTACGCCAAGGAGGT 1
RESULT 223
AAZ65443/C
ID AAZ65443 standard; DNA; 17 BP.
XX
XX AAZ65443;
AC
XX
XX 30-MAR-2000 (first entry)
DT
DE
DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-3.
XX
XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;
KW glomerulonephritis; acute respiratory distress syndrome; ss;
KW atherosclerosis.
XX
XX Unidentified.
OS
XX
XX WO963975-A2.
PN
XX
XX 16-DEC-1999.
PD
XX
XX 10-JUN-1999; 99WO-EP004013.
PF
XX
XX 10-JUN-1998; 98EP-00110709.
PR
XX 25-JUL-1998; 98EP-00113974.
PR
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
PA
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
PI
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
PT adversely affects the immune response, for treating cancers and
PT infections.
XX
XX Claim 10; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
CC used in the invention. The invention relates to a composition which
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
CC transforming growth factor TGF-beta, vascular endothelial growth factor
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
CC that adversely affects the immune response. The composition also includes
CC at least one stimulant that positively affects the immune response. This
CC oligonucleotide is an example of an inhibitor that is used in the
CC composition. The composition is used as an immunostimulant for the
CC treatment of neoplasms and infections, particularly hyperproliferation;
CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
CC most of which are directed against TGFbeta or VEGF, are inhibitors of
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
CC colitis, diabetes, glomerulonephritis, acute respiratory distress
CC syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1343 GCAGATCCTCTGAGCAAGC 1359
DB 17 GCAGATCCTCTGAGCAAGC 1
RESULT 224
ADJ76724
ID ADJ76724 standard; DNA; 17 BP.
XX
XX ADJ76724;
AC
XX
XX 20-MAY-2004 (first entry)
DT
DE
DE TGFbeta reverse PCR primer SEQ ID NO:1976.
XX
XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker; PCR; primer; ss.
XX
XX Mus musculus.
OS
XX Synthetic.
XX
XX EP1394274-A2.
PN
XX
XX 03-MAR-2004.
PD
XX
XX 04-AUG-2003; 2003EP-00254857.
PF
XX
XX 06-AUG-2002; 2002JP-00229312.
PR
XX 20-MAR-2003; 2003JP-00077212.
PR
XX (GENO-) GENOX RES INC.
PA
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
PI
XX WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
XX Example 11; SEQ ID NO 1976; 241pp; English.
XX

```

XX The present invention describes a method of testing for bronchial asthma  
 CC or chronic obstructive pulmonary disease. The method comprises  
 CC determining the expression level of a marker gene in a biological sample  
 CC from a subject, comparing the expression level determined with the  
 CC expression level of the marker gene in a biological sample from a healthy  
 CC subject, and judging whether the subject has bronchial asthma or chronic  
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
 CC genes (S1) whose expression levels increase when respiratory epithelial  
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
 CC whose expression levels decrease when respiratory epithelial cells are  
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for  
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
 CC (2) a kit for screening for a candidate compound for a therapeutic agent  
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
 CC an animal model for bronchial asthma or chronic obstructive pulmonary  
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
 CC method for producing an animal model for bronchial asthma or chronic  
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
 CC a marker gene or an antisense nucleic acid corresponding to a portion of  
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
 CC expression of the gene through an RNAi effect or an antibody recognising  
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
 CC probe has been immobilised to assay a marker gene. (I) has respiratory  
 CC and antiasthmatic activities, and can be used in gene therapy. The method  
 CC is useful for testing for or screening for a therapeutic agent for  
 CC bronchial asthma or chronic obstructive pulmonary disease. The present  
 CC invention is used in the exemplification of the present invention.

XX Sequence 17 BP; 4 A; 9 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 CGCAGCCACGCGCCCA 308  
 Db 1 CGCAGCCACGCGCCCA 17

RESULT 225

AAQ05125/c

ID AAQ05125 standard; DNA; 20 BP.

XX AAQ05125;

AC AAQ05125;

XX 25-MAR-2003 (revised)

DT 02-NOV-1990 (first entry)

XX Probe used to screen cDNA library for human TGF-Beta2 precursor.

XX Human TGF-Beta2 precursor; cancer; tumorcide; ss.

XX Synthetic.

XX EP376785-A.

XX 04-JUL-1990.

PD 14-DEC-1989; 89EP-00403480.

XX 16-DEC-1988; 88US-00285140.

PR 05-DEC-1989; 89US-00446020.

XX (ONCO ) ONCOGEN LP.

PA Purchio AF, Madisen L, Webb N;

XX WPI; 1990-203127/27.

DR Cloning and expression of transforming growth factor beta 2 - used for

XX

PT treatment of tumours or for augmenting wound healing.

XX Example 6; Page 14; 58pp; English.

CC TGF-Beta2 may be used in treatment of tumors at effective doses, and may

CC also be useful in augmenting wound healing by stimulating cell

CC proliferation. The growth factor can be produced at high levels from a

CC CHO expression system. (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 20 BP; 4 A; 4 C; 1 G; 5 T; 0 U; 6 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;

Best Local Similarity 70.0%; Pred. No. 1.6e+02;

Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2142 TGGTTTAGAAATGTGCAGGA 2161

Db 20 TGYTTYAGRAAYGTNCARGA 1

RESULT 226

AAQ04119/c

ID AAQ04119 standard; DNA; 20 BP.

XX AAQ04119;

AC AAQ04119;

XX 25-MAR-2003 (revised)

DT 28-MAY-1996 (first entry)

XX Human transforming growth factor-beta2 precursor degenerate probe.

XX TGF-beta1; TGF-beta2; transforming growth factor; protein;

XX cell differentiation; cell proliferation; CHO; Chinese hamster; ovary;

XX COS; monkey kidney; animal; mammal; DNA probe; ss.

XX Synthetic.

XX EP676474-A1.

PN 11-OCT-1995.

XX 14-DEC-1989; 95EP-00104223.

XX 16-DEC-1988; 88US-00285140.

PR 05-DEC-1989; 89US-00446020.

XX (ONCO ) ONCOGEN LP.

XX Purchio AF, Madisen L, Webb N;

XX WPI; 1995-346094/45.

XX Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used to

XX produce biologically active, mature TGF-beta-2.

XX Example 6; Page 13; 52pp; English.

XX This probe is used during a procedure for the cloning of TGF-beta2

XX precursor from human prostate adenocarcinoma cell line PC-3. DS cDNA was

XX synthesized from polyadenylated RNACC isolated from PC-3 cells treated

XX with tamoxifen for 24 hr. cDNA fractions larger than 1000 bases were

XX cloned into phage lambda gt10. The library was first screened in duplicate

XX with a 32P-labelled 24-mer degenerate probe (AAQ04118) complimentary to

XX DNA encoding AA WKWIEP which are conserved between TGF-beta1 and TGF-

XX beta2. Positive clones were then screened with this 2nd degenerate probe

XX (AAQ04119). (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 20 BP; 4 A; 4 C; 1 G; 5 T; 0 U; 6 Other;

Query Match 0.4%; Score 17; DB 1; Length 20;

Best Local Similarity 70.0%; Pred. No. 1.6e+02;

Matches 14; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

|            |  |                       |      |    |   |   |  |
|------------|--|-----------------------|------|----|---|---|--|
| QY         | 2142   | TGCTTTAGAAATGTCAGGA   | 2161 | DT | 06-JUL-2001   | (first entry)   |  |
| Db         | 20   | TGYTTAGRAAYGTNCARGA   | 1    | XX | Human glutathione S-transferase pi promoter (GSTP1) PCR primer N-F1.      |   |  |
| RESULT 227 |  |                       |      | XX | Human; glutathione S-transferase pi; GSTP1; CpG island; diagnosis;        |   |  |
| AAZ05389/c |  |                       |      | KW | hepatic cell proliferative disorder; liver cancer; anticancer;            |   |  |
| ID         | AAZ05389   | standard; DNA; 20 BP. |      | KW | tumorigenesis; detection; PCR primer; ss.                                 |   |  |
| XX         | AAZ05389;  |                       |      | XX | Homo sapiens.   |   |  |
| AC         | AAZ05389;  |                       |      | XX | WO200126536-A2.   |   |  |
| XX         | 07-OCT-1999  | (first entry)         |      | PN | 19-APR-2001.  |   |  |
| DT         | PCR primer used to amplify an ORF of Chlamydia trachomatis.                  |                       |      | PD | 12-OCT-2000; 2000WO-US028427.   |   |  |
| XX         | Vaccine; eye disease; conventional trachoma; nonendemic trachoma;            |                       |      | XX | 13-OCT-1999; 99US-0159168P.   |   |  |
| XX         | paratrachoma; inclusion conjunctivitis; genital disease; perithecitis;       |                       |      | XX | (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.                               |   |  |
| KW         | nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer; |                       |      | PA | Nelson WG, Lin X, Tchou JC, Bakker J;                                     |   |  |
| KW         | bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.               |                       |      | XX | WPI; 2001-290647/30.  |   |  |
| XX         | Synthetic.   |                       |      | PI | Detecting hepatic cell proliferative disorder useful for detecting        |   |  |
| OS         | Chlamydia trachomatis.   |                       |      | XX | hepatocellular carcinoma comprises detecting a methylated CpG-containing  |   |  |
| XX         | WO9928475-A2.  |                       |      | DR | glutathione-S-transferase nucleic acid.                                   |   |  |
| PN         | 10-JUN-1999.   |                       |      | XX | Claim 83; Page 42; 64pp; English.   |   |  |
| XX         | 27-NOV-1998; 98WO-IB001939.  |                       |      | XX | The present invention describes a method for detecting hepatic cell       |   |  |
| XX         | 28-NOV-1997; 97FR-00015041.  |                       |      | CC | proliferative disorders. The method comprises detecting a methylated CpG- |   |  |
| PR         | 17-DEC-1997; 97FR-00016034.  |                       |      | CC | containing glutathione-S-transferase (GST) nucleic acid (I) in a hepatic  |   |  |
| PR         | 04-NOV-1998; 98US-0107077P.  |                       |      | CC | specimen or a biological fluid, where a methylated GST nucleic acid is    |   |  |
| XX         | (GEST ) GENSET.  |                       |      | CC | indicative of a hepatic cell proliferative disorder. The method can be    |   |  |
| PA         | Griffais R;  |                       |      | CC | used to diagnose hepatocellular carcinoma, and to monitor progress of its |   |  |
| XX         | WPI; 1999-371125/31.   |                       |      | CC | treatment. Increasing the level of GST is useful in the treatment of      |   |  |
| XX         | Genome sequence of Chlamydia trachomatis.                                    |                       |      | CC | liver cancer, in humans or animals. The method can detect the early       |   |  |
| PT         | Disclosure; Page 1766; 1755pp; English.                                      |                       |      | CC | stages of tumorigenesis in liver cells simply. The present sequence       |   |  |
| XX         | PCR primers AA201426-206209 were used to amplify open reading frames         |                       |      | CC | represents a PCR primer which is used in the amplification of the human   |   |  |
| XX         | (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs     |                       |      | CC | glutathione S-transferase pi gene (GSTP1) promoter in an example from the |   |  |
| CC         | encode polypeptides (see AA36754-Y37949) which can be used as vaccines       |                       |      | CC | present invention for mapping somatic GSTP1 CpG island DNA                |   |  |
| CC         | against Chlamydia trachomatis. Antisense and ribozyme sequences can also     |                       |      | CC | hypermethylation changes by genomic sequencing after bisulfite treatment  |   |  |
| CC         | be used to control growth of the microorganism. Chlamydia trachomatis is     |                       |      | XX | Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;                        |   |  |
| CC         | responsible for a large number of diseases, e.g. eye diseases such as        |                       |      | QY | Query Match 0.4%; Score 17; DB 1; Length 20;                              |   |  |
| CC         | conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion      |                       |      | Db | Best Local Similarity 100.0%; Pred. No. 1.6e+02;                          |   |  |
| CC         | conjunctivitis; genital diseases such as nongonococcal urethritis;           |                       |      |    | Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;               |   |  |
| CC         | epididymitis, cervicitis, salpingitis, perithecitis, bartholinitis;          |                       |      |    | QY 2574 TTAAAAAATAAAAAAATT 2590   |   |  |
| CC         | pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.    |                       |      |    | Db 19 TTAAAAAATAAAAAAATT 3  |   |  |
| CC         | diseases   |                       |      |    | RESULT 229  |   |  |
| XX         | Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;                            |                       |      |    | AAZ05389/c  |   |  |
| SQ         | Query Match 0.4%; Score 17; DB 1; Length 20;                                 |                       |      |    | ID  | AAZ05389 standard; DNA; 20 BP.  |  |
|            | Best Local Similarity 100.0%; Pred. No. 1.6e+02;                             |                       |      |    | XX  | AAZ05389;   |  |
|            | Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                  |                       |      |    | AC  | AAZ05389;   |  |
|            | QY 2111 GCGGAGAGCGCGCTT 2127   |                       |      |    | XX  | 07-AUG-2003 (first entry)   |  |
| Db         | 17 GCGGAGAGCGCGCTT 1   |                       |      |    | DT  | Human FGFR-3 antisense oligonucleotide, ISIS #125161.                   |  |
| RESULT 228 |  |                       |      |    | DE  | Human; antisense; fibroblast growth factor receptor 3; prophylaxis;     |  |
| AAF87713/c |  |                       |      |    | XX  | developmental disorder; hyperproliferative disorder; antisense therapy; |  |
| ID         | AAF87713 standard; DNA; 20 BP.   |                       |      |    | KW  | FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.                  |  |
| XX         | AAF87713;  |                       |      |    | XX  | Homo sapiens.   |  |
| AC         | AAF87713;  |                       |      |    | OS  | Synthetic.  |  |
| XX         |  |                       |      |    | XX  | Key   |  |
|            |  |                       |      |    | FX  | Location/Qualifiers   |  |

|            |   |  |
|------------|---|--|
| FT         | modified_base   | 1..20  |
| FT         | /*tag=  | a  |
| FT         | /mod_base=  | OTHER  |
| FT         | /note=  | "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines" |
| FT         | modified_base   | 1..5   |
| FT         | /*tag=  | b  |
| FT         | /mod_base=  | OTHER  |
| FT         | /note=  | "2'-methoxyethyl (2'-MOE) nucleotides"                                   |
| FT         | modified_base   | 16..20   |
| FT         | /*tag=  | c  |
| FT         | /mod_base=  | OTHER  |
| FT         | /note=  | "2 -methoxyethyl (2'-MOE) nucleotides"                                   |
| XX         |   |  |
| XX         | WO2003023004-A2.  |  |
| PN         |   |  |
| PD         | 20-MAR-2003.  |  |
| XX         |   |  |
| XX         | 06-SEP-2002;  | 2002WO-US028549.   |
| PF         |   |  |
| XX         | 10-SEP-2001;  | 2001US-00953047.   |
| PR         |   |  |
| XX         | (ISIS-) ISIS PHARM INC.   |  |
| PA         |   |  |
| XX         | Monia BP, Wyatt JR;   |  |
| PI         |   |  |
| XX         | WPI; 2003-313244/30.  |  |
| DR         |   |  |
| XX         |   |  |
| PT         | Novel compound targeted to a nucleic acid molecule encoding fibroblast growth factor receptor 3, useful for inhibiting the expression of the receptor and for treating an animal having cancer or developmental disorder.   |  |
| PT         |   |  |
| PT         |   |  |
| XX         | Claim 3; Page 79; 120pp; English.   |  |
| PS         |   |  |
| XX         |   |  |
| CC         | The invention relates to antisense compounds targetted to a nucleic acid molecule encoding fibroblast growth factor (FGF) receptor 3 (also known as FGFR-3, ACH, JTK4 and CER2) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with FGFR-3 such as developmental disorders or hyperproliferative disorders, especially cancer of colorectal, bladder, bone, lung, cervical, breast or skin. They are useful as research reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion of the genes expressed within cells and tissues. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human FGFR-3 |  |
| XX         |   |  |
| SQ         | Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;   |  |
|            | Query Match   | 0.4%; Score 17; DB 1; Length 20;   |
|            | Best Local Similarity   | 100.0%; Pred. No. 1.6e+02;   |
|            | Matches   | 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                      |
| QY         | 2351 TTGCTGTGTGCCAGG 2367   |  |
| DB         | 17 TTGCTGTGTGCCAGG 1  |  |
|            |   |  |
| RESULT 230 |   |  |
| ID         | AAQ75726/c  |  |
| XX         | AAQ75726 standard; DNA; 21 BP.  |  |
| AC         |   |  |
| XX         | AAQ75726;   |  |
| DT         |   |  |
| XX         | 04-AUG-1995 (first entry)   |  |
| DE         |   |  |
| XX         | Reverse transcription primer used in cDNA analysis technique.   |  |
| XX         |   |  |
| KW         | Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.  |  |
| XX         |   |  |
| OS         | Synthetic.  |  |
|            |   |  |
| RESULT 231 |   |  |
| ID         | AAQ78450/c  |  |
| XX         | AAQ78450 standard; DNA; 20 BP.  |  |
| AC         |   |  |
| XX         | AAQ78450;   |  |
| DT         | 25-MAR-2003 (revised)   |  |
| DT         | 27-JUN-1995 (first entry)   |  |
| XX         |   |  |
| DE         | TGF-beta gene phosphorothioate antisense oligonucleotide.   |  |
| XX         |   |  |
| KW         | Transforming growth factor beta; TGF-beta; antisense; treatment; tumour; angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma; carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut; immunosuppression; oligonucleotide; ss.   |  |
| XX         |   |  |
| OS         | Synthetic.  |  |
| XX         |   |  |
| PN         | WO9425588-A2.   |  |
| XX         |   |  |
| PD         | 10-NOV-1994.  |  |
| XX         |   |  |
| PF         | 29-APR-1994;  | 94WO-EP001362.   |
| XX         |   |  |
| PR         | 30-APR-1993;  | 93EP-00107089.   |
| PR         | 13-MAY-1993;  | 93EP-00107849.   |
| XX         |   |  |
| PA         | (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  |  |
| XX         |   |  |
| PI         | Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R; Bogdahn U;   |  |
| XX         |   |  |
| DR         | WPI; 1994-358266/44,  |  |
| XX         |   |  |
| PT         | New transforming growth factor beta anti:sense oligo:nucleotide(s) - for  |  |

PT treating immunosuppression, tumours, etc.  
 XX Claim 6; Page 52; 74pp; English.  
 XX  
 CC The antisense oligonucleotides are useful in the treatment of tumours in  
 CC which expression of TGF-beta is of relevance for pathogenicity and/or  
 CC inhibition of pathological angiogenesis. They are used especially for the  
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
 CC of skin carcinogenesis, and treatment of oesophageal and gastric  
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESBQ files  
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
 CC beta 1. The sequences given in GENESBQ files AAQ78408-78487 are antisense  
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1928 CATCATCCCAATAAAGCG 1947  
 Db ||||||| |||||||  
 20 CATCATCCCAATAAAGTG 1  
 RESULT 232  
 AAT48166  
 ID AAT48166 standard; DNA; 20 BP.  
 AC AAT48166;  
 XX  
 XX 19-SEP-1997 (first entry)  
 DT  
 DE Escherichia coli chromosomal PCR primer beta21079.  
 XX  
 XX Escherichia coli; heterologous non-bacterial protein; host cell;  
 KW IGF-I fusion gene; chromosomal transfer DNA; polymerase chain reaction;  
 KW ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9640722-A1.  
 PN  
 XX  
 XX 19-DEC-1996.  
 PD  
 XX 05-JUN-1996; 96WO-US009006.  
 PF  
 XX 07-JUN-1995; 95US-00482182.  
 PR  
 XX (CELT-) CELTRIX PHARM INC.  
 PA  
 XX Mascarenhas D, Olson PS;  
 PI  
 XX WPI; 1997-065167/06.  
 DR  
 XX  
 XX Prodn. of heterologous non-bacterial protein in bacteria - using a  
 PT chromosomal transfer DNA contg. a gene which has not been cloned in a  
 PT multi-copy vector.  
 PT  
 XX Example 6; Page 40; 80pp; English.  
 PS  
 XX A method has been produced for the production of a heterologous,  
 CC preferably non-bacterial, protein in a bacterial host cell such as  
 CC Escherichia coli. The method involves: transferring a chromosomal DNA  
 CC into a bacterial host cell preferably comprising a chromosome, where the  
 CC chromosomal DNA contains at least one copy of a gene encoding the  
 CC heterologous protein and a selectable marker; selecting for integration  
 CC of the chromosomal DNA into the cell resulting in a host cell chromosome  
 CC comprising a gene encoding the heterologous protein operably linked to a

CC promoter functional in the host cell and a selectable marker flanked by  
 CC duplicate DNA; and expressing the gene, where the gene is at no time  
 CC operably linked to a promoter, functional in the host cell, on a  
 CC multicopy number plasmid vector during construction of the transfer DNA  
 CC and where the heterologous protein accumulates within the host cell to a  
 CC level in excess of 0.1% of total cell protein. The present sequence is  
 CC PCR primer beta21079, which is part of a primer pair used to confirm the  
 CC proper integration of intact chromosomal transfer DNA. The method is  
 CC especially useful for producing eukaryotic protein, especially mammalian  
 CC protein. The method of construction avoids the generation of low or high  
 CC multicopy plasmid where expression of a small amount of the foreign  
 CC protein may be toxic to the cell. The method allows high accumulation of  
 CC the foreign protein (about 20% of total cell protein) from low  
 CC (approximately 2) copies of the gene encoding the heterologous protein  
 XX  
 SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2212 GGAAATGGATCCATGAACCC 2231  
 Db ||||||| |||||||  
 1 GGAAATGGATACACGAACCC 20  
 RESULT 233  
 AA47680  
 ID AA47680 standard; DNA; 20 BP.  
 XX  
 AC AA47680;  
 XX  
 XX 20-NOV-1998 (first entry)  
 DT  
 XX  
 DE Unmethylated CpG dinucleotide 1631.  
 XX  
 KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;  
 KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;  
 KW pulmonary disorder; asthma; environmentally induced airway disease;  
 KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;  
 KW inflammatory bowel disease; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9837919-A1.  
 PN  
 XX  
 XX 03-SEP-1998.  
 PD  
 XX 25-FEB-1999; 98WO-US003678.  
 PF  
 XX 28-FEB-1997; 97US-0039405P.  
 PR  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA  
 XX Schwartz DA, Krieg AM;  
 PI  
 XX WPI; 1998-480941/41.  
 DR  
 XX  
 XX Use of nucleic acids containing an unmethylated CpG - for treating a  
 PT subject having or at risk of having an acute decrement in air flow or  
 PT inhibiting an inflammatory response.  
 PT  
 XX Claim 35; Page 27; 65pp; English.  
 PS  
 XX This sequence represents an unmethylated CpG dinucleotide, and can be  
 CC used in the method of the invention. The method is for treating a subject  
 CC having, or at risk of having an acute decrement in air flow, comprising  
 CC administering a nucleic acid sequence containing at least one  
 CC unmethylated CpG. The nucleic acids containing an unmethylated CpG  
 CC dinucleotide affect an immune response in a subject by activating natural  
 CC killer cells (NK) or redirecting a subject's immune response from a Th2  
 CC to a Th1 response by inducing monocytic and other cells to produce Th1  
 CC cytokines. They can be used to treat pulmonary disorders having an



CC immunologic component, such as asthma or environmentally induced airway  
 CC disease. They can also be used to treat diseases associated with Gram-  
 CC positive bacterial infections or endotoxaemia including bacterial  
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease  
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal  
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or  
 CC an inflammatory response to lipopolysaccharide

XX  
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
 Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 234  
 AAV47680/c  
 ID AAV47680 standard; DNA; 20 BP.  
 XX  
 AC AAV47680;  
 XX  
 DT 20-NOV-1998 (first entry)  
 XX  
 DE Unmethylated CpG dinucleotide 1631.  
 XX  
 KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;  
 KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;  
 KW pulmonary disorder; asthma; environmentally induced airway disease;  
 KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;  
 KW inflammatory bowel disease; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9837919-A1.  
 XX  
 PD 03-SEP-1998.  
 XX  
 PF 25-FEB-1998; 98WO-US003678.  
 XX  
 PR 28-FEB-1997; 97US-0039405P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Schwartz DA, Krieg AM;  
 XX  
 PS WPI; 1998-480941/41.  
 XX  
 DR Use of nucleic acids containing an unmethylated CpG - for treating a  
 PT subject having or at risk of having an acute decrement in air flow or  
 PT inhibiting an inflammatory response.  
 XX  
 PS Claim 35; Page 27; 65pp; English.  
 XX  
 CC This sequence represents an unmethylated CpG dinucleotide, and can be  
 CC used in the method of the invention. The method is for treating a subject  
 CC having, or at risk of having an acute decrement in air flow, comprising  
 CC administering a nucleic acid sequence containing at least one  
 CC unmethylated CpG. The nucleic acids containing an unmethylated CpG  
 CC dinucleotide affect an immune response in a subject by activating natural  
 CC killer cells (NK) or redirecting a subject's immune response from a Th2  
 CC to a Th1 response by inducing monocyte and other cells to produce Th1  
 CC cytokines. They can be used to treat pulmonary disorders having an  
 CC immunologic component, such as asthma or environmentally induced airway  
 CC disease. They can also be used to treat diseases associated with Gram-  
 CC positive bacterial infections or endotoxaemia including bacterial  
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease,  
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal  
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or  
 CC an inflammatory response to lipopolysaccharide

XX  
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635  
 Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 235  
 AAV48940/c  
 ID AAV48940 standard; DNA; 20 BP.  
 XX  
 AC AAV48940;  
 XX  
 DT 15-OCT-1998 (first entry)  
 XX  
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-11.  
 XX  
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN EP856579-A1.  
 XX  
 PD 05-AUG-1998.  
 XX  
 PF 31-JAN-1997; 97EP-00101531.  
 XX  
 PR 31-JAN-1997; 97EP-00101531.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Brysch W;  
 XX  
 DR WPI; 1998-400910/35.  
 XX  
 PT Preparation of antisense oligonucleotide(s) which lack long runs of  
 PT consecutive guanosine or inosine - and have specific ratio of residues  
 PT able to form two or three hydrogen bonds, have greater activity and  
 PT reduced toxicity, used therapeutically or to modulate growth of cells in  
 PT culture.  
 XX  
 PS Claim 10; Fig 8a; 286pp; English.  
 XX  
 CC AAV48930-49007 represent antisense oligonucleotides directed against  
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only  
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
 CC little effect. The oligonucleotides exemplify the invention. The  
 CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 CC which contain at most 8 nucleotides that can each form three hydrogen  
 CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 CC form three H-bonds each to four consecutive cytosines; do not contain two  
 CC sequences of three consecutive nucleotides each able to form three H-  
 CC bonds to three consecutive cytosines, and the ratio between residues able  
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 CC genes, particularly the genes for p53, ErbB-2, JunB, JunD, TGF-beta 1 or  
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 CC keratinocytes). The oligonucleotides can also be used to analyse function  
 CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 CC stimulating the immune system

XX  
 SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1523 GGTATTAAATCGACATGC 1542  
 ||||| ||||| ||||| |||||  
 Db 20 GGTTCACAAATAGACATGC 1

RESULT 236  
 AAV74258  
 ID AAV74258 standard; DNA; 20 BP.  
 XX  
 AC AAV74258;  
 XX  
 DT 20-MAR-2003 (revised)  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE CpG-N motif oligonucleotide #5.  
 XX  
 KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation;  
 KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;  
 KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon;  
 KW hormone; clotting factor; ligand; receptor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9852581-A1.  
 XX  
 PD 26-NOV-1998.  
 XX  
 PF 20-MAY-1998; 98WO-US010408.  
 XX  
 PR 20-MAY-1997; 97US-0047209P.  
 PR 20-MAY-1997; 97US-0047233P.  
 XX  
 PA (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (QIAG-) QIAGEN GMBH.  
 XX  
 PI Davis HL, Krieg AM, Schorr J, Wu T;  
 XX WPI; 1999-059712/05.  
 DR  
 XX Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for  
 PT enhancing the immunostimulatory effect of an antigen or enhancing the  
 PT expression of a therapeutic polypeptide.  
 XX  
 PS Example 5; Page 73; 109pp; English.  
 XX  
 CC AAV74254-V74261 are oligonucleotides used to describe a method for  
 CC enhancing the immunostimulatory effect of an antigen encoded by nucleic  
 CC acid contained in a nucleic acid construct. The method involves  
 CC determining the CpG-N and CpG-S motifs present in the construct, removing  
 CC neutralising CpG (CpG-N) motifs and optionally inserting stimulatory CpG  
 CC (CpG-S) motifs in the construct, thereby producing a nucleic acid  
 CC construct having enhanced immunostimulatory efficacy. The method can be  
 CC used for immunisation against viral antigens, e.g. from hepatitis B virus  
 CC (HBV), bacterial antigens or an antigen derived from a parasite. They can  
 CC also be used for expression of a therapeutic polypeptide, e.g. growth  
 CC factors, toxins, tumour suppressors, cytokines, apoptotic proteins,  
 CC interferons, hormones, clotting factors, ligands and receptors. (Updated  
 CC on 20-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634  
 ||||| ||||| ||||| |||||  
 Db 1 GCGCGCGCGCGCGCGCGC 20

RESULT 238  
 AAZ65448/c  
 ID AAZ65448 standard; DNA; 20 BP.  
 XX  
 AC AAZ65448;

RESULT 237  
 AAV74258/c  
 ID AAV74258 standard; DNA; 20 BP.  
 XX  
 AC AAV74258;  
 XX  
 DT 20-MAR-2003 (revised)  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE CpG-N motif oligonucleotide #5.  
 XX  
 KW CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation;  
 KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;  
 KW toxin; tumour suppressor; cytokine; apoptotic protein; interferon;  
 KW hormone; clotting factor; ligand; receptor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9852581-A1.  
 XX  
 PD 26-NOV-1998.  
 XX  
 PF 20-MAY-1998; 98WO-US010408.  
 XX  
 PR 20-MAY-1997; 97US-0047209P.  
 PR 20-MAY-1997; 97US-0047233P.  
 XX  
 PA (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (QIAG-) QIAGEN GMBH.  
 XX  
 PI Davis HL, Krieg AM, Schorr J, Wu T;  
 XX WPI; 1999-059712/05.  
 DR  
 XX Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for  
 PT enhancing the immunostimulatory effect of an antigen or enhancing the  
 PT expression of a therapeutic polypeptide.  
 XX  
 PS Example 5; Page 73; 109pp; English.  
 XX  
 CC AAV74254-V74261 are oligonucleotides used to describe a method for  
 CC enhancing the immunostimulatory effect of an antigen encoded by nucleic  
 CC acid contained in a nucleic acid construct. The method involves  
 CC determining the CpG-N and CpG-S motifs present in the construct, removing  
 CC neutralising CpG (CpG-N) motifs and optionally inserting stimulatory CpG  
 CC (CpG-S) motifs in the construct, thereby producing a nucleic acid  
 CC construct having enhanced immunostimulatory efficacy. The method can be  
 CC used for immunisation against viral antigens, e.g. from hepatitis B virus  
 CC (HBV), bacterial antigens or an antigen derived from a parasite. They can  
 CC also be used for expression of a therapeutic polypeptide, e.g. growth  
 CC factors, toxins, tumour suppressors, cytokines, apoptotic proteins,  
 CC interferons, hormones, clotting factors, ligands and receptors. (Updated  
 CC on 20-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCGC 634  
 ||||| ||||| ||||| |||||  
 Db 20 GCGCGCGCGCGCGCGCGC 1

RESULT 238  
 AAZ65448/c  
 ID AAZ65448 standard; DNA; 20 BP.  
 XX  
 AC AAZ65448;

XX DT 30-MAR-2000 (first entry)

XX DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-8.

XX KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;

XX KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;

XX KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;

XX KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;

XX KW glomerulonephritis; acute respiratory distress syndrome; ss;

XX KW atherosclerosis.

XX OS Unidentified.

XX PN WO963975-A2.

XX PD 16-DEC-1999.

XX PF 10-JUN-1999; 99WO-EP004013.

XX PR 10-JUN-1998; 98EP-00110709.

XX PR 25-JUL-1998; 98EP-00113974.

XX PA (BIOG-) BIOGOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX PI Schlingensiepen K, Schlingensiepen R, Brysch W;

XX DR WPI; 2000-097470/08.

XX PT Composition containing immune stimulant and inhibitor of agent that

XX PT adversely affects the immune response, for treating cancers and

XX PT infections.

XX PS Claim 5; Fig 1; 30pp; English.

XX CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is

CC used in the invention. The invention relates to a composition which

CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.

CC transforming growth factor TGF-beta, vascular endothelial growth factor

CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)

CC that adversely affects the immune response. The composition also includes

CC at least one stimulant that positively affects the immune response. This

CC oligonucleotide is an example of an inhibitor that is used in the

CC composition. The composition is used as an immunostimulant for the

CC treatment of neoplasms and infections, particularly hyperproliferation;

CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,

CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,

CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,

CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,

CC most of which are directed against TGFbeta or VEGF, are inhibitors of

CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-

CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative

CC colitis, diabetes, glomerulonephritis, acute respiratory distress

CC syndrome and the formation of atherosclerotic plaque

XX SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1523 GGTATTATAAATCGACATGC 1542

||||| ||||| ||||| |||||

DB 20 GGTTTACAAATAGACATGC 1

RESULT 239

AAZ57138

ID AAZ57138 standard; DNA; 20 BP.

XX AC AAZ57138;

XX DT 24-MAR-2000 (first entry)

XX DE Self complementary intermolecular duplex SEQ ID NO:13.

XX KW Quadruplex DNA; antibody; binding; detection; isolation; purification;

XX KW ss.

XX OS Synthetic.

XX PN US6001657-A.

XX PD 14-DEC-1999.

XX PF 11-OCT-1996; 96US-00729598.

XX PR 12-OCT-1995; 95US-0005242P.

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.

PA (JACK-) JACKSON LAB.

XX PI Roberts JF, Pelsue SC, Hardin CC, Brown BA;

XX DR WPI; 2000-096139/08.

XX PT Quadruplex nucleic acid and antibody binding assay useful for detecting

XX PT and purifying antibodies and nucleic acids from a biological sample.

XX PS Example 4; Col 10; 11pp; English.

XX CC A method has been developed for binding quadruplex nucleic acids. The

CC method comprises contacting a quadruplex nucleic acid with a monoclonal

CC antibody that selectively binds to quadruplex nucleic acid to form an

CC antibody-quadruplex nucleic acid complex. The method can be used for

CC detecting antibodies that bind to quadruplex nucleic acids and to collect

CC antibodies that bind to quadruplex nucleic acids. The method is also

CC suitable for detecting, isolating and purifying quadruplex nucleic acids.

CC The detecting step can be carried out on a biological sample such as

CC cerebrospinal fluid, tissues samples, blood samples or other sample

CC suspected of containing quadruplex nucleic acids. The method can be used

CC for the purification of quadruplex nucleic acids from solutions and to

CC purify aptamers from combinatorial libraries or heterogeneous solutions,

CC in particular to purify or detect DNA aptamers that specifically bind the

CC thrombin molecule critical in the thrombin-catalysed, fibrin-clot

CC formation cascade of blood platelets. The antibodies can then be used to

CC detect levels of a known therapeutic aptamer in a patient and monitor

CC clearance and dosage levels in a treatment protocol involving the

CC aptamer. The present sequence represents an oligonucleotide used in the

CC exemplification of the present invention

XX SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635

||||| ||||| ||||| |||||

DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 240

AAZ57138/C

ID AAZ57138 standard; DNA; 20 BP.

XX AC AAZ57138;

XX DT 24-MAR-2000 (first entry)

XX DE Self complementary intermolecular duplex SEQ ID NO:13.

XX KW Quadruplex DNA; antibody; binding; detection; isolation; purification;

XX KW ss.

XX OS Synthetic.

XX DE Self complementary intermolecular duplex SEQ ID NO:13.

XX KW Quadruplex DNA; antibody; binding; detection; isolation; purification;

XX KW ss.

XX OS Synthetic.

XX PN US6001657-A.

XX PD 14-DEC-1999.

XX PF 11-OCT-1996; 96US-00729598.

XX PR 12-OCT-1995; 95US-0005242P.

XX PA (UYNC-) UNIV NORTH CAROLINA STATE.

PA (JACK-) JACKSON LAB.

XX PI Roberts JF, Pelsue SC, Hardin CC, Brown BA;

XX DR WPI; 2000-096139/08.

XX PT Quadruplex nucleic acid and antibody binding assay useful for detecting

XX PT and purifying antibodies and nucleic acids from a biological sample.

XX PS Example 4; Col 10; 11pp; English.

XX CC A method has been developed for binding quadruplex nucleic acids. The

CC method comprises contacting a quadruplex nucleic acid with a monoclonal

CC antibody that selectively binds to quadruplex nucleic acid to form an

CC antibody-quadruplex nucleic acid complex. The method can be used for

CC detecting antibodies that bind to quadruplex nucleic acids and to collect

CC antibodies that bind to quadruplex nucleic acids. The method is also

CC suitable for detecting, isolating and purifying quadruplex nucleic acids.

CC The detecting step can be carried out on a biological sample such as

CC cerebrospinal fluid, tissues samples, blood samples or other sample

CC suspected of containing quadruplex nucleic acids. The method can be used

CC for the purification of quadruplex nucleic acids from solutions and to

CC purify aptamers from combinatorial libraries or heterogeneous solutions,

CC in particular to purify or detect DNA aptamers that specifically bind the

CC thrombin molecule critical in the thrombin-catalysed, fibrin-clot

CC formation cascade of blood platelets. The antibodies can then be used to

CC detect levels of a known therapeutic aptamer in a patient and monitor

CC clearance and dosage levels in a treatment protocol involving the

CC aptamer. The present sequence represents an oligonucleotide used in the

CC exemplification of the present invention

XX SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635

||||| ||||| ||||| |||||

DB 1 CGCGCGCGCGCGCGCGCG 20

RESULT 240

AAZ57138/C

ID AAZ57138 standard; DNA; 20 BP.

XX AC AAZ57138;

XX DT 24-MAR-2000 (first entry)

XX DE Self complementary intermolecular duplex SEQ ID NO:13.

XX KW Quadruplex DNA; antibody; binding; detection; isolation; purification;

XX KW ss.

XX OS Synthetic.

XX US6001657-A.  
 PN  
 XX  
 PD 14-DEC-1999.  
 XX  
 XX  
 PF 11-OCT-1996; 96US-00729598.  
 PR  
 PR 12-OCT-1995; 95US-0005242P.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA (JACK-) JACKSON LAB.  
 XX  
 XX Roberts JF, Pelsue SC, Hardin CC, Brown BA;  
 PI WPI; 2000-096139/08.  
 XX  
 XX Quadruplex nucleic acid and antibody binding assay useful for detecting  
 PT and purifying antibodies and nucleic acids from a biological sample.  
 XX  
 XX Example 4; Col 10; 11pp; English.  
 XX  
 CC A method has been developed for binding quadruplex nucleic acids. The  
 CC method comprises contacting a quadruplex nucleic acid with a monoclonal  
 CC antibody that selectively binds to quadruplex nucleic acid to form an  
 CC antibody-quadruplex nucleic acid complex. The method can be used for  
 CC detecting antibodies that bind to quadruplex nucleic acids and to collect  
 CC antibodies that bind to quadruplex nucleic acids. The method is also  
 CC suitable for detecting, isolating and purifying quadruplex nucleic acids.  
 CC The detecting step can be carried out on a biological sample such as  
 CC cerebrospinal fluid, tissues samples, blood samples or other sample  
 CC suspected of containing quadruplex nucleic acids. The method can be used  
 CC for the purification of quadruplex nucleic acids from solutions and to  
 CC purify aptamers from combinatorial libraries or heterogeneous solutions.  
 CC in particular to purify or detect DNA aptamers that specifically bind the  
 CC thrombin molecule critical in the thrombin-catalysed, fibrin-clot  
 CC formation cascade of blood platelets. The antibodies can then be used to  
 CC detect levels of a known therapeutic aptamer in a patient and monitor  
 CC clearance and dosage levels in a treatment protocol involving the  
 CC aptamer. The present sequence represents an oligonucleotide used in the  
 CC amplification of the present invention  
 XX  
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 616 CGCGCGCGCACGCGCGCG 635  
 DB 20 CGCGCGCGCGCGCGCGCG 1  
 RESULT 241  
 AAF99391  
 ID AAF99391 standard; DNA; 20 BP.  
 AC AAF99391;  
 XX  
 XX 12-JUN-2001 (first entry)  
 DT  
 XX  
 XX Immunostimulatory nucleic acid #507.  
 DE  
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200122972-A2.  
 PN  
 XX 05-APR-2001.  
 PD  
 XX 25-SEP-2000; 2000WO-US026383.  
 PF  
 XX 25-SEP-1999; 99US-0156113P.  
 PR  
 XX 27-SEP-1999; 99US-0156135P.  
 PR  
 XX 23-AUG-2000; 2000US-0227436P.  
 PR  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PA

PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 DR  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 XX Claim 101; Page 48; 338pp; English.  
 PS  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 616 CGCGCGCGCACGCGCGCG 635  
 DB 1 CGCGCGCGCGCGCGCGCG 20  
 RESULT 242  
 AAF99391/c  
 ID AAF99391 standard; DNA; 20 BP.  
 AC AAF99391;  
 XX  
 XX 12-JUN-2001 (first entry)  
 DT  
 XX  
 XX Immunostimulatory nucleic acid #507.  
 DE  
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200122972-A2.  
 PN  
 XX 05-APR-2001.  
 PD  
 XX 25-SEP-2000; 2000WO-US026383.  
 PF  
 XX 25-SEP-1999; 99US-0156113P.  
 PR  
 XX 27-SEP-1999; 99US-0156135P.  
 PR  
 XX 23-AUG-2000; 2000US-0227436P.  
 PR  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PA

XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX Claim 101; Page 48; 338pp; English.  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 616 CGCGCGCGCACGCACGCGCG 635  
 Db 20 CGCGCGCGCGCGCGCGCG 1  
 RESULT 243  
 AAF99569  
 ID AAF99569 standard; DNA; 20 BP.  
 XX AAF99569;  
 XX 12-JUN-2001 (first entry)  
 XX Immunostimulatory nucleic acid #685.  
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 DE immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX Synthetic.  
 XX WO200122972-A2.  
 XX 05-APR-2001.  
 XX 25-SEP-2000; 2000WO-US026383.  
 XX 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX

PS Claim 101; Page 53; 338pp; English.  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 616 CGCGCGCGCACGCACGCGCG 635  
 Db 1 CGCGCGCGCGCGCGCGCG 20  
 RESULT 244  
 AAF99569/c  
 ID AAF99569 standard; DNA; 20 BP.  
 XX AAF99569;  
 XX 12-JUN-2001 (first entry)  
 XX Immunostimulatory nucleic acid #685.  
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 DE immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX Synthetic.  
 XX WO200122972-A2.  
 XX 05-APR-2001.  
 XX 25-SEP-2000; 2000WO-US026383.  
 XX 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX Claim 101; Page 53; 338pp; English.  
 XX The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX

CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC hemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone

XX  
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 616 CGCGCGCGCGACGACGCGCG 635  
||||||| ||| |||||  
Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 245  
ABA91532  
ID ABA91532 standard; DNA; 20 BP.  
XX  
AC ABA91532;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE DNA oligonucleotide AGT02020 used to test RNase H cleavage.

XX Nucleic acid detection; probe; mismatch; ss.  
XX  
OS Synthetic.

Key Location/Qualifiers  
FH misc\_feature 13  
FT /\*tag= a  
FT /note= "mismatch to target DNA"

XX WO200206531-A2.  
XX  
XX 24-JAN-2002.  
XX  
XX 12-JUL-2001; 2001WO-US022166.  
XX  
XX 14-JUL-2000; 2000US-00616761.  
XX  
XX 30-MAR-2001; 2001US-00823647.  
XX  
XX (GENE-) APPLIED GENE TECHNOLOGIES INC.

XX Dattagupta N;  
XX  
XX WPI; 2002-171819/22.

XX Probes for detecting target nucleotide sequence in sample, has sequence  
XX that forms hairpin structure having a double-stranded segment and single-  
XX stranded loop collectively forming region complementary to target  
XX sequence.

XX Example 5; Page 49; 72pp; English.

XX The present sequence is that of oligonucleotide AGT02020, which contains  
XX a single mismatch with a target DNA oligonucleotide (see ABA91531). It is  
XX one of a set of oligonucleotides (see ABA91532-37) containing  
XX mismatch(es) to the target DNA that were tested in a hybridisation/RNase  
XX H cleavage assay. The results showed that 2 mismatches between the target  
XX and the probe ablated RNase H cleavage. The effect of one mismatch site  
XX was less than that of two mismatch sites, and showed a polarity effect,  
XX with stronger inhibition shown in assays with AGT02020 than in assays  
XX using an oligonucleotide in which the mismatch was at an adjacent  
XX position. The invention provides probes for nucleic acid hybridisation.  
XX The probes form a hairpin structure comprising a double-stranded stem and  
XX a single-stranded loop, and are capable of both intramolecular and

CC intermolecular hybridisation. The double-stranded stem may comprise a  
CC methylphosphonate DNA:RNA hybrid that is resistant to RNase H cleavage.  
CC When the probe hybridises with a target DNA, the RNA strand in the  
CC DNA:RNA duplex becomes sensitive to RNase H treatment and can be removed.  
CC Arrays and methods for nucleic acid hybridisation using the probes are  
CC provided

XX  
SQ Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2580 AAAAAAAAAATTGGAGAAAAA 2599  
||||||| ||| |||||  
Db 1 AAAAAAAAAATTGAAAAAAA 20

RESULT 246  
ABA91533  
ID ABA91533 standard; DNA; 20 BP.  
XX  
AC ABA91533;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE DNA oligonucleotide AGT02021 used to test RNase H cleavage.

XX Nucleic acid detection; probe; mismatch; ss.  
XX  
OS Synthetic.

Key Location/Qualifiers  
FH misc\_feature 12  
FT /\*tag= a  
FT /note= "mismatch to target DNA"

XX WO200206531-A2.  
XX  
XX 24-JAN-2002.  
XX  
XX 12-JUL-2001; 2001WO-US022166.  
XX  
XX 14-JUL-2000; 2000US-00616761.  
XX  
XX 30-MAR-2001; 2001US-00823647.  
XX  
XX (GENE-) APPLIED GENE TECHNOLOGIES INC.

XX Dattagupta N;  
XX  
XX WPI; 2002-171819/22.

XX Probes for detecting target nucleotide sequence in sample, has sequence  
XX that forms hairpin structure having a double-stranded segment and single-  
XX stranded loop collectively forming region complementary to target  
XX sequence.

XX Example 5; Page 50; 72pp; English.

XX The present sequence is that of oligonucleotide AGT02021, which contains  
XX a single mismatch with a target DNA oligonucleotide (see ABA91531). It is  
XX one of a set of oligonucleotides (see ABA91532-37) containing  
XX mismatch(es) to the target DNA that were tested in a hybridisation/RNase  
XX H cleavage assay. The results showed that 2 mismatches between the target  
XX and the probe ablated RNase H cleavage. The effect of one mismatch site  
XX was less than that of two mismatch sites, and showed a polarity effect,  
XX with weaker inhibition shown in assays with AGT02021 than in assays using  
XX an oligonucleotide in which the mismatch was at an adjacent position.  
XX Oligonucleotides in which the mismatch was C or A rather than G showed  
XX similar inhibition of RNase H cleavage. The invention provides probes for  
XX nucleic acid hybridisation. The probes form a hairpin structure  
XX comprising a double-stranded stem and a single-stranded loop, and are  
XX capable of both intramolecular and intermolecular hybridisation. The

CC double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that  
CC is resistant to RNase H cleavage. When the probe hybridises with a target  
CC DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H  
CC treatment and can be removed. Arrays and methods for nucleic acid  
CC hybridisation using the probes are provided

XX  
SQ Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2580 AAAAAAAAAATTGGAGAAAA 2599  
Db 1 AAAAAAAAAATTGTAAGAAAA 20  
|||||

## RESULT 247

ABS78285  
ID ABS78285 standard; DNA; 20 BP.

XX AC ABS78285;  
XX  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #769.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX Synthetic.  
OS  
XX  
XX WO200253141-A2.  
XX  
XX  
PD 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US048458.  
XX  
XX 14-DEC-2000; 2000US-0255534P.  
XX  
XX (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;  
XX  
XX WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.

XX Claim 2; Page 33; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGG 635  
Db 1 CGCGCGCGCGCGCGCGG 20  
|||||

## RESULT 248

ABS78285/c  
ID ABS78285 standard; DNA; 20 BP.

XX AC ABS78285;  
XX  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #769.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX Synthetic.

OS  
WO200253141-A2.

XX 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US048458.

XX 14-DEC-2000; 2000US-0255534P.

XX (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

XX WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.

XX Claim 2; Page 33; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGG 635  
|||||

|            |   |  |
|------------|---|--|
| AC         | AB578036;   |  |
| XX         |   |  |
| DT         | 13-DEC-2002 (first entry)   |  |
| XX         |   |  |
| DE         | Angiogenesis inhibitory oligonucleotide #520.                             |  |
| XX         |   |  |
| KW         | Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;            |  |
| KW         | tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  |  |
| KW         | diabetic retinopathy; retinopathy of prematurity; macular degeneration;   |  |
| KW         | corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;   |  |
| KW         | rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;                 |  |
| KW         | plaque neovascularisation; telangiectasia; haemophilic joint;             |  |
| KW         | angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;    |  |
| KW         | scleroderma; hypertrophic scar.   |  |
| XX         |   |  |
| OS         | Synthetic.  |  |
| XX         |   |  |
| PN         | WO200253141-A2.   |  |
| XX         |   |  |
| PD         | 11-JUL-2002.  |  |
| XX         |   |  |
| PF         | 14-DEC-2001; 2001WO-US048458.   |  |
| XX         |   |  |
| PR         | 14-DEC-2000; 2000US-0255534P.   |  |
| XX         |   |  |
| PA         | (COLE-) COLEY PHARM GROUP INC.  |  |
| XX         |   |  |
| FI         | Bratzler RL;  |  |
| XX         |   |  |
| DR         | WPI; 2002-566690/60.  |  |
| XX         |   |  |
| XX         | Inhibiting angiogenesis in a subject, involves administering at least one |  |
| PT         | antiangiogenic nucleic acid molecule to the subject.                      |  |
| XX         |   |  |
| PS         | Claim 2; Page 28; 276pp; English.   |  |
| XX         |   |  |
| CC         | The invention relates to inhibiting angiogenesis in a subject, comprising |  |
| CC         | administering at least one antiangiogenic nucleic acid molecule. Also     |  |
| CC         | included is a kit comprising a first container housing the antiangiogenic |  |
| CC         | nucleic acids, and instructions for administering them to a subject       |  |
| CC         | having a condition characterised by unwanted angiogenesis. The method is  |  |
| CC         | useful for inhibiting angiogenesis associated with solid tumour growth,   |  |
| CC         | tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  |  |
| CC         | diabetic retinopathy, retinopathy of prematurity, macular degeneration,   |  |
| CC         | corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,   |  |
| CC         | rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque          |  |
| CC         | neovascularisation, telangiectasia, haemophilic joints, angiofibroma,     |  |
| CC         | wound granulation, intestinal adhesions, atherosclerosis, scleroderma and |  |
| CC         | hypertrophic scars. The present sequence is an antiangiogenic nucleic     |  |
| CC         | acid of the invention   |  |
| XX         |   |  |
| SQ         | Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;                       |  |
|            | Query Watch 0.4%; Score 16.8; DB 1; Length 20;                            |  |
|            | Best Local Similarity 90.0%; Pred. No. 1.7e+02;                           |  |
|            | Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0                |  |
| Qy         | 616 CGCGCGCGCACGCGCGCG 635  |  |
|            |   |  |
| Db         | 20 CGCGCGCGCGCGCGCGCG 1   |  |
|            |   |  |
| RESULT 251 |   |  |
| ABL38812   |   |  |
| ID         | ABL38812 standard; DNA; 20 BP.  |  |
| XX         |   |  |
| AC         | ABL38812;   |  |
| XX         |   |  |
| DT         | 16-APR-2002 (first entry)   |  |
| XX         |   |  |
| DE         | Immunostimulatory nucleic acid SEQ ID NO: 193.                            |  |
| XX         |   |  |
| KW         | Antibody-induced cell lysis; cancer; immunostimulatory; CD20;             |  |





DR WPI; 2002-154611/20.

XX Treating or preventing cancer, such as basal cell carcinoma, comprises

PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer.

XX

XX Disclosure; Page 144; 312pp; English.

XX The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder

CC cancer, bone cancer, brain and central nervous system (CNS) cancer,

CC breast cancer, cervical cancer, colon and rectum cancer, connective

CC tissue cancer, oesophageal cancer, eye cancer, Hodgkin's lymphoma, non-

CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian

CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin

CC cancer, stomach cancer, testicular cancer, and uterine cancer. The

CC present sequence is an immunostimulatory oligonucleotide described in the

CC exemplification of the invention

XX

XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

SQ

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635

Db 1 CGCGCGCGCGCGCGCGCG 20

RESULT 254

ABL38811/c

ID ABL38811 standard; DNA; 20 BP.

AC ABL38811;

XX

XX 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 192.

DE

DE Antibody-induced cell lysis; cancer; immunostimulatory; CD20;

XX angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.

KW

KW Synthetic.

OS

XX

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= a

FT /\*mod\_base= OTHER

FT /\*note= "phosphorothioate backbone"

XX

XX WO200197843-A2.

PN

XX

XX 27-DEC-2001.

XX

XX 22-JUN-2001; 2001WO-US020154.

PF

XX

XX 22-JUN-2000; 2000US-0213346P.

PR

XX

XX (IOWA ) UNIV IOWA RES FOUND.

PA

XX

XX Weiner G, Hartmann G;

PI

XX

XX WPI; 2002-154611/20.

DR

XX

XX Treating or preventing cancer, such as basal cell carcinoma, comprises

PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer.

PT developing cancer.

XX

XX Disclosure; Page 144; 312pp; English.

XX The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder

CC cancer, bone cancer, brain and central nervous system (CNS) cancer,

CC breast cancer, cervical cancer, colon and rectum cancer, connective

CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx

CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-

CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian

CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin

CC cancer, stomach cancer, testicular cancer, and uterine cancer. The

CC present sequence is an immunostimulatory oligonucleotide described in the

CC exemplification of the invention

XX

XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

SQ

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGACGCGCG 635

Db 20 CGCGCGCGCGCGCGCGCG 1

RESULT 255

ABA97650/c

ID ABA97650 standard; DNA; 20 BP.

XX

XX ABA97650;

XX

XX 11-APR-2002 (first entry)

DT

DE probe u.

DE

XX ss; fluorochrome; nucleic acid probe; fluorescence.

KW

XX Unidentified.

OS

XX JP2001286300-A.

PN

XX 16-OCT-2001.

PD

XX

XX 20-APR-2000; 2000JP-00120097.

PF

XX

XX 20-APR-1999; 99JP-00111601.

PR

XX 24-AUG-1999; 99JP-00236666.

PR

XX 30-AUG-1999; 99JP-00242693.

PR

XX 01-FEB-2000; 2000JP-00028896.

PR

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA

XX (KANK-) KANKYO ENG KK.

PA

XX (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIJUTSU SOGO KEN.

XX

XX WPI; 2002-134193/18.

DR

XX

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

PT

XX

XX Example 6; Page 18; 34pp; Japanese.

PS

XX

XX This invention relates to a method for measuring nucleic acids using a

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

CC target nucleic acid, the decrease in the fluorescence is measured. The

CC method can be used for measuring a target nucleic acid

XX

XX Sequence 20 BP; 15 A; 0 C; 0 G; 5 T; 0 U; 0 Other;

SQ

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1152 TTTCTTTTATATATATTT 1171  
 DB 20 TTTTATATATATATAT 1

RESULT 256  
 ACH03107  
 ID ACH03107 standard; DNA; 20 BP.  
 XX AC ACH03107;  
 XX AC ACH03107;  
 DT 25-SEP-2003 (first entry)  
 XX Immunostimulatory nucleic acid #742.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX Synthetic.  
 OS US2003050268-A1.  
 PN 13-MAR-2003.  
 XX 29-MAR-2002; 2002US-00112653.  
 XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX Krieg AM, Berg DJ;  
 PI WPI; 2003-521815/49.  
 DR Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX Disclosure; Page 29; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid

XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 616 CGCGCGCGCACGCGCGCG 635  
 DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 258  
 ACD99811  
 ID ACD99811 standard; DNA; 20 BP.  
 XX AC ACD99811;  
 XX AC ACD99811;  
 DT 25-SEP-2003 (first entry)  
 XX Immunostimulatory nucleic acid #497.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX Synthetic.  
 OS US2003050268-A1.  
 PN 13-MAR-2003.

XX 25-SEP-2003 (first entry)  
 DT Immunostimulatory nucleic acid #742.  
 XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX Synthetic.  
 OS US2003050268-A1.  
 PN 13-MAR-2003.  
 XX 29-MAR-2002; 2002US-00112653.  
 XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX Krieg AM, Berg DJ;  
 PI WPI; 2003-521815/49.  
 DR Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX Disclosure; Page 29; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid

XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 616 CGCGCGCGCACGCGCGCG 635  
 DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 258  
 ACD99811  
 ID ACD99811 standard; DNA; 20 BP.  
 XX AC ACD99811;  
 XX AC ACD99811;  
 DT 25-SEP-2003 (first entry)  
 XX Immunostimulatory nucleic acid #497.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX Synthetic.  
 OS US2003050268-A1.  
 PN 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.  
 XX  
 XX 29-MAR-2001; 2001US-0279642P.  
 XX  
 XX (KRIE/) KRIEG A M.  
 XX (BERG/) BERG D J.  
 XX  
 XX Krieg AM, Berg DJ;  
 XX WPI; 2003-521815/49.  
 XX  
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 XX allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 XX disease by administering an immunostimulatory nucleic acid.  
 XX  
 XX Disclosure; Page 22; 229pp; English.  
 XX  
 XX The invention describes a method of treating non-allergic inflammatory  
 XX disease comprising administering to a subject having or at risk of  
 XX developing a non-allergic inflammatory disease an immunostimulatory  
 XX nucleic acid for prevention or treatment of the disease. The method is  
 XX useful for treating non-allergic inflammatory diseases, such as  
 XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 XX This sequence represents an immunostimulatory nucleic acid  
 XX  
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX 616 CGCGCGCGCACGACGCGCG 635  
 XX 1 CGCGCGCGCGCGCGCGCG 20  
 XX  
 XX RESULT 259  
 XX ACD9811/c  
 XX ID ACD9811 standard; DNA; 20 BP.  
 XX  
 XX ACD9811;  
 XX  
 XX 25-SEP-2003 (first entry)  
 XX  
 XX Immunostimulatory nucleic acid #497.  
 XX  
 XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 XX antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX  
 XX Synthetic.  
 XX  
 XX US2003050268-A1.  
 XX  
 XX 13-MAR-2003.  
 XX  
 XX 29-MAR-2002; 2002US-00112653.  
 XX  
 XX 29-MAR-2001; 2001US-0279642P.  
 XX  
 XX (KRIE/) KRIEG A M.  
 XX (BERG/) BERG D J.  
 XX  
 XX Krieg AM, Berg DJ;  
 XX WPI; 2003-521815/49.  
 XX  
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 XX allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 XX disease by administering an immunostimulatory nucleic acid.

XX  
 XX Disclosure; Page 22; 229pp; English.  
 XX  
 XX The invention describes a method of treating non-allergic inflammatory  
 XX disease comprising administering to a subject having or at risk of  
 XX developing a non-allergic inflammatory disease an immunostimulatory  
 XX nucleic acid for prevention or treatment of the disease. The method is  
 XX useful for treating non-allergic inflammatory diseases, such as  
 XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 XX This sequence represents an immunostimulatory nucleic acid  
 XX  
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX 616 CGCGCGCGCACGACGCGCG 635  
 XX 20 CGCGCGCGCGCGCGCGCG 1  
 XX  
 XX RESULT 260  
 XX ADB37071  
 XX ID ADB37071 standard; DNA; 20 BP.  
 XX  
 XX ADB37071;  
 XX  
 XX 04-DEC-2003 (first entry)  
 XX  
 XX Immunostimulatory nucleic acid #685.  
 XX  
 XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
 XX hypo-responsive subject; immunostimulatory.  
 XX  
 XX Synthetic.  
 XX  
 XX US2003087848-A1.  
 XX  
 XX 08-MAY-2003.  
 XX  
 XX 02-FEB-2001; 2001US-00776479.  
 XX  
 XX 03-FEB-2000; 2000US-0179991P.  
 XX  
 XX (BRAT/) BRATZLER R L.  
 XX (PETE/) PETERSEN D M.  
 XX (FOUR/) FOURON Y.  
 XX  
 XX Bratzler RL, Petersen DM, Fouron Y;  
 XX WPI; 2003-657977/62.  
 XX  
 XX Treating and/or preventing allergy or asthma using an immunostimulatory  
 XX nucleic acid alone or in combination with an asthma/allergy medicament.  
 XX  
 XX Disclosure; Page 16; 221pp; English.  
 XX  
 XX The invention relates to a method of treating or preventing allergy or  
 XX asthma which comprises administering to a subject a poly-G nucleic acid  
 XX in an aerosol formulation. The methods and compositions of the present  
 XX invention are useful for diagnosing and/or treating asthma and allergy  
 XX especially in a hypo-responsive subject. The present sequence represents  
 XX an immunostimulatory nucleic acid of the invention.  
 XX  
 XX Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX 616 CGCGCGCGCACGACGCGCG 635

```

Db      1 CGCGCGCGCGCGCGCGCG 20
|||||
RESULT 261
ADB37071/c
ID      ADB37071 standard; DNA; 20 BP.
XX
AC      ADB37071;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Immunostimulatory nucleic acid #685.
XX
KW      ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX      hypo-responsive subject; immunostimulatory.
XX
OS      Synthetic.
XX
PN      US2003087848-A1.
XX
PD      08-MAY-2003.
XX
PF      02-FEB-2001; 2001US-00776479.
XX
PR      03-FEB-2000; 2000US-0179991P.
XX
PA      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
PA      (FOUR/) FOURON Y.
XX
PI      Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX
Disclosure; Page 16; 22ipp; English.
XX
The invention relates to a method of treating or preventing allergy or
asthma which comprises administering to a subject a poly-G nucleic acid
in an aerosol formulation. The methods and compositions of the present
invention are useful for diagnosing and/or treating asthma and allergy
especially in a hypo-responsive subject. The present sequence represents
an immunostimulatory nucleic acid of the invention.
XX
Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
XX
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCGCGCG 635
Db      20 CGCGCGCGCGCGCGCGCG 1
|||||
RESULT 262
ADB36893
ID      ADB36893 standard; DNA; 20 BP.
XX
AC      ADB36893;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Immunostimulatory nucleic acid #507.
XX
KW      ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX      hypo-responsive subject; immunostimulatory.
XX
OS      Synthetic.
XX
PN      US2003087848-A1.
XX
PD      08-MAY-2003.
XX
PF      02-FEB-2001; 2001US-00776479.
XX
PR      03-FEB-2000; 2000US-0179991P.
XX
PA      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
PA      (FOUR/) FOURON Y.
XX
PI      Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX
Disclosure; Page 16; 22ipp; English.
XX
The invention relates to a method of treating or preventing allergy or
asthma which comprises administering to a subject a poly-G nucleic acid
in an aerosol formulation. The methods and compositions of the present
invention are useful for diagnosing and/or treating asthma and allergy
especially in a hypo-responsive subject. The present sequence represents
an immunostimulatory nucleic acid of the invention.
XX
Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
XX
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCGCGCG 635
Db      20 CGCGCGCGCGCGCGCGCG 1
|||||

```

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PN      US2003087848-A1.
XX
PD      08-MAY-2003.
XX
PF      02-FEB-2001; 2001US-00776479.
XX
PR      03-FEB-2000; 2000US-0179991P.
XX
PA      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
PA      (FOUR/) FOURON Y.
XX
PI      Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX
Disclosure; Page 12; 22ipp; English.
XX
The invention relates to a method of treating or preventing allergy or
asthma which comprises administering to a subject a poly-G nucleic acid
in an aerosol formulation. The methods and compositions of the present
invention are useful for diagnosing and/or treating asthma and allergy
especially in a hypo-responsive subject. The present sequence represents
an immunostimulatory nucleic acid of the invention.
XX
Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
XX
Query Match      0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      616 CGCGCGCGCACGCGCGCG 635
Db      1 CGCGCGCGCGCGCGCGCG 20
|||||
RESULT 263
ADB36893/c
ID      ADB36893 standard; DNA; 20 BP.
XX
AC      ADB36893;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Immunostimulatory nucleic acid #507.
XX
KW      ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX      hypo-responsive subject; immunostimulatory.
XX
OS      Synthetic.
XX
PN      US2003087848-A1.
XX
PD      08-MAY-2003.
XX
PF      02-FEB-2001; 2001US-00776479.
XX
PR      03-FEB-2000; 2000US-0179991P.
XX
PA      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
PA      (FOUR/) FOURON Y.
XX
PI      Bratzler RL, Petersen DM, Fouron Y;
XX
WPI; 2003-657977/62.
XX
Treating and/or preventing allergy or asthma using an immunostimulatory
nucleic acid alone or in combination with an asthma/allergy medicament.
XX

```

```
PS Disclosure; Page 12; 22lpp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 264
ADF86263
ID ADF86263 standard; DNA; 20 BP.
XX
AC ADF86263;
XX
DT 26-FEB-2004 (first entry)
XX
DE Rat TGF-beta 2 PCR primer related to liver regeneration SeqID9.
XX
KW liver regeneration promoter; hepatic disorder; anti-kallikrein antibody;
KW hepatotropic; antiinflammatory; virucide; TGF;
KW transforming growth factor-beta; liver tissue fibrosis; liver cirrhosis;
KW hepatitis; liver regeneration insufficiency; PCR; primer; ss; rat;
KW TGF-beta 2.
XX
OS Rattus sp.
XX
PN JP2003252792-A.
XX
PD 10-SEP-2003.
XX
PF 04-MAR-2002; 2002JP-00057253.
XX
PR 04-MAR-2002; 2002JP-00057253.
XX
PA (RIKA ) RIKAGAKU KENKYUSHO.
PA (GIFU-) GIFU DAIGAKUCHO.
XX
DR WPI; 2003-857283/80.
XX
PT Liver regeneration promoter for treating and preventing hepatic disorder,
PT contains anti-kallikrein antibody as active ingredient.
XX
PS Disclosure; SEQ ID NO 9; 25pp; Japanese.
XX
CC This invention relates to a novel liver regeneration promoter for
CC treating and preventing a hepatic disorder, which contains anti-
CC kallikrein antibody as an active ingredient. The invention may be useful
CC in the development of compositions with hepatotropic, antiinflammatory or
CC virucide activities as a transforming growth factor (TGF)-agonist. The
CC invention may be useful for treating and preventing hepatic disorders
CC resulting from the effect of transforming growth factor-beta, liver
CC tissue fibrosis, liver cirrhosis, hepatitis or liver regeneration
CC insufficiency.
XX
SQ Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1965 TTTCGAGGTATGATGGCAC 1984

PS Disclosure; Page 12; 22lpp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 20 BP; 0 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGCG 635
DB 20 CGCGCGCGCGCGCGCGCG 1

RESULT 265
ADF86264/c
ID ADF86264 standard; DNA; 20 BP.
XX
AC ADF86264;
XX
DT 26-FEB-2004 (first entry)
XX
DE Rat TGF-beta 2 PCR primer related to liver regeneration SeqID10.
XX
KW liver regeneration promoter; hepatic disorder; anti-kallikrein antibody;
KW hepatotropic; antiinflammatory; virucide; TGF;
KW transforming growth factor-beta; liver tissue fibrosis; liver cirrhosis;
KW hepatitis; liver regeneration insufficiency; PCR; primer; ss; rat;
KW TGF-beta 2.
XX
OS Rattus sp.
XX
PN JP2003252792-A.
XX
PD 10-SEP-2003.
XX
PF 04-MAR-2002; 2002JP-00057253.
XX
PR 04-MAR-2002; 2002JP-00057253.
XX
PA (RIKA ) RIKAGAKU KENKYUSHO.
PA (GIFU-) GIFU DAIGAKUCHO.
XX
DR WPI; 2003-857283/80.
XX
PT Liver regeneration promoter for treating and preventing hepatic disorder,
PT contains anti-kallikrein antibody as active ingredient.
XX
PS Disclosure; SEQ ID NO 10; 25pp; Japanese.
XX
CC This invention relates to a novel liver regeneration promoter for
CC treating and preventing a hepatic disorder, which contains anti-
CC kallikrein antibody as an active ingredient. The invention may be useful
CC in the development of compositions with hepatotropic, antiinflammatory or
CC virucide activities as a transforming growth factor (TGF)-agonist. The
CC invention may be useful for treating and preventing hepatic disorders
CC resulting from the effect of transforming growth factor-beta, liver
CC tissue fibrosis, liver cirrhosis, hepatitis or liver regeneration
CC insufficiency.
XX
SQ Sequence 20 BP; 6 A; 3 C; 8 G; 3 T; 0 U; 0 Other;

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2159 GGATAATTGCTGCTTGCC 2178
DB 20 GCATAATTCTGCTTGCC 1

RESULT 266
ABZ86060/c
ID ABZ86060 standard; DNA; 20 BP.
XX
AC ABZ86060;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
```

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX Homo sapiens.  
XX WO200285308-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013135.  
XX 24-APR-2001; 2001US-0286137P.  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX Claim 15; SEQ ID NO 1302; 872pp; English.  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antinflammatory steroid and ubiquinone. A composition of the invention  
CC has antinflammatory, antiasthmatic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 20 BP; 0 A; 1 C; 5 G; 14 T; 0 U; 0 Other;  
XX  
XX Query Match 0.4%; Score 16.8; DB 1; Length 20;  
XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX QY 2667 CAGCAACACACACACAAAA 2686  
XX 20 CAGCAACACACACACAAAAA 1  
XX  
XX RESULT 267  
XX ABZ89592/c  
XX ID ABZ89592 standard; DNA; 20 BP.  
XX XX  
XX AC ABZ89592;  
XX XX  
XX DT 17-OCT-2003 (first entry)  
XX XX  
XX DE Human oligonucleotide sequence.  
XX XX  
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX KW antinflammatory steroid; ubiquinone; antinflammatory; antiasthmatic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX Homo sapiens.  
XX WO200285308-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013135.  
XX 24-APR-2001; 2001US-0286137P.  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX Disclosure; SEQ ID NO 4834; 872pp; English.  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antinflammatory steroid and ubiquinone. A composition of the invention  
CC has antinflammatory, antiasthmatic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 20 BP; 8 A; 3 C; 0 G; 9 T; 0 U; 0 Other;  
XX  
XX Query Match 0.4%; Score 16.8; DB 1; Length 20;  
XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX QY 2749 TTTTITTAAGGAAAAATA 2768  
XX 20 TTTTITTAAGGAAAAAAGA 1  
XX  
XX RESULT 268  
XX ABD22290/c  
XX ID ABD22290 standard; DNA; 20 BP.  
XX XX  
XX AC ABD22290;  
XX XX  
XX DT 29-JUL-2004 (first entry)  
XX XX  
XX DE Human stannocalcin-derived oligo SEQ ID 1302.  
XX XX  
XX KW Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;  
XX KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;

KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX  
XX Homo sapiens.  
XX  
XX W0200285309-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013143.  
XX  
XX 24-APR-2001; 2001US-0286036P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-093058/08.  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
XX oligonucleotide containing less percentage of adenosine, targeted to  
XX nucleic acids associated with lung airway or lung dysfunction, and  
XX bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 1302; 763pp; English.  
XX  
XX This invention describes a novel composition (a) a first active agent,  
XX comprising oligonucleotides, effective for alleviating  
XX bronchoconstriction, respiratory tract inflammation, allergies and  
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
XX surfactant depletion or hyposecretion, when administered to a mammal. The  
XX oligonucleotides are derived from a gene encoding or regulating  
XX expression of a target polypeptide associated with lung airway or lung  
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
XX The invention also describes a kit, that comprises: (a) a delivery  
XX device, in separate containers, (b) the oligonucleotides, (c)  
XX instructions for adding a carrier and for use of the kit. The composition  
XX of the invention has antiasthmatic, antiinflammatory, antiasthmatic,  
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
XX beta-adrenergic agonist. The composition is useful for preventing or  
XX treating a respiratory, lung or malignant disease. The administered  
XX composition comprises oligo and is administered to reduce the production  
XX or availability, or to increase the degradation of the target mRNA or to  
XX reduce the amount of target polypeptide present in the lungs. The  
XX pulmonary obstruction, and/or surfactant hypoproduction are associated  
XX with inflammation, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
XX transplantation rejection, pulmonary infections, bronchitis or cancer.  
XX The reduced adenosine content of the anti-sense oligos corresponding to  
XX thymidines present in the target RNA serves to prevent the breakdown of  
XX the oligonucleotides into products that free adenosine into the system  
XX e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to  
XX prevent any unwanted effects due to it  
XX  
XX Sequence 20 BP; 0 A; 1 C; 5 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2667 CAGCAACAAACACCAAAA 2686  
Db 20 CAGCAACAAACACCAAAA 1

RESULT 269  
ABD25822/c  
ID ABD25822 standard; DNA; 20 BP.  
XX  
XX ABD25822;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX AI085559-derived oligonucleotide SEQ ID 4834.  
XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX pulmonary transplantation rejection; ss; primer.  
XX  
XX Homo sapiens.  
XX  
XX W0200285309-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013143.  
XX  
XX 24-APR-2001; 2001US-0286036P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-093058/08.  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
XX oligonucleotide containing less percentage of adenosine, targeted to  
XX nucleic acids associated with lung airway or lung dysfunction, and  
XX bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 4834; 763pp; English.  
XX  
XX This invention describes a novel composition (a) a first active agent,  
XX comprising oligonucleotides, effective for alleviating  
XX bronchoconstriction, respiratory tract inflammation, allergies and  
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
XX surfactant depletion or hyposecretion, when administered to a mammal. The  
XX oligonucleotides are derived from a gene encoding or regulating  
XX expression of a target polypeptide associated with lung airway or lung  
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
XX The invention also describes a kit, that comprises: (a) a delivery  
XX device, in separate containers, (b) the oligonucleotides, (c)  
XX instructions for adding a carrier and for use of the kit. The composition  
XX of the invention has antiasthmatic, antiinflammatory, antiasthmatic,  
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
XX beta-adrenergic agonist. The composition is useful for preventing or  
XX treating a respiratory, lung or malignant disease. The administered  
XX composition comprises oligo and is administered to reduce the production  
XX or availability, or to increase the degradation of the target mRNA or to  
XX reduce the amount of target polypeptide present in the lungs. The  
XX pulmonary obstruction, and/or surfactant hypoproduction are associated  
XX with inflammation, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
XX transplantation rejection, pulmonary infections, bronchitis or cancer.  
XX The reduced adenosine content of the anti-sense oligos corresponding to  
XX thymidines present in the target RNA serves to prevent the breakdown of  
XX the oligonucleotides into products that free adenosine into the system  
XX e.g., lung, brain, heart, kidney, etc., tissue environment and thereby, to  
XX prevent any unwanted effects due to it



```
XX SQ Sequence 20 BP; 8 A; 3 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2749 TTTTAAAGGAAAAAATA 2768
Db 20 TTTTAAAGGAAAAAAGA 1

RESULT 270
ADH67307
ID ADH67307 standard; DNA; 20 BP.
XX
AC ADH67307;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human glucocorticoid receptor-specific antisense oligonucleotide #4141.
XX
KW antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
OS Homo sapiens.
XX
PN WO2003099215-A2.
XX
PD 04-DEC-2003.
XX
PF 20-MAY-2003; 2003WO-US016084.
XX
PR 20-MAY-2002; 2002US-0381857P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Crosby SD, NaLeeth AB;
XX
DR WPI; 2004-035034/03.
XX
New antisense compound targeted to a nucleic acid molecule encoding
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
XX
PS Claim 4; SEQ ID NO 4141; 985pp; English.
XX
The invention comprises an antisense oligonucleotides that are targeted
CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
CC antisense oligonucleotides of the invention are useful for preventing or
CC delaying infection, inflammation or tumour formation. The antisense
CC oligonucleotides are also useful for treating diabetes, obesity,
CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
CC present DNA sequence represents an antisense oligonucleotide that targets
CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 16 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2804 AAAAAAATCAATCAAAAC 2823
Db 1 AAAAAAATCAATCAAAAC 20

RESULT 271
ADH67307
ID ADH67307 standard; DNA; 20 BP.
XX
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```
XX AC ADH67307;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID NO 181.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytosolic; notropic; neuroprotective; immunosuppressive;
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
KW immune; ss; human.
XX
OS Homo sapiens.
XX
PN US2004006030-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00189267.
XX
PR 02-JUL-2002; 2002US-00189267.
XX
(ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM, Dobie KW;
XX
DR WPI; 2004-081742/08.
XX
New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT neurodegenerative disorder, or a disease involving hyperactivation of
PT immune response.
XX
PS Example 16; SEQ ID NO 181; 135pp; English.
XX
The invention relates to a novel antisense compound of 8-80 nucleobases
CC in length targeted to, and which specifically hybridizes with, a nucleic
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC inhibits the expression of TGF-beta 2. The invention further relates to:
CC a compound 8-80 nucleobases in length that specifically hybridizes with
CC at least an 8-nucleobase portion of an active site on a nucleic acid
CC molecule encoding TGF-beta 2; a composition comprising the compound and a
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC tissues by contacting the cells or tissues with the compound so that
CC expression of TGF-beta 2 is inhibited; treating an animal having a
CC disease or condition associated with TGF-beta 2 by administering to the
CC animal a therapeutic or prophylactic amount of the compound so that
CC expression of TGF-beta 2 is inhibited; and screening an antisense
CC compound. The antisense compound has cytostatic, notropic,
CC neuroprotective, and immunosuppressive activities. The compound,
CC composition and methods are useful for treating a disease or condition
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC cancer, a neurodegenerative disorder, or a disease or condition involving
CC hyperactivation of an immune response. This polynucleotide sequence
CC represents a preferred target DNA region of TGF-beta 2 of the invention.
XX
SQ Sequence 20 BP; 7 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2094 TCACAAACAGTCACGCGCG 2113
Db 1 TCACAAACAGTCACGCGCG 20

RESULT 272
ADH67307/c
ID ADH67307 standard; DNA; 20 BP.
XX
AC ADH67307;
XX
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DT 22-APR-2004 (first entry)  
 XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 71.  
 DE  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 XX cytosatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US2004006030-A1.  
 XX 08-JAN-2004.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX Example 15; SEQ ID NO 71; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX Sequence 20 BP; 6 A; 7 C; 2 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3056 TGGATGGCTTAAGGAGTTTG 3075  
 DB 20 TGGATGGCTTAAGGAACTTG 1  
 RESULT 273  
 ADI80187  
 ID ADI80187 standard; DNA; 20 BP.  
 XX  
 AC ADI80187;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX Human transforming growth factor-beta 2 target DNA region, SEQ ID No 188.  
 DE

XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosatic; nontropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 XX Homo sapiens.  
 OS  
 XX US2004006030-A1.  
 XX 08-JAN-2004.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX Example 16; SEQ ID NO 188; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, nontropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2127 TTGGATGCTGCTACTGCTT 2146  
 DB 1 TTGGATGCGGCTATTGCTT 20  
 RESULT 274  
 ADI80040/c  
 ID ADI80040 standard; DNA; 20 BP.  
 XX  
 AC ADI80040;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 41.  
 DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytosatic; nontropic; neuroprotective; immunosuppressive;  
 KW

KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 XX immune; ss; human.  
 OS Homo sapiens.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 PI Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 DR  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 15; SEQ ID NO 41; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents an antisense oligonucleotide of the invention.  
 XX  
 SQ Sequence 20 BP; 7 A; 4 C; 1 G; 8 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1870 TGGGGTTTAAATAAGTTTA 1889  
 Db 20 TGGGATTTAAATAAGCTTA 1  
 RESULT 275  
 AD180185  
 ID AD180185 standard; DNA; 20 BP.  
 XX  
 AC AD180185;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 186.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; ss; human.  
 XX

OS Homo sapiens.  
 XX  
 PN US2004006030-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-JUL-2002; 2002US-00189267.  
 XX  
 PR 02-JUL-2002; 2002US-00189267.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 PI Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 DR  
 XX  
 PT New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX  
 PS Example 16; SEQ ID NO 186; 135pp; English.  
 XX  
 CC The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX  
 SQ Sequence 20 BP; 8 A; 1 C; 4 G; 7 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1870 TGGGGTTTAAATAAGTTTA 1889  
 Db 1 TGGGATTTAAATAAGCTTA 20  
 RESULT 276  
 AD180006  
 ID AD180006 standard; DNA; 20 BP.  
 XX  
 AC AD180006;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human transforming growth factor-beta 2 PCR probe.  
 XX  
 KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 KW immune; human; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004006030-A1.

XX 08-JAN-2004.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 XX neurodegenerative disorder, or a disease involving hyperactivation of  
 XX immune response.  
 XX Example 13; SEQ ID NO 7; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 XX in length targeted to, and which specifically hybridizes with, a nucleic  
 XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 XX inhibits the expression of TGF-beta 2. The invention further relates to:  
 XX a compound 8-80 nucleobases in length that specifically hybridizes with  
 XX at least an 8-nucleobase portion of an active site on a nucleic acid  
 XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
 XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 XX tissues by contacting the cells or tissues with the compound so that  
 XX expression of TGF-beta 2 is inhibited; treating an animal having a  
 XX disease or condition associated with TGF-beta 2 by administering to the  
 XX animal a therapeutic or prophylactic amount of the compound so that  
 XX expression of TGF-beta 2 is inhibited; and screening an antisense  
 XX compound. The antisense compound has cytostatic, neurotropic,  
 XX neuroprotective, and immunosuppressive activities. The compound,  
 XX composition and methods are useful for treating a disease or condition  
 XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 XX cancer, a neurodegenerative disorder, or a disease or condition involving  
 XX hyperactivation of an immune response. This polynucleotide sequence  
 XX represents a probe used in the exemplification of the invention.  
 XX Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2119 AGCGGCTTTGGATGCTGCC 2138  
 DB 1 AGCGTCTTTGGATGCGGCC 20  
 RESULT 277  
 ADI80034/c  
 ID ADI80034 standard; DNA; 20 BP.  
 AC ADI80034;  
 XX 22-APR-2004 (first entry)  
 XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 35.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 XX cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 XX immune; ss; human.  
 XX Homo sapiens.  
 XX US2004006030-A1.  
 XX 08-JAN-2004.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.

PF 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 XX nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 XX neurodegenerative disorder, or a disease involving hyperactivation of  
 XX immune response.  
 XX Example 15; SEQ ID NO 35; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 XX in length targeted to, and which specifically hybridizes with, a nucleic  
 XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 XX inhibits the expression of TGF-beta 2. The invention further relates to:  
 XX a compound 8-80 nucleobases in length that specifically hybridizes with  
 XX at least an 8-nucleobase portion of an active site on a nucleic acid  
 XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
 XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 XX tissues by contacting the cells or tissues with the compound so that  
 XX expression of TGF-beta 2 is inhibited; treating an animal having a  
 XX disease or condition associated with TGF-beta 2 by administering to the  
 XX animal a therapeutic or prophylactic amount of the compound so that  
 XX expression of TGF-beta 2 is inhibited; and screening an antisense  
 XX compound. The antisense compound has cytostatic, neurotropic,  
 XX neuroprotective, and immunosuppressive activities. The compound,  
 XX composition and methods are useful for treating a disease or condition  
 XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 XX cancer, a neurodegenerative disorder, or a disease or condition involving  
 XX hyperactivation of an immune response. This polynucleotide sequence  
 XX represents an antisense oligonucleotide of the invention.  
 XX Sequence 20 BP; 1 A; 4 C; 8 G; 7 T; 0 U; 0 Other;  
 XX  
 Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2094 TCACACAGTCCAGCGCGC 2113  
 DB 20 TCACACAGACACACCGCG 1  
 RESULT 278  
 ADI80022/c  
 ID ADI80022 standard; DNA; 20 BP.  
 AC ADI80022;  
 XX 22-APR-2004 (first entry)  
 XX Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 23.  
 XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 XX cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 XX immune; ss; human.  
 XX Homo sapiens.  
 XX US2004006030-A1.  
 XX 08-JAN-2004.  
 XX 02-JUL-2002; 2002US-00189267.  
 XX 02-JUL-2002; 2002US-00189267.

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XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.
XX PT New compounds, particularly antisense oligonucleotides targeted to a
XX PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a
XX PT neurodegenerative disorder, or a disease involving hyperactivation of
XX PT immune response.
XX PS Example 15; SEQ ID NO 23; 135pp; English.
XX CC The invention relates to a novel antisense compound of 8-80 nucleobases
XX CC in length targeted to, and which specifically hybridizes with, a nucleic
XX CC acid molecule encoding transforming growth factor (TGF)-beta 2, and
XX CC inhibits the expression of TGF-beta 2. The invention further relates to:
XX CC a compound 8-80 nucleobases in length that specifically hybridizes with
XX CC at least an 8-nucleobase portion of an active site on a nucleic acid
XX CC molecule encoding TGF-beta 2; a composition comprising the compound and a
XX CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
XX CC tissues by contacting the cells or tissues with the compound so that
XX CC expression of TGF-beta 2 is inhibited; treating an animal having a
XX CC disease or condition associated with TGF-beta 2 by administering to the
XX CC animal a therapeutic or prophylactic amount of the compound so that
XX CC expression of TGF-beta 2 is inhibited; and screening an antisense
XX CC compound. The antisense compound has cytostatic, neurotropic,
XX CC neuroprotective, and immunosuppressive activities. The compound,
XX CC composition and methods are useful for treating a disease or condition
XX CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
XX CC cancer, a neurodegenerative disorder, or a disease or condition involving
XX CC hyperactivation of an immune response. This polynucleotide sequence
XX CC represents an antisense oligonucleotide of the invention.
XX SQ Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2349 CTTGCTGTGCTGCCAGGA 2368
DB 20 CTTGCTGTGCTGCCAGA 1

RESULT 279
ADI80043/c
ID ADI80043 standard; DNA; 20 BP.
XX AC ADI80043;
XX DT 22-APR-2004 (first entry)
XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 44.
XX DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; human.
XX OS Homo sapiens.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PP 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.

(ISIS-) ISIS PHARM INC.
Monia BP, Freier SM, Dobie KW;
WPI; 2004-081742/08.
New compounds, particularly antisense oligonucleotides targeted to a
nucleic acid encoding TGF-beta 2, useful for treating cancer, a
neurodegenerative disorder, or a disease involving hyperactivation of
immune response.
Example 15; SEQ ID NO 23; 135pp; English.
The invention relates to a novel antisense compound of 8-80 nucleobases
in length targeted to, and which specifically hybridizes with, a nucleic
acid molecule encoding transforming growth factor (TGF)-beta 2, and
inhibits the expression of TGF-beta 2. The invention further relates to:
a compound 8-80 nucleobases in length that specifically hybridizes with
at least an 8-nucleobase portion of an active site on a nucleic acid
molecule encoding TGF-beta 2; a composition comprising the compound and a
carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
tissues by contacting the cells or tissues with the compound so that
expression of TGF-beta 2 is inhibited; treating an animal having a
disease or condition associated with TGF-beta 2 by administering to the
animal a therapeutic or prophylactic amount of the compound so that
expression of TGF-beta 2 is inhibited; and screening an antisense
compound. The antisense compound has cytostatic, neurotropic,
neuroprotective, and immunosuppressive activities. The compound,
composition and methods are useful for treating a disease or condition
associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
cancer, a neurodegenerative disorder, or a disease or condition involving
hyperactivation of an immune response. This polynucleotide sequence
represents an antisense oligonucleotide of the invention.
Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2349 CTTGCTGTGCTGCCAGGA 2368
DB 20 CTTGCTGTGCTGCCAGA 1

RESULT 279
ADI80043/c
ID ADI80043 standard; DNA; 20 BP.
XX AC ADI80043;
XX DT 22-APR-2004 (first entry)
XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 44.
XX DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; human.
XX OS Homo sapiens.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PP 02-JUL-2002; 2002US-00189267.
XX PR 02-JUL-2002; 2002US-00189267.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.

Monia BP, Freier SM, Dobie KW;
WPI; 2004-081742/08.
New compounds, particularly antisense oligonucleotides targeted to a
nucleic acid encoding TGF-beta 2, useful for treating cancer, a
neurodegenerative disorder, or a disease involving hyperactivation of
immune response.
Example 15; SEQ ID NO 44; 135pp; English.
The invention relates to a novel antisense compound of 8-80 nucleobases
in length targeted to, and which specifically hybridizes with, a nucleic
acid molecule encoding transforming growth factor (TGF)-beta 2, and
inhibits the expression of TGF-beta 2. The invention further relates to:
a compound 8-80 nucleobases in length that specifically hybridizes with
at least an 8-nucleobase portion of an active site on a nucleic acid
molecule encoding TGF-beta 2; a composition comprising the compound and a
carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
tissues by contacting the cells or tissues with the compound so that
expression of TGF-beta 2 is inhibited; treating an animal having a
disease or condition associated with TGF-beta 2 by administering to the
animal a therapeutic or prophylactic amount of the compound so that
expression of TGF-beta 2 is inhibited; and screening an antisense
compound. The antisense compound has cytostatic, neurotropic,
neuroprotective, and immunosuppressive activities. The compound,
composition and methods are useful for treating a disease or condition
associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
cancer, a neurodegenerative disorder, or a disease or condition involving
hyperactivation of an immune response. This polynucleotide sequence
represents an antisense oligonucleotide of the invention.
Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2127 TTGGATGCTGCCTACTGCTT 2146
DB 20 TTGGATGCGGCTATTGCTT 1

RESULT 280
ADI80173
ID ADI80173 standard; DNA; 20 BP.
XX AC ADI80173;
XX DT 22-APR-2004 (first entry)
XX DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 174.
XX DE antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
XX KW cytostatic; neurotropic; neuroprotective; immunosuppressive;
XX KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
XX KW immune; ss; human.
XX OS Homo sapiens.
XX PN US2004006030-A1.
XX PD 08-JAN-2004.
XX PF 02-JUL-2002; 2002US-00189267.
XX PP 02-JUL-2002; 2002US-00189267.
XX PR (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM, Dobie KW;
XX DR WPI; 2004-081742/08.

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XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 16; SEQ ID NO 174; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2349 CTTGCTGTGTGTCACGGA 2368  
DB 1 CCTTGCTGCTGTGTCACGGA 20  
RESULT 281  
AD180045/C  
ID AD180045 standard; DNA; 20 BP.  
XX  
AC AD180045;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 46.  
XX  
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
KW cytostatic; neurotropic; neuroprotective; immunosuppressive;  
KW hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
KW immune; ss; human.  
XX  
OS Homo sapiens.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a

PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX Example 15; SEQ ID NO 46; 135pp; English.  
XX  
CC The invention relates to a novel antisense compound of 8-80 nucleobases  
CC in length targeted to, and which specifically hybridizes with, a nucleic  
CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
CC inhibits the expression of TGF-beta 2. The invention further relates to:  
CC a compound 8-80 nucleobases in length that specifically hybridizes with  
CC at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
CC tissues by contacting the cells or tissues with the compound so that  
CC expression of TGF-beta 2 is inhibited; treating an animal having a  
CC disease or condition associated with TGF-beta 2 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of TGF-beta 2 is inhibited; screening an antisense  
CC compound. The antisense compound has cytostatic, neurotropic,  
CC neuroprotective, and immunosuppressive activities. The compound,  
CC composition and methods are useful for treating a disease or condition  
CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
CC cancer, a neurodegenerative disorder, or a disease or condition involving  
CC hyperactivation of an immune response. This polynucleotide sequence  
CC represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.4%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2446 CTTGTAATGCGAGCTAAAGT 2465  
DB 20 CTTGCAATGCGAGCTAAAT 1  
RESULT 282  
ADK79195  
ID ADK79195 standard; DNA; 20 BP.  
XX  
AC ADK79195;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #5529.  
XX  
KW Nav1.3; Analgesic; Neurotropic; Neuroprotective; post-herpetic neuralgia;  
KW diabetic neuropathy; arthritic pain; migraine headache;  
KW infantile epilepsy; ataxia; ss.  
XX  
OS Synthetic.  
XX  
PN WO2004016754-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 14-AUG-2003; 2003WO-US025465.  
XX  
PR 14-AUG-2002; 2002US-0403416P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX  
PI Robert SL;  
XX  
DR WPI; 2004-203785/19.  
XX  
PT New antisense compound targeted to a nucleic acid molecule encoding  
PT Nav1.3, useful for useful for treating a disease or condition associated  
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
PT disorder, or ataxia.  
XX  
PS Claim 4; SEQ ID NO 529; 417pp; English.

XX The present invention relates to an antisense compound targeted to a  
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
 CC compound and composition are useful for treating a disease or condition  
 CC associated with Nav1.3, e.g. pain including but not limited to  
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
 CC headache; seizure disorder such as childhood seizure disorder, including  
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
 CC sequence represents a chimeric phosphorothioate oligonucleotide with  
 CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of  
 CC human Nav1.3 expression, the oligonucleotides are designed to target  
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 13 A; 2 C; 1 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACATCAA 2820  
 DB 1 TGAATAAAAAAAAAACATCTA 20

RESULT 283  
 ADOS3074/C  
 ID ADOS3074 standard; DNA; 20 BP.  
 AC  
 AC ADOS3074;  
 XX  
 XX 15-JUL-2004 (first entry)  
 XX Farnesoid X receptor gene expression antisense inhibitory oligo #447.  
 DE ss; antidiabetic; immunosuppressive; cardiovascular; antilipemic;  
 XX antiarteriosclerotic; hepatotropic; litholytic; anorectic;  
 KW neuroprotective; vasotropic; antisense; gene therapy;  
 KW Farnesoid X receptor; diabetes; immunological disorder;  
 KW cardiovascular disorder; dyslipidemia; atherosclerosis;  
 KW high density lipoprotein; low density lipoprotein; hypercholesterolemia;  
 KW gallstones; hypertriglyceridemia; obesity; neurological disorder;  
 KW ischemia; reperfusion; diagnostics; prophylaxis.  
 XX Homo sapiens.  
 OS  
 XX WO2004030750-A1.  
 PN  
 XX 15-APR-2004.  
 PD  
 XX 25-SEP-2003; 2003WO-US030353.  
 PF  
 XX 25-SEP-2002; 2002US-0413588P.  
 PR (PHAA ) PHARMACIA CORP.  
 XX  
 XX Kane CD;  
 PI  
 XX WPI; 2004-347928/32.  
 DR  
 XX New antisense oligonucleotides useful for modulating expression of  
 PT Farnesoid X Receptor (FXR) or for treating diseases associated with FXR,  
 PT e.g. diabetes, immunological disorders, cardiovascular disorders,  
 PT gallstones or obesity.  
 XX  
 XX Claim 4; SEQ ID NO 447; 150pp; English.  
 PS  
 XX The invention relates to an antisense compound 8-30 nucleobases in length  
 CC targeted to a nucleic acid molecule encoding Farnesoid X receptor (FXR),  
 CC where the antisense compound specifically hybridizes with and inhibits  
 CC the expression of FXR. The composition and methods are useful for

CC inhibiting the expression of FXR (Farnesoid X receptor) in cells or  
 CC tissues, or for treating diseases or conditions associated with FXR, such  
 CC as diabetes, immunological disorders, cardiovascular disorders, e.g.  
 CC dyslipidemia and its symptoms, atherosclerosis, low HDL (high density  
 CC lipoprotein), elevated LDL (low density lipoprotein) or  
 CC hypercholesterolemia, gallstones, hypertriglyceridemia, obesity,  
 CC neurological disorders, or ischemia/reperfusion injury. In addition, the  
 CC composition is used for diagnostics, prophylaxis, or as research reagents  
 CC or kits. This sequence corresponds to an antisense oligonucleotide of the  
 CC invention.

XX Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3346 TCAGACTTTTGACCGTGAAG 3365  
 DB 20 TCAGACTTTGGACCATGAAG 1

RESULT 284  
 AAQ73754/C  
 ID AAQ73754 standard; DNA; 21 BP.  
 XX  
 AC AAQ73754;  
 XX  
 XX 10-JUL-1995 (first entry)  
 DT Rice starch branching enzyme promoter 3'-primer.  
 DE Starch branching enzyme promoter; rice; starch content; PCR primer; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX JP06261767-A.  
 PN  
 XX 20-SEP-1994.  
 PD  
 XX 22-OCT-1993; 93JP-00265171.  
 PF  
 XX 29-OCT-1992; 92JP-00291719.  
 PR (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.  
 PA  
 XX WPI; 1994-337418/42.  
 DR  
 XX New gene of branching enzyme of rice starch - useful for increasing  
 PT starch yield of grain.  
 PT  
 XX Example 2; Page 13; 13pp; Japanese.  
 PS  
 XX The rice starch branching enzyme gene promoter was amplified using a 5'-  
 CC primer (AAQ73753) and a 3'-primer (AAQ73754) corresponding to nucleotides  
 CC 4-23 and 995-1115, respectively, of the promoter sequence. The promoter  
 CC can be operatively linked to the branching enzyme gene or to heterologous  
 CC genes for expression in plant seeds

XX Sequence 21 BP; 0 A; 3 C; 12 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 2e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 629 ACGCGGCACACCGGCACAC 648  
 DB 21 ACGCGGCACACCGGCACAC 2

RESULT 285  
 AAQ75791/C  
 ID AAQ75791 standard; DNA; 21 BP.



XX AC AAQ75791;  
 XX DT 04-AUG-1995 (first entry)  
 XX DE Reverse transcription primer used in cDNA analysis technique.  
 XX DE Analysis; Gene expression; reverse transcription; primer; cDNA;  
 XX KW aggregate; restriction enzyme; ss.  
 XX OS Synthetic.  
 XX XX JP06303997-A.  
 XX PD 01-NOV-1994.  
 XX PF 16-APR-1993; 93JP-00112515.  
 XX PR 16-APR-1993; 93JP-00112515.  
 XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 XX DR WPI; 1995-018287/03.  
 XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 XX PT by digestion with restriction enzymes.  
 XX PS Disclosure; Page 9; 11pp; Japanese.  
 XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 XX CC and using the aggregate of mRNAs as the template for each reverse  
 XX CC transcription primer; (b) digesting each of the prepared aggregates of  
 XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
 XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 XX CC method can be used to analyse gene expression rapidly and easily  
 XX SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.8; DB 1; Length 21;  
 Best Local Similarity 90.0%; Pred. No. 2e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 925 CAGGAGAAAAAACAACAAA 944  
 Db 21 CAGGAAAAAACAACAAA 2  
 RESULT 286  
 ADD29304/c  
 ID ADD29304 standard; DNA; 24 BP.  
 XX AC ADD29304;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE Molecular and biological process inhibiting oligonucleotide seq id 67.  
 XX KW molecular process inhibition; monomeric unit;  
 XX KW oligonucleotide interaction; polynucleotide interaction;  
 XX KW enzyme interaction; local interaction; ss.  
 XX OS Synthetic.  
 XX XX US6548251-B1.  
 XX PD 15-APR-2003.  
 XX PF 05-SEP-2000; 2000US-00655804.  
 XX PR 05-SEP-2000; 2000US-00655804.

PA (FIDE-) FIDELITY SYSTEMS INC.  
 XX FI Kozyavkin SA, Malykh AG, Polouchine NN, Slesarev AI;  
 XX DR WPI; 2003-786284/74.  
 XX PT Inhibiting nucleic acid hybridization and/or extension in a sample  
 XX PT comprises administering to the sample a modified oligonucleotide or  
 XX PT polynucleotide that contains at least one monomeric unit.  
 XX PS Disclosure; SEQ ID NO 67; 38pp; English.  
 XX XX The invention describes a method of inhibiting a molecular process  
 XX CC involving the interaction between nucleic acids in a sample capable of  
 XX CC undergoing the molecular process. The method comprises administering to  
 XX CC the sample an oligonucleotide or polynucleotide that contains at least  
 XX CC one monomeric unit having a specific formula. The method is useful in  
 XX CC inhibiting undesired molecular interaction between oligonucleotides and  
 XX CC their complexes with polynucleotides and enzymes, including local  
 XX CC interactions between their chemical units (nucleotides or amino acids).  
 XX CC This sequence represents an oligonucleotide used to inhibit undesired  
 XX CC molecular interaction between oligonucleotides and their complexes with  
 XX CC polynucleotides and enzymes.  
 XX SQ Sequence 24 BP; 11 A; 3 C; 0 G; 10 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.6; DB 1; Length 24;  
 Best Local Similarity 82.6%; Pred. No. 2.9e+02;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2732 AAAAGAAAACATCTTTTTTTTTT 2754  
 Db 24 AAAAAAAAAGTGTGTGTGT 2  
 RESULT 287  
 AAQ78427/c  
 ID AAQ78427 standard; DNA; 18 BP.  
 XX AC AAQ78427;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 27-JUN-1995 (first entry)  
 XX DE TGF-beta gene phosphorothioate antisense oligonucleotide.  
 XX KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
 XX KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
 XX KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
 XX KW immunosuppression; oligonucleotide; ss.  
 XX OS Synthetic.  
 XX PN WO9425588-A2.  
 XX PD 10-NOV-1994.  
 XX PF 29-APR-1994; 94WO-EP001362.  
 XX PR 30-APR-1993; 93EP-00107089.  
 XX PR 13-MAY-1993; 93EP-00107849.  
 XX PA (BIOG-) BIOGNOSTIK GES BIOWOLEKULARE DIAGNOSTIK.  
 XX PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
 XX PI Bogdahn U;  
 XX DR WPI; 1994-358266/44.  
 XX XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for  
 XX PT treating immunosuppression, tumours, etc.  
 XX PS Claim 6; Page 46; 74pp; English.



XX The antisense oligonucleotides are useful in the treatment of tumours in  
 CC which expression of TGF-beta is of relevance for pathogenicity and/or  
 CC inhibition of pathological angiogenesis. They are used especially for the  
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
 CC and malignant gliomas, and treatment of oesophageal and gastric  
 CC skin carcinogenesis, and treatment of oesophageal and gastric  
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files  
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
 CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense  
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 18 BP; 6 A; 2 C; 5 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 ACCCTACTTCAGAAATCGT 1606  
 |||||  
 DB 18 ACCCTACTTCAGAAATGTT 1

RESULT 288  
 AAQ78484/C  
 ID AAQ78484 standard; DNA; 18 BP.  
 XX  
 AC AAQ78484;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-JUN-1995 (first entry)  
 XX  
 DE TGF-beta gene phosphorothioate antisense oligonucleotide.  
 XX  
 KW Transforming growth factor beta; TGF-beta; antisense; tumour;  
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
 KW immunosuppression; oligonucleotide; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9425588-A2.  
 XX  
 PD 10-NOV-1994.  
 XX  
 PF 29-APR-1994; 94WO-EP001362.  
 XX  
 PR 30-APR-1993; 93EP-00107089.  
 PR 13-MAY-1993; 93EP-00107849.  
 XX  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA  
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
 PI Bogdahn U;  
 XX  
 DR WPI; 1994-358266/44.  
 XX  
 PT New transforming growth factor beta anti-sense oligo:nucleotide(s) - for  
 PT treating immunosuppression, tumours, etc.  
 XX  
 XX Claim 6; Page 62; 74pp; English.  
 PS  
 XX The antisense oligonucleotides are useful in the treatment of tumours in  
 CC which expression of TGF-beta is of relevance for pathogenicity and/or  
 CC inhibition of pathological angiogenesis. They are used especially for the  
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
 CC of skin carcinogenesis, and treatment of oesophageal and gastric

CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files  
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
 CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense  
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 18 BP; 4 A; 3 C; 4 G; 7 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2446 CTTGTAAATGCAGCTAAA 2463  
 |||||  
 DB 18 CTTGCAATGCAGCTAAA 1

RESULT 289  
 AA265452/C  
 ID AA265452 standard; DNA; 18 BP.  
 XX  
 AC AA265452;  
 XX  
 DT 30-MAR-2000 (first entry)  
 XX  
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-12.  
 XX  
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; ss;  
 KW atherosclerosis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9963975-A2.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 10-JUN-1999; 99WO-EP004013.  
 XX  
 PR 10-JUN-1998; 98EP-00110709.  
 PR 25-JUL-1998; 98EP-00113974.  
 XX  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA  
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;  
 PI WPI; 2000-097470/08.  
 XX  
 DR Composition containing immune stimulant and inhibitor of agent that  
 XX adversely affects the immune response, for treating cancers and  
 PT infections.  
 PT  
 XX Claim 5; Fig 1; 30pp; English.  
 PS  
 XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
 CC used in the invention. The invention relates to a composition which  
 CC contains at least one inhibitor (less than 100 kb) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor  
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes  
 CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-

CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
 CC syndrome and the formation of atherosclerotic plaque  
 XX  
 SQ Sequence 18 BP; 6 A; 2 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1589 ACCCTACTTCAGATCGT 1606  
 |||||  
 Db 18 ACCCTACTTCAGATTCGT 1

RESULT 290  
 AAZ65510/C  
 ID AAZ65510 standard; DNA; 18 BP.  
 XX  
 AC AAZ65510;  
 XX  
 AC  
 XX  
 DT 30-MAR-2000 (first entry)  
 XX  
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta-123-2262.  
 XX  
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; as;  
 KW atherosclerosis.  
 XX  
 OS Unidentified.  
 XX  
 OS  
 XX  
 PN WO9963975-A2.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 10-JUN-1999; 99WO-EP004013.  
 XX  
 PR 10-JUN-1998; 98EP-00110709.  
 XX  
 PR 25-JUL-1998; 98EP-00113974.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;  
 XX  
 DR WPI; 2000-097470/08.  
 XX  
 PT Composition containing immune stimulant and inhibitor of agent that  
 PT adversely affects the immune response, for treating cancers and  
 PT infections.  
 XX  
 PS Claim 10; Fig 1; 30pp; English.  
 XX  
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
 CC used in the invention. The invention relates to a composition which  
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor  
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes  
 CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress

CC syndrome and the formation of atherosclerotic plaque  
 XX  
 SQ Sequence 18 BP; 5 A; 3 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2237 GTACATGCTAACTTCGT 2254  
 |||||  
 Db 18 GTACATGCCAACTTCGT 1

RESULT 291  
 AAZ65466/C  
 ID AAZ65466 standard; DNA; 18 BP.  
 XX  
 AC AAZ65466;  
 XX  
 AC  
 XX  
 DT 30-MAR-2000 (first entry)  
 XX  
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-26.  
 XX  
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; as;  
 KW atherosclerosis.  
 XX  
 OS Unidentified.  
 XX  
 OS  
 XX  
 PN WO9963975-A2.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 10-JUN-1999; 99WO-EP004013.  
 XX  
 PR 10-JUN-1998; 98EP-00110709.  
 XX  
 PR 25-JUL-1998; 98EP-00113974.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;  
 XX  
 DR WPI; 2000-097470/08.  
 XX  
 PT Composition containing immune stimulant and inhibitor of agent that  
 PT adversely affects the immune response, for treating cancers and  
 PT infections.  
 XX  
 PS Claim 5; Fig 1; 30pp; English.  
 XX  
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
 CC used in the invention. The invention relates to a composition which  
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor  
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes  
 CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
 CC inflammatories for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
 CC syndrome and the formation of atherosclerotic plaque

SQ Sequence 18 BP; 4 A; 3 C; 4 G; 7 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2446 CTTGTAATGCAGCTAAA 2463  
 ||||| ||||| ||||| |||||  
 Db 18 CTTGCAATGCAGCTAAA 1

RESULT 292  
 ABA97624/C  
 ID ABA97624 standard; DNA; 18 BP.  
 XX AC ABA97624;  
 XX DT 11-APR-2002 (first entry)  
 XX DE Probe c.  
 XX ss; fluorochrome; nucleic acid probe; fluorescence.  
 XX Unidentified.  
 OS JP2001286300-A.  
 PN JP2001286300-A.  
 XX PD 16-OCT-2001.  
 XX PF 20-APR-2000; 2000JP-00120097.  
 XX PR 20-APR-1999; 99JP-00111601.  
 PR 24-AUG-1999; 99JP-00236666.  
 PR 30-AUG-1999; 99JP-00242693.  
 PR 01-FEB-2000; 2000JP-00028896.  
 XX (BIOI-) BIOINDUSTRY KYOKAI SH.  
 PA (KANK-) KANKYO ENG KK.  
 PA (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIUTSU SOGO KEN.  
 XX WPI; 2002-134193/18.  
 XX Measurement of nucleic acids, using a nucleic acid probe and analysis of  
 PT the obtained data.  
 PS Example 5; Page 17; 34pp; Japanese.  
 XX This invention relates to a method for measuring nucleic acids using a  
 CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe  
 CC decreases the fluorescence of the fluorochrome when hybridised with a  
 CC target nucleic acid, the decrease in the fluorescence is measured. The  
 CC method can be used for measuring a target nucleic acid

SQ Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1151 GTTCTCTTTTATATATA 1168  
 ||||| ||||| ||||| |||||  
 Db 18 GTTTTCTTTTATATATA 1

RESULT 293  
 ABL95897/C  
 ID ABL95897 standard; DNA; 18 BP.  
 XX AC ABL95897;  
 XX DT 19-JUN-2002 (first entry)  
 XX DE Probe c for assaying nucleic acids.

XX Probe; polymorphism detection; mutation detection; disease diagnosis;  
 KW microbial identification; ss.  
 XX Unidentified.  
 XX WO200208414-A1.  
 XX 31-JAN-2002.  
 XX 27-JUN-2001; 2001WO-1B001147.  
 XX 27-JUN-2000; 2000JP-00193133.  
 PR 03-AUG-2000; 2000JP-00236115.  
 PR 26-SEP-2000; 2000JP-00292483.  
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (KANK-) KANKYO ENG CO LTD.  
 XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
 PI Yokomaku T;  
 XX WPI; 2002-195876/25.  
 DR Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
 XX their polymorphism and mutation, particularly useful in science and  
 PT medicine for e.g. analytical applications, disease diagnosis and  
 PT microbial identification.  
 XX Example 12; Page 60; 152pp; Japanese.  
 CC The present invention relates to nucleic acid probes, which are useful  
 CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
 CC which a single-stranded oligonucleotide is labelled with a fluorescent  
 CC substance and a quencher in a manner that the fluorescence intensity of  
 CC the hybridisation reaction system is increased after completion of the  
 CC hybridisation but no stem loop structure is formed. The probes are useful  
 CC for assaying nucleic acids and their polymorphism and mutation,  
 CC particularly useful for e.g. analytical applications, disease diagnosis  
 CC and microbial identification. The present sequence was used to illustrate  
 CC the invention

SQ Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 18;  
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1151 GTTCTCTTTTATATATA 1168  
 ||||| ||||| ||||| |||||  
 Db 18 GTTTTCTTTTATATATA 1

RESULT 294  
 AAA85942/C  
 ID AAA85942 standard; DNA; 19 BP.  
 XX AC AAA85942;  
 XX DT 04-DEC-2000 (first entry)  
 XX DE Cdc 25 hs ribozyme binding site #50.  
 XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
 XX OS Mammalia.  
 XX PN WO200032765-A2.  
 XX PD 08-JUN-2000.  
 XX PF 06-DEC-1999; 99WO-US028772.  
 XX

```
PR 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 100; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 924 CCAGGAGAAAAAACAAC 941
DB 18 CCAGGAGAAAAAACAAC 1
RESULT 295
AAA85941/C
ID AAA85941 standard; DNA; 19 BP.
XX
XX AAA85941;
XX
XX 04-DEC-2000 (first entry)
XX
XX Cdc 25 hs ribozyme binding site #49.
XX
XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX Mammalia.
XX
XX WO200032765-A2.
XX
XX 08-JUN-2000.
XX
XX
XX 06-DEC-1999; 99WO-US028772.
XX
XX 04-DEC-1998; 98US-0110954P.
XX (IMMU-) IMMUSOL INC.
XX
XX Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX PCNA and Cyclin B1.
XX
XX Disclosure; Page 100; 109pp; English.
XX
XX The present invention relates to a hairpin or hammerhead ribozyme,
XX designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
XX other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
XX Representative examples of ribozyme recognition sites are given in
XX AAA82415 to AAA86787. The ribozyme of the invention is useful for
XX inhibiting restenosis by introduction of the ribozyme into cells. The
XX ribozyme is resistant to endonuclease activity and hence is efficient in
XX restenosis treatment
XX
XX Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 924 CCAGGAGAAAAAACAAC 941
DB 19 CCAGGAGAAAAAACAAC 2
RESULT 296
AAH61103/C
ID AAH61103 standard; DNA; 19 BP.
XX
XX AAH61103;
XX
XX 10-SEP-2001 (first entry)
XX
XX Cdc25 hs ribozyme binding site SEQ ID NO:3527.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX recognition site; target; ribozyme binding site; eye disease; vulneryary;
XX proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
XX matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX antipsoziatic; dermatological; antiseborrheic; antidiabetic; virucide;
XX antisickling; ophthalmological; keratolytic; Gene therapy; viral wart;
XX atopic dermatitis; actinic keratosis; squamous cell carcinoma;
XX basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
XX sickle cell retinopathy; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200130362-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
XX (IMMU-) IMMUSOL INC.
XX
XX Robbins JM, Tritz R;
XX WPI; 2001-300427/31.
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
XX that cleave RNA encoding cytokines involved in inflammation, matrix
XX metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 328; 408pp; English.
XX
XX The present invention describes a method for treating a proliferative
XX skin or eye disease and scarring. The method involves administering a
XX ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX dependent kinase, growth factor or a reductase, or administering a
XX nucleic acid molecule (II) comprising a promoter operably linked to a
XX nucleic acid segment encoding (I). (I) can have antipsoziatic,
XX dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
XX ophthalmological, vulneryary, keratolytic and virucide activities, and
XX cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX in gene therapy. (I) and (II) are useful for treating proliferative skin
XX diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX also be used for treating proliferative eye diseases such as diabetic
```

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
 CC prematurity and retinal detachment, and for treating and preventing  
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
 CC scar. AAH57577 to AAH62099 represent sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 19 BP; 0 A; 3 C; 5 G; 11 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 924 CCAGGAGAAAAAAAC 941  
 |||||  
 Db 19 CCAGGAGAAAAAAAC 2  
 |||||  
 RESULT 297  
 AAH61104/C  
 ID AAH61104 standard; DNA; 19 BP.  
 XX  
 AC AAH61104;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Cdc25 hs ribozyme binding site SEQ ID NO:3528.  
 XX  
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;  
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytosolic;  
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;  
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;  
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;  
 KW sickle cell retinopathy; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200130362-A2.  
 XX  
 PD 03-MAY-2001.  
 XX  
 XX 26-OCT-2000; 2000WO-US029500.  
 XX  
 PR 26-OCT-1999; 99US-0161532P.  
 XX  
 XX (IMMU-) IMMUSOL INC.  
 PA  
 XX Robbins JM, Tritz R;  
 PI  
 XX WPI; 2001-300427/31.  
 DR  
 XX  
 PT Treating proliferative skin or eye diseases and scarring, using ribozymes  
 PT that cleave RNA encoding cytokines involved in inflammation, matrix  
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
 XX  
 PS Example 1; Page 328; 408pp; English.  
 XX  
 CC The present invention describes a method for treating a proliferative  
 CC skin or eye disease and scarring. The method involves administering a  
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
 CC dependent kinase, growth factor or a reductase, or administering a  
 CC nucleic acid molecule (II) comprising a promoter operably linked to a  
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,  
 CC dermatological, cytosolic, antiseborrheic, antidiabetic, antisickling,  
 CC ophthalmological, vulnery, keratolytic and virucide activities, and  
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
 CC also be used for treating proliferative eye diseases such as diabetic  
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
 CC prematurity and retinal detachment, and for treating and preventing  
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
 CC scar. AAH57577 to AAH62099 represent sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 924 CCAGGAGAAAAAAAC 941  
 |||||  
 Db 18 CCAGGAGAAAAAAAC 1  
 |||||  
 RESULT 298  
 ADQ60911  
 ID ADQ60911 standard; RNA; 19 BP.  
 XX  
 AC ADQ60911;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Anti-BMX siRNA related DNA sequence SEQ ID NO:613.  
 XX  
 KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;  
 KW RNA interference.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004045543-A2.  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 14-NOV-2003; 2003WO-US036787.  
 XX  
 PR 14-NOV-2002; 2002US-0426137P.  
 PR 10-SEP-2003; 2003US-0502050P.  
 XX  
 XX (DHAR-) DHARMA CON INC.  
 PA  
 XX Anastasia K, Angela R, Devin L, William M, Stephen S;  
 PI  
 XX WPI; 2004-420527/39.  
 DR  
 XX  
 XX Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases  
 XX by selecting a target gene and measuring the functionality of the  
 XX nucleotide sequences that are complementary to a stretch of nucleotides  
 XX of the target sequence.  
 PS  
 XX Example 12; SEQ ID NO 613; 199pp; English.  
 XX  
 CC The invention relates to a novel method for selecting siRNA (short  
 CC interfering RNA) comprising selecting an siRNA molecule of 19-25  
 CC nucleoside bases by selecting a target gene and measuring the  
 CC functionality of sequences of 19-25 nucleotides in length that are  
 CC substantially complementary to a stretch of nucleotides of the target  
 CC sequence, where the functionality is dependent upon non-target specific  
 CC criteria. Also claimed are methods for gene-silencing, developing an  
 CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved  
 CC functionality, selecting hyperfunctional siRNA, an siRNA molecule  
 CC effective at silencing Bcl-2, and a kit for gene silencing comprising the  
 CC siRNA. The siRNA molecule comprises a sequence substantially similar to a  
 CC sequence consisting of GGGAGUAGUGAUGAUGA; GAAGUACUCCUAGUAG;  
 CC GUACGACACCGGAGUA; AGAUAGUAGUAGUAGU; UGAAGACUCUGCUCAGUUU;  
 CC GUAGGCGCUCUGUUUGA; UCGGCGCUCUGUUUGA; GAGUAGUGAUGAUGA;  
 CC GGAGUAGUGAUGAUGA; and GAAGACUCUCUGCUCAGUUU. The siRNA molecule  
 CC comprises a sense strand and an anti-sense strand. The siRNA molecule  
 CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 bases

CC pairs. The kit comprises at least two siRNA, comprising a first optimised  
CC siRNA and a second optimised siRNA. The method is useful in selecting  
CC siRNA for generating a gene silencing reagent. The present sequence is  
CC used in the exemplification of the invention. The sequence is shown in  
CC the specification as DNA, but described as siRNA.

XX SQ Sequence 19 BP; 8 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 938 AAACAAACCTTCTTACT 955  
Db 1 AAACAAACCTTCTTACT 18

## RESULT 299

ADS90660  
ID ADS90660 standard; DNA; 19 BP.

XX AC ADS90660;

XX DT 18-NOV-2004 (first entry)

XX DE Oligonucleotide of the invention SEQ ID NO:1676.

XX KW ss; cell proliferative disorder; breast; methylation; cytostatic;  
XX KW gene therapy; single nucleotide polymorphism; SNP.

XX OS Unidentified.

XX PN WO2004035803-A2.

XX PD 29-APR-2004.

XX PF 01-OCT-2003; 2003WO-EP010881.

XX PR 01-OCT-2002; 2002DE-01045779.

XX PR 07-JAN-2003; 2003DE-01000096.

XX PR 17-APR-2003; 2003DE-01017955.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;  
XX PI Nimmrich I, Rajan T, Schmitt A, Schmitt M, Look MP, Marx A;

XX DR WPI; 2004-348469/32.

XX PT Predicting responsiveness of a subject with breast cell proliferative  
XX PT disorder, useful for treating or differentiating breast cell  
XX PT proliferative disorders comprises analyzing methylation pattern of a  
XX PT genomic DNA from the subject.

XX PS Disclosure; SEQ ID NO 1676; 104pp; English.

XX CC The invention relates to a novel method for predicting the responsiveness  
XX CC of a subject with a cell proliferative disorder of the breast tissues to  
XX CC a therapy comprising analysing the methylation pattern of a target  
XX CC nucleic acid by contacting at least one of the target nucleic acids in a  
XX CC biological sample obtained from the subject prior to or during treatment.  
XX CC The method of the invention has cytostatic activity, and may have a use  
XX CC in gene therapy. The set of oligonucleotides comprising at least two of  
XX CC the oligomers are useful for detecting the cytosine methylation state  
XX CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The  
XX CC methods, nucleic acid, oligonucleotide, and kit are useful for the  
XX CC treatment, characterization, classification and/or differentiation, of  
XX CC breast cell proliferative disorders. The method is also useful for  
XX CC predicting the responsiveness of a subject with a cell proliferative  
XX CC disorder of the breast tissues to a therapy. The present sequence is used  
XX CC in the exemplification of the invention.

XX SQ Sequence 19 BP; 5 A; 0 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTTCCTTTTAAAGGAA 2762  
Db 1 TTTTTCCTTTTAAAGGAA 18

## RESULT 300

AAX32003  
ID AAX32003 standard; DNA; 20 BP.

XX AC AAX32003;

XX DT 14-JUN-1999 (first entry)

XX DE MSH2 gene specific primer.

XX KW Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;  
XX KW CPTN; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;  
XX KW Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;  
XX KW colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;  
XX KW BAP1 gene; PCR primer; ss.

XX OS Synthetic.

XX PN WO9906598-A2.

XX PD 11-FEB-1999.

XX PF 04-AUG-1998; 98WO-US016574.

XX PR 04-AUG-1997; 97US-00905772.

XX PR 22-MAY-1998; 98US-00084471.

XX PA (ONCO-) ONCORMED INC.

XX PI Murphy PD;

XX DR WPI; 1999-153820/13.

XX PT Determining common functional alleles in a population - useful in the  
XX PT diagnosis of disease associated with allelic heterogeneity.

XX PS Example 1; Page 24; 78pp; English.

XX CC The invention relates to methods of determining a functional allele  
XX CC profile of a gene in a population. Functional allele profiles comprise  
XX CC the commonly occurring alleles in a population, and the relative  
XX CC frequencies at which such alleles of a given gene occur. The methods are  
XX CC used to identify and determine the frequency of the functional alleles of  
XX CC genes which display extensive allelic heterogeneity, particularly those  
XX CC implicated in disease or conditions, such as the BRCA1 gene associated  
XX CC with breast cancer, CPTN associated with cystic fibrosis, dystrophin  
XX CC associated with Duchenne muscular dystrophy and Becker muscular  
XX CC dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can  
XX CC also be employed for diseases where allelic and genetic heterogeneity  
XX CC exist, such as breast cancer, neurofibromatosis, and hereditary non-  
XX CC polyposis colorectal cancer. Identification of functional alleles is  
XX CC necessary for identification of mutations which may be implicated in the  
XX CC disease. Sequences AAX32001-172 represent primers for determining the  
XX CC functional allele profiles of various genes. The primers are specific for  
XX CC genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene  
XX CC

SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2743 TCTTTTTCCTTTTAAAGG 2760



11-MAR-2004 (first entry)

Human talin phosphorothioate antisense oligonucleotide, SEQ ID NO:10.

Human; talin; cellular adhesion; muscle strength; cardiac function; cardiomyocyte; platelet; prostate; androgen downregulation; prostate cancer; talin-related disorder; cellular adhesion-related disorder; expression inhibition; antisense therapy; phosphorothioate; antisense oligonucleotide; ss.

Homo sapiens.

Key Location/Qualifiers  
modified\_base 1..20  
/\*tag= a  
/mod\_base  
/note= "This oligonucleotide has a phosphorothioate backbone and 2'-methoxyethyl (2'-MOR) wings at the 5' and 3' ends, which are 5 nucleotides in length. Also all cytosine nucleotides are 5-methylcytosines"

WO200268446-A1.

06-SEP-2002.

30-OCT-2001; 2001WO-US048435.

22-FEB-2001; 2001US-00791942.

(ISIS-) ISIS PHARM INC.  
(BOEH) BOEHRINGER INGELHEIM PHARM INC.

Bennett CF, Rothlein R, Kishimoto TK, Cowsett LM;  
WPI; 2002-691651/74.

New antisense oligonucleotides targeted to nucleic acid molecules encoding human Talin, useful for inhibiting the expression of human Talin and for treating a human having a disease or condition associated with Talin.

Example 15; SEQ ID NO 10; 114pp; English.

Sequences ADG90460-ADG90539 represent phosphorothioate targeted to the human talin gene, which inhibit its expression. The antisense were designed to target different regions of human talin RNA, and were analysed for their effect on talin expression by quantitative real-time PCR. Talin is a cytoplasmic protein which links cytoskeletal proteins such as actin, myosin and vinculin to integrins, thereby linking the extracellular matrix to other cells. It is thought to be involved in the regulation of cellular adhesion and cell morphology. Talin is highly expressed in platelets, and may play a role in platelet adhesion as its subcellular distribution differs between resting non-adhesive platelets and activated adhesive platelets. It could also play a major role in determining muscle strength and cardiac function as it has been found to participate in the transmission of contractile force to the extracellular matrix in cardiomyocytes, and exhibits mechanical loading-dependent expression at myotendinous junctions. The expression of talin is downregulated by androgens in prostate tissues, a phenomenon known to contribute to the development of prostate cancer. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of talin-related disorders, such as those related to cellular adhesion. The present sequence represents a human c-Ha-ras phosphorothioate antisense oligonucleotide used as a positive control in determining optimal oligonucleotide concentration for a particular cell line.

Sequence 20 BP; 2 A; 5 C; 3 G; 10 T; 0 U; 0 Other;  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3393 TCCTTGTCTTGGTATAT 3410

||||| |||||||

2 TCCTTGTCTTGGTATAT 19

Db

RESULT 304  
ADA45244

ID ADA45244 standard; DNA; 20 BP.

XX  
AC ADA45244;

XX  
DT 20-NOV-2003 (first entry)

XX  
DE Human MSH2 gene PCR primer #3.

XX  
KW Functional allele profile; genetic inheritance; haplotype; population; disease; pharmacogenetic application; selective pressure; human; MSH2; MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; PCR; primer; ss.

XX  
OS Homo sapiens.

XX  
PN US2003096236-A1.

XX  
PD 22-MAY-2003.

XX  
PF 08-AUG-2001; 2001US-00923327.

XX  
PR 12-FEB-1996; 96US-00598591.

XX  
PR 12-FEB-1997; 97US-00798691.

XX  
PR 04-AUG-1997; 97US-00905772.

XX  
PR 22-MAY-1998; 98US-00084471.

XX  
PR 04-AUG-1998; 98US-00129134.

XX  
PR 14-MAR-2000; 2000US-00524794.

XX  
PA (ONCO-) ONCORMED INC.

XX  
PI Murphy PD;

XX  
DR WPI; 2003-576875/54.

XX  
PT Determining a functional allele profile of a gene in a population by identifying the nucleotide sequence of a gene of genomic DNA from each of the individuals with a family history of functional alleles of the gene of interest.

XX  
PS Example 1; Page 9; 28pp; English.

XX  
CC The present invention relates to a method for determining a functional allele profile of a gene in a population. The method comprises identifying the nucleotide sequence of a gene of interest out of genomic DNA from each of a population of individuals identified as having a family history which indicates inheritance of functional alleles of the gene of interest, and rank ordering the frequency of occurrence of each haplotype, where the identity of the alleles containing each haplotype and the determination of their relative frequencies constitutes the functional allele profile of the gene of interest in the population. The method is useful for determining functional allele profiles which are useful in the treatment and diagnosis of diseases, for genetic and pharmacogenetic applications, and for evaluating the degree to which the gene(s) are under selective pressure. The present sequence represents a PCR primer used in the method of the invention.

XX  
SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2743 TCCTTTTAAAAA 2760  
|||||

Db 1 TTTTAAAAA 18

RESULT 305



```

ABZ86070/c
ID ABZ86070 standard; DNA; 20 BP.
XX
AC ABZ86070;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PY Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Claim 15; SEQ ID NO 1312; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 426 GCAGCAGCGCGGCTGCA 443
DB 18 GCAGCAGCGCGGCGAGCA 1

ABZ89593/c
ID ABZ89593 standard; DNA; 20 BP.
XX
AC ABZ89593;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PY Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Disclosure; SEQ ID NO 4835; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 12 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2745 TTTTITTTTTTAGGAAA 2762
DB 18 TTTTITTTTTTAGGAAA 1

RESULT 307

```

ABZ89178  
ID ABZ89178 standard; DNA; 20 BP.  
XX  
AC ABZ89178;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200285308-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013135.  
XX  
XX 24-APR-2001; 2001US-0286137P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
XX Disclosure; SEQ ID NO 4420; 872bp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytosstatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 13 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. NO. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTTAAAAA 2588  
DB 2 TGTTTTAAAAA 19

RESULT 308

ABZ97995/c  
ID ABZ97995 standard; DNA; 20 BP.  
XX  
AC ABZ97995;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human RANTES oligonucleotide sequence.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200285308-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013135.  
XX  
XX 24-APR-2001; 2001US-0286137P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
XX Disclosure; SEQ ID NO 13237; 872bp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytosstatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 6 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. NO. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2670 CAACACACACACAAAA 2687  
DB 20 CAACACACACACAAAA 3

RESULT 309

ABD25408  
ID ABD25408 standard; DNA; 20 BP.  
AC ABD25408;  
XX  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX AI122807-derived oligonucleotide SEQ ID 4420.  
XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX  
XX Homo sapiens.  
OS  
XX WO200285309-A2.  
PN  
XX  
XX 31-OCT-2002.  
PD  
XX  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-093058/08.  
DR  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 4420; 763pp; English.  
PS  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytosstatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX

SQ Sequence 20 BP; 13 A; 0 C; 1 G; 6 T; 0 U; 0 Other;  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2571 TGTATAAAAAAAAAAAAAA 2588  
Db 2 TGTATAAAAAAAAAAAAAA 19  
RESULT 310  
ABD31026/c  
ID ABD31026 standard; DNA; 20 BP.  
XX  
AC ABD31026;  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
XX Human RANTES-derived oligonucleotide SEQ ID 13237.  
DE  
XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ss; primer.  
XX  
XX Homo sapiens.  
OS  
XX WO200285309-A2.  
PN  
XX  
XX 31-OCT-2002.  
PD  
XX  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-093058/08.  
DR  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 13237; 763pp; English.  
PS  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytosstatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX

CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 0 A; 1 C; 6 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2670 CAACAACACCAACAAAA 2687  
 Db 20 CAACAACACCAACAAAA 3  
 ||||| ||||| |||||

RESULT 311  
 ABD22300/C  
 ID ABD22300 standard; DNA; 20 BP.  
 XX  
 AC ABD22300;  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human stanniocalcin-derived oligo SEQ ID 1312.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.

XX  
 XX WO200285309-A2.  
 XX  
 XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 XX Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 1312; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 426 GCAGCAGCGCGGCTGCA 443  
 Db 18 GCAGCAGCGCGGCGAGCA 1  
 ||||| ||||| |||||

RESULT 312  
 ABD25823/C  
 ID ABD25823 standard; DNA; 20 BP.

XX ABD25823;

XX 29-JUL-2004 (first entry)

XX AI085559-derived oligonucleotide SEQ ID 4835.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 XX Miller S, Tang L, Shahabuddin S;  
 XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and  
 XX bronchodilating agent.  
 PS Claim 15; SEQ ID NO 4835; 763pp; English.  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

XX SQ Sequence 20 BP; 12 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2745 TTTT TTTT TTTT TTTT AAGGAAA 2762  
 DB 18 TTTT TTTT TTTT TTTT AAGGAAA 1

RESULT 313  
 ADI80176  
 ID ADI80176 standard; DNA; 20 BP.  
 XX AC ADI80176;  
 XX DT 22-APR-2004 (first entry)  
 XX DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 177.  
 XX antisease; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 XX cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 XX immune; ss; human.  
 XX OS Homo sapiens.  
 XX PN US2004006030-A1.  
 XX PD 08-JAN-2004.  
 XX PF 02-JUL-2002; 2002US-00189267.  
 XX PR 02-JUL-2002; 2002US-00189267.  
 XX PA (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM, Dobie KW;  
 XX WPI; 2004-081742/08.  
 XX New compounds, particularly antisense oligonucleotides targeted to a  
 PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
 PT neurodegenerative disorder, or a disease involving hyperactivation of  
 PT immune response.  
 XX Example 16; SEQ ID NO 177; 135pp; English.  
 XX The invention relates to a novel antisense compound of 8-80 nucleobases  
 CC in length targeted to, and which specifically hybridizes with, a nucleic  
 CC acid molecule encoding transforming growth factor (TGF)-beta 2, and  
 CC inhibits the expression of TGF-beta 2. The invention further relates to:  
 CC a compound 8-80 nucleobases in length that specifically hybridizes with  
 CC at least an 8-nucleobase portion of an active site on a nucleic acid  
 CC molecule encoding TGF-beta 2; a composition comprising the compound and a  
 CC carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
 CC tissues by contacting the cells or tissues with the compound so that  
 CC expression of TGF-beta 2 is inhibited; treating an animal having a  
 CC disease or condition associated with TGF-beta 2 by administering to the  
 CC animal a therapeutic or prophylactic amount of the compound so that  
 CC expression of TGF-beta 2 is inhibited; and screening an antisense  
 CC compound. The antisense compound has cytostatic, neurotropic,  
 CC neuroprotective, and immunosuppressive activities. The compound,  
 CC composition and methods are useful for treating a disease or condition  
 CC associated with TGF-beta 2, such as a hyperproliferative disorder e.g.  
 CC cancer, a neurodegenerative disorder, or a disease or condition involving  
 CC hyperactivation of an immune response. This polynucleotide sequence  
 CC represents a preferred target DNA region of TGF-beta 2 of the invention.  
 XX SQ Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1683 AACCCCAAAAGCCAGAGTG 1700  
 DB 2 AACCCCAAAAGCCAGAGTG 19

RESULT 314  
 ADI80026/c  
 ID ADI80026 standard; DNA; 20 BP.  
 XX AC ADI80026;  
 XX DT 22-APR-2004 (first entry)  
 XX DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 27.  
 XX antisease; transforming growth factor; TGF; beta 2; TGF-beta 2;  
 XX cytostatic; neurotropic; neuroprotective; immunosuppressive;  
 XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
 XX immune; ss; human.  
 XX OS Homo sapiens.  
 XX PN US2004006030-A1.  
 XX PD 08-JAN-2004.  
 XX PF 02-JUL-2002; 2002US-00189267.  
 XX PR 02-JUL-2002; 2002US-00189267.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM, Dobie KW;  
 XX

```

DR  WPI; 2004-081742/08.
XX
PT  New compounds, particularly antisense oligonucleotides targeted to a
PT  nucleic acid encoding TGF-beta 2, useful for treating cancer, a
PT  neurodegenerative disorder, or a disease involving hyperactivation of
PT  immune response.
XX
PS  Example 15; SEQ ID NO 27; 135pp; English.
XX
CC  The invention relates to a novel antisense compound of 8-80 nucleobases
CC  in length targeted to, and which specifically hybridizes with, a nucleic
CC  acid molecule encoding transforming growth factor (TGF)-beta 2, and
CC  inhibits the expression of TGF-beta 2. The invention further relates to:
CC  a compound 8-80 nucleobases in length that specifically hybridizes with
CC  at least an 8-nucleobase portion of an active site on a nucleic acid
CC  molecule encoding TGF-beta 2; a composition comprising the compound and a
CC  carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or
CC  tissues by contacting the cells or tissues with the compound so that
CC  expression of TGF-beta 2 is inhibited; treating an animal having a
CC  disease or condition associated with TGF-beta 2 by administering to the
CC  animal a therapeutic or prophylactic amount of the compound so that
CC  expression of TGF-beta 2 is inhibited; and screening an antisense
CC  compound. The antisense compound has cytostatic, neurotropic,
CC  neuroprotective, and immunosuppressive activities. The compound,
CC  composition and methods are useful for treating a disease or condition
CC  associated with TGF-beta 2, such as a hyperproliferative disorder e.g.
CC  cancer, a neurodegenerative disorder, or a disease or condition involving
CC  hyperactivation of an immune response. This polynucleotide sequence
CC  represents an antisense oligonucleotide of the invention.
XX
SQ  Sequence 20 BP; 1 A; 5 C; 6 G; 8 T; 0 U; 0 Other;.
    Query Match          0.4%; Score 16.4; DB 1; Length 20;
    Best Local Similarity 94.4%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
    Matches 17; Conservative 0; Mismatches 1;
QY  1683 AACCCCAAAGCCAGAGTG 1700
    ||||| ||||| ||||| |||||
DB  19 AACCCCAAAGCCAGAGTG 2
RESULT 315
ADJ59860/C
ID  ADJ59860 standard; DNA; 20 BP.
XX  AC ADJ59860;
XX  AC ADJ59860;
DT  06-MAY-2004 (first entry)
XX  Oligonucleotide associated to RANTES #109.
XX  interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW  airway inflammation; allergy; asthma; impeded respiration;
KW  cystic fibrosis; acute respiratory distress syndrome;
KW  pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW  ss.
XX  Homo sapiens.
XX  OS
XX  WO2004011613-A2.
XX  PN
XX  PD 05-FEB-2004.
XX  XX
XX  25-JUL-2003; 2003WO-US023509.
XX  XX
XX  29-JUL-2002; 2002US-0399076P.
XX  XX
XX  (EPIG-) EPIGENESIS PHARM INC.
XX  PA
XX  Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI  Shahabuddin S, Lu H, Cong H;
XX  WPI; 2004-203534/19.
XX  DR

```

CC The present invention relates to an antisense compound targeted to a  
CC nucleic acid molecule encoding Nav1.3, where the antisense compound  
CC specifically hybridizes with and inhibits the expression of Nav1.3. The  
CC compound and composition are useful for treating a disease or condition  
CC associated with Nav1.3, e.g. pain including but not limited to  
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
CC pain from burns, migraine headache, cluster headache, mild-to-moderate  
CC headache, seizure disorder such as childhood seizure disorder, including  
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present  
CC sequence represents a chimeric phosphorothioate oligonucleotide with  
CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of  
CC human Nav1.3 expression, the oligonucleotides are designed to target  
CC different regions of the human Nav1.3 RNA.  
XX  
SQ Sequence 20 BP; 12 A; 2 C; 1 G; 5 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2801 TGAATAAAAAAAAAAACATC 2818  
Db 2 TGAATAAAAAAAAAAACATC 19  
  
RESULT 317  
ADK80967  
ID ADK80967 standard; DNA; 20 BP.  
AC ADK80967;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #8301.  
XX  
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;  
KW diabetic neuropathy; arthritic pain; migraine headache;  
KW infantile epilepsy; ataxia; ss.  
XX  
OS Synthetic.  
XX  
PN WO2004016754-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 14-AUG-2003; 2003WO-US025465.  
XX  
PR 14-AUG-2002; 2002US-0403416P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX  
PI Robert's SL;  
XX  
XX WPI; 2004-203785/19.  
DR  
PT New antisense compound targeted to a nucleic acid molecule encoding  
PT Nav1.3, useful for treating a disease or condition associated  
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure  
PT disorder, or ataxia.  
XX  
XX Claim 4; SEQ ID NO 8301; 417pp; English.  
XX  
XX The present invention relates to an antisense compound targeted to a  
XX nucleic acid molecule encoding Nav1.3, where the antisense compound  
XX specifically hybridizes with and inhibits the expression of Nav1.3. The  
XX compound and composition are useful for treating a disease or condition  
XX associated with Nav1.3, e.g. pain including but not limited to  
XX neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,  
XX diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,  
XX pain from burns, migraine headache, cluster headache, mild-to-moderate  
XX headache; seizure disorder such as childhood seizure disorder, including  
XX but not limited to neonatal or infantile epilepsy; or ataxia. The present

CC sequence represents a chimeric phosphorothioate oligonucleotide with  
CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of  
CC human Nav1.3 expression, the oligonucleotides are designed to target  
CC different regions of the human Nav1.3 RNA.  
XX  
SQ Sequence 20 BP; 12 A; 2 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2801 TGAATAAAAAAAAAAACATC 2818  
Db 3 TGAATAAAAAAAAAAACATC 20  
  
RESULT 318  
ADL58169/C  
ID ADL58169 standard; DNA; 20 BP.  
XX  
AC ADL58169;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human ESM-1 antisense oligonucleotide seqid 418.  
XX  
KW cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;  
KW gene therapy; endothelial specific molecule-1; ESM-1;  
KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
KW angiogenic disorder; immunological disorder; cardiovascular disorder;  
KW neurological disorder; antisense technology; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= phosphorothioate backbone. All cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
XX  
PN WO2004021978-A2.  
XX  
PD 18-MAR-2004.  
XX  
PF 19-AUG-2003; 2003WO-US025833.  
XX  
PR 19-AUG-2002; 2002US-0404495P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX  
PI Weinstein EJ, Griggs DW;  
XX  
XX WPI; 2004-248358/23.  
DR  
PT New antisense compound, having a sequence targeted to a nucleic acid  
PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
PT composition for treating e.g., diabetes, cancer or cardiovascular  
PT disorder.  
XX  
XX Claim 3; SEQ ID NO 418; 555pp; English.  
XX  
XX The invention describes a new antisense compound, having a sequence  
XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
XX specific molecule-1 (ESM-1), that specifically hybridizes with the



CC nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 CC treating an animal having a disease or condition associated with ESM-1.  
 CC The compound is useful for preparing a composition for treating diabetes,  
 CC cancer, ischaemia or reperfusion injury, or angiogenic, immunological,  
 CC cardiovascular or neurological disorder. This sequence represents an  
 CC antisense oligonucleotide that can be used to modulate expression of  
 CC endothelial specific molecule-1 (ESM-1).  
 XX  
 SQ Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 362 TGGCGCGCTGGAGCAAGA 379  
 Db 18 TGGCGCGCTGGAGCAATA 1  
 RESULT 319  
 ADL58390/c  
 ID ADL58390 standard; DNA; 20 BP.  
 XX AC ADL58390;  
 XX AC  
 DT 03-JUN-2004 (first entry)  
 DE Human ESM-1 antisense oligonucleotide seqid 639.  
 XX  
 KW cytostatic; antidiabetic; immunomodulator; cardiact; neuroprotective;  
 KW gene therapy; endothelial specific molecule-1; ESM-1;  
 KW ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
 KW angiogenic disorder; immunological disorder; cardiovascular disorder;  
 KW neurological disorder; antisense technology; ss.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= Phosphorothioate backbone. All cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 XX  
 PN WO2004021978-A2.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 19-AUG-2003; 2003WO-US025833.  
 XX  
 PR 19-AUG-2002; 2002US-0404495P.  
 XX  
 XX (PHAA ) PHARMACIA CORP.  
 XX Weinstein EJ, Griggs DW;  
 PI WPI; 2004-248358/23.  
 XX  
 DR New antisense compound, having a sequence targeted to a nucleic acid  
 PT encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 PT composition for treating e.g., diabetes, cancer or cardiovascular  
 PT disorder.  
 XX  
 XX Claim 3; SEQ ID NO 639; 555pp; English.

XX  
 CC The invention describes a new antisense compound, having a sequence  
 CC comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 CC specific molecule-1 (ESM-1), that specifically hybridises with the  
 CC nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 CC composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 CC treating an animal having a disease or condition associated with ESM-1.  
 CC The compound is useful for preparing a composition for treating diabetes,  
 CC cancer, ischaemia or reperfusion injury, or angiogenic, immunological,  
 CC cardiovascular or neurological disorder. This sequence represents an  
 CC antisense oligonucleotide that can be used to modulate expression of  
 CC endothelial specific molecule-1 (ESM-1).  
 XX  
 SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16.4; DB 1; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 2e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 363 GGCGCGCTGGAGCAAGAA 380  
 Db 20 GGCGCGCTGGAGCAATAA 3  
 RESULT 320  
 ADO45350/c  
 ID ADO45350 standard; DNA; 20 BP.  
 XX AC ADO45350;  
 XX AC  
 DT 15-JUL-2004 (first entry)  
 DE Human oligonucleotide #716.  
 XX  
 KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
 KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; tryptase a;  
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;  
 KW asthma; lung allergy; inflammation; inflammatory disease;  
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
 KW acute respiratory distress syndrome; pulmonary hypertension;  
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.  
 XX Homo sapiens.  
 OS  
 XX US2004049022-A1.  
 PN  
 XX 11-MAR-2004.  
 PD  
 XX 25-JUL-2003; 2003US-00627930.  
 PF  
 XX 23-APR-2002; 2002WO-US013135.  
 PR  
 XX 23-APR-2002; 2002WO-US013143.  
 XX  
 XX (NYCE/) NYCE J W.  
 XX (SAND/) SANDRASAGRA A.  
 XX (TANG/) TANG L.  
 XX (AGUI/) AGUILAR D.  
 XX (MILL/) MILLER S.  
 XX (SHAH/) SHAHABUDDIN S.  
 XX (LUHH/) LU H.  
 XX (CONG/) CONG H.  
 XX  
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;  
 PI Shahabuddin S, Lu H, Cong H;  
 PI WPI; 2004-293804/27.  
 DR Novel single or multiple target oligonucleotide anti-sense to e.g.  
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,  
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
 PT asthma.



XX  
PS Claim 2; SEQ ID NO 716; 174pp; English.  
XX  
CC The invention relates to oligonucleotides anti-sense to an initiation  
CC codon, coding region, 5' or 3' intron-exon junction, intron or region  
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
CC triptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
CC also relates to a method of screening a candidate compound that binds to  
CC one or more nucleic acid target(s) or expressed product(s), for the  
CC prevention and/or treatment of a respiratory or lung disease. The  
CC oligonucleotides are useful for reducing or inhibiting expression of a  
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, triptase a,  
CC triptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
CC useful for preventing or treating a respiratory or lung disease. The  
CC respiratory or lung disease is associated with hyper-responsiveness to  
CC receptor(s), and/or asthma and/or lung allergies associated with  
CC inflammation or an inflammatory disease. The respiratory or lung disease  
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,  
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
CC hypertension, lung inflammation, bronchitis, airway obstruction or  
CC bronchoconstriction. This sequence represents an oligonucleotide of the  
CC invention.  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 6 G; 13 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2670 CAACACACACACACAAAA 2687  
DB 20 CAACACACACACACAAAA 3  
  
RESULT 321  
ADP85665  
ID ADP85665 standard; DNA; 20 BP.  
XX  
AC ADP85665;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Human Talin antisense oligonucleotide, ISIS #109109.  
XX  
KW Antisense; Talin; muscular disorder; haematologic disorder;  
KW cardiac disorder; hyperproliferative disorder; cancer; human;  
KW phosphorothioate; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone where all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 16..20  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX  
PN US2004110705-A1.  
XX

PD 10-JUN-2004.  
XX  
PF 11-SEP-2003; 2003US-00415463.  
XX  
PR 30-OCT-2000; 2000US-00702251.  
PR 30-OCT-2001; 2001WO-US047585.  
XX  
PA (BENN/) BENNETT C F.  
PA (COWS/) COWSERT L M.  
XX  
PI Bennett CF, Cowsert LM;  
XX WPI; 2004-440384/41.  
DR  
XX New compounds, particularly antisense oligonucleotides targeted to a  
XX nucleic acid encoding talin, useful for treating muscular, cardiac,  
XX hematologic, or hyperproliferative disorders.  
PT  
XX Example 15; SEQ ID NO 10; 48pp; English.  
PS  
XX The invention relates to novel antisense compounds targeted to a nucleic  
XX acid molecule encoding human Talin to and inhibit its expression. The  
XX invention is useful for treating a disease or condition associated with  
XX talin such as a disease or condition e.g. muscular, haematologic, cardiac  
XX or hyperproliferative disorder such as cancer. The present sequence is an  
XX antisense oligonucleotide targeted to human Talin DNA.  
XX  
SQ Sequence 20 BP; 2 A; 5 C; 3 G; 10 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3393 TCCTTGTCTGTGTATAT 3410  
DB 2 TCCTTGTCTGTGTATAT 19  
  
RESULT 322  
ADP69475/C  
ID ADP69475 standard; DNA; 20 BP.  
XX  
AC ADP69475;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human mitONEET-specific antisense oligonucleotide #369.  
XX  
KW human; antisense oligonucleotide; mitochondrial membrane;  
KW insulin sensitising antidiabetic thiazolidinediones; mitONEET; diabetes;  
KW immunological disorder; cardiovascular disorder; including hypertension;  
KW neurological disorders; ischaemia; reperfusion; ss.  
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.  
XX  
OS Homo sapiens.  
XX  
PN WO2004053060-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 25-NOV-2003; 2003WO-US037621.  
XX  
PR 06-DEC-2002; 2002US-0431529P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX Colca JR;  
XX WPI; 2004-468836/44.  
DR  
XX New antisense oligonucleotides encoding mitONEET, useful for modulating  
XX mitONEET expression or for treating diseases associated with mitONEET,  
XX e.g. diabetes, immunological disorders or cardiovascular disorders.  
PT

XX Claim 4; SEQ ID NO 369; 226pp; English.  
PS The invention comprises antisense oligonucleotides that are targeted to  
CC the nucleic acids encoding a family of human proteins from mitochondrial  
CC membranes, which bind insulin sensitising, antidiabetic  
CC thiazolidinediones (referred to as: mitONEET). The antisense  
CC oligonucleotides of the invention are useful for modulating mitONEET  
CC expression and for treating diseases or conditions associated with  
CC mitONEET, such as: diabetes, immunological disorders, cardiovascular  
CC disorders including hypertension, neurological disorders, and  
CC ischaemia/reperfusion injuries. The present DNA sequence represents a  
CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The  
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a  
CC phosphorothioate backbone.  
SQ Sequence 20 BP; 5 A; 1 C; 1 G; 13 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2571 TGTTTAAAAA 2588  
DB 19 TGTTTAAACAAAAA 2  
  
RESULT 323  
ADP69581/c  
ID ADP69581 standard; DNA; 20 BP.  
XX  
AC ADP69581;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human mitONEET-specific antisense oligonucleotide #475.  
XX  
KW human; antisense oligonucleotide; mitochondrial membrane;  
KW insulin sensitising antidiabetic thiazolidinediones; mitONEET; diabetes;  
KW immunological disorder; cardiovascular disorder; including hypertension;  
KW neurological disorders; ischaemia; reperfusion; ss;  
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.  
XX  
OS Homo sapiens.  
XX  
PN WO2004053060-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 25-NOV-2003; 2003WO-US037621.  
XX  
PR 06-DEC-2002; 2002US-0431529P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX  
PI Colca JR;  
XX  
DR WPI; 2004-468836/44.  
XX  
PT New antisense oligonucleotides encoding mitONEET, useful for modulating  
PT mitONEET expression or for treating diseases associated with mitONEET,  
PT e.g. diabetes, immunological disorders or cardiovascular disorders.  
XX  
PS Claim 4; SEQ ID NO 475; 226pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are targeted to  
CC the nucleic acids encoding a family of human proteins from mitochondrial  
CC membranes, which bind insulin sensitising, antidiabetic  
CC thiazolidinediones (referred to as: mitONEET). The antisense  
CC oligonucleotides of the invention are useful for modulating mitONEET  
CC expression and for treating diseases or conditions associated with  
CC mitONEET, such as: diabetes, immunological disorders, cardiovascular  
CC disorders including hypertension, neurological disorders, and

CC ischaemia/reperfusion injuries. The present DNA sequence represents a  
CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The  
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a  
CC phosphorothioate backbone.  
SQ Sequence 20 BP; 6 A; 1 C; 1 G; 12 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2571 TGTTTAAAAA 2588  
DB 18 TGTTTAAACAAAAA 1  
  
RESULT 324  
ADP69398/c  
ID ADP69398 standard; DNA; 20 BP.  
XX  
AC ADP69398;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Human mitONEET-specific antisense oligonucleotide #292.  
XX  
KW human; antisense oligonucleotide; mitochondrial membrane;  
KW insulin sensitising antidiabetic thiazolidinediones; mitONEET; diabetes;  
KW immunological disorder; cardiovascular disorder; including hypertension;  
KW neurological disorders; ischaemia; reperfusion; ss;  
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.  
XX  
OS Homo sapiens.  
XX  
PN WO2004053060-A2.  
XX  
PD 24-JUN-2004.  
XX  
PF 25-NOV-2003; 2003WO-US037621.  
XX  
PR 06-DEC-2002; 2002US-0431529P.  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX  
PI Colca JR;  
XX  
DR WPI; 2004-468836/44.  
XX  
PT New antisense oligonucleotides encoding mitONEET, useful for modulating  
PT mitONEET expression or for treating diseases associated with mitONEET,  
PT e.g. diabetes, immunological disorders or cardiovascular disorders.  
XX  
PS Claim 4; SEQ ID NO 292; 226pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are targeted to  
CC the nucleic acids encoding a family of human proteins from mitochondrial  
CC membranes, which bind insulin sensitising, antidiabetic  
CC thiazolidinediones (referred to as: mitONEET). The antisense  
CC oligonucleotides of the invention are useful for modulating mitONEET  
CC expression and for treating diseases or conditions associated with  
CC mitONEET, such as: diabetes, immunological disorders, cardiovascular  
CC disorders including hypertension, neurological disorders, and  
CC ischaemia/reperfusion injuries. The present DNA sequence represents a  
CC mitONEET-specific antisense oligonucleotide of the invention. NOTE: The  
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a  
CC phosphorothioate backbone.  
SQ Sequence 20 BP; 4 A; 1 C; 1 G; 14 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 2571 TGTTTAAAAA 2588
Db 20 TGTTTAAACAAAAA 3

RESULT 325
AAQ78464/c
ID AAQ78464 standard; DNA; 16 BP.
XX
AC AAQ78464;
XX
DT 25-MAR-2003 (revised)
DT 27-JUN-1995 (first entry)
XX
DE TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO9425588-A2.
XX
PD 10-NOV-1994.
XX
PF 29-APR-1994; 94WO-EP001362.
PR 30-APR-1993; 93EP-00107089.
PR 13-MAY-1993; 93EP-00107849.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI Bogdahn U;
XX
DR WPI; 1994-358266/44.
XX
PT New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
PT treating immunosuppression, tumours, etc.
XX
PS Claim 6; Page 56; 74pp; English.
XX
CC The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 16 BP; 5 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2153 TGTGCAGGATAATTC 2168
Db 16 TGTGCAGGATAATTC 1

RESULT 326
AAQ78456/c
ID AAQ78456 standard; DNA; 16 BP.
XX
Qy 2571 TGTTTAAAAA 2588
Db 20 TGTTTAAACAAAAA 3

RESULT 325
AAQ78464/c
ID AAQ78464 standard; DNA; 16 BP.
XX
AC AAQ78464;
XX
DT 25-MAR-2003 (revised)
DT 27-JUN-1995 (first entry)
XX
DE TGF-beta gene phosphorothioate antisense oligonucleotide.
XX
KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO9425588-A2.
XX
PD 10-NOV-1994.
XX
PF 29-APR-1994; 94WO-EP001362.
PR 30-APR-1993; 93EP-00107089.
PR 13-MAY-1993; 93EP-00107849.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI Bogdahn U;
XX
DR WPI; 1994-358266/44.
XX
PT New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
PT treating immunosuppression, tumours, etc.
XX
PS Claim 6; Page 56; 74pp; English.
XX
CC The antisense oligonucleotides are useful in the treatment of tumours in
CC which expression of TGF-beta is of relevance for pathogenicity and/or
CC inhibition of pathological angiogenesis. They are used especially for the
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
CC of skin carcinogenesis, and treatment of oesophageal and gastric
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 16 BP; 5 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2153 TGTGCAGGATAATTC 2168
Db 16 TGTGCAGGATAATTC 1

RESULT 326
AAQ78456/c
ID AAQ78456 standard; DNA; 16 BP.
XX

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KW presclempsia; pregnancy; choriocarcinoma; phosphorothioate; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9840747-A1.  
 XX 17-SEP-1998.  
 PD 05-MAR-1998; 98WO-CA000180.  
 PF 07-MAR-1997; 97US-0039919P.  
 XX (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
 XX Caniggia I, Post M, Lye S;  
 XX WPI; 1998-520837/44.  
 DR Regulation of trophoblast invasion - by, e.g. transforming growth factor-beta3 inhibitor, useful for detecting or treating preeclampsia in pregnant women.  
 XX Example 4; Page 22; 59pp; English.  
 XX AAV63225-26 represent phosphorothioate oligonucleotides directed against nucleic acid encoding human transforming growth factor-beta 2 (TGF-beta2). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclampsia in pregnant women or choriocarcinomas  
 XX Sequence 16 BP; 5 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1217 CATGCACACTACTGTGTG 1232  
 Db 16 CATGCACACTACTGTGTG 1  
 RESULT 328  
 AAV63226  
 ID AAV63226 standard; DNA; 16 BP.  
 XX AAV63226;  
 XX 14-JAN-1999 (first entry)  
 DE Phosphorothioate oligonucleotide directed against TGF-beta2.  
 XX Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;  
 KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;  
 KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;  
 KW preeclampsia; pregnancy; choriocarcinoma; phosphorothioate; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9840747-A1.  
 XX 17-SEP-1998.  
 PD 05-MAR-1998; 98WO-CA000180.  
 PF 07-MAR-1997; 97US-0039919P.  
 XX (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
 XX Caniggia I, Post M, Lye S;  
 XX WPI; 1998-520837/44.  
 DR Regulation of trophoblast invasion - by, e.g. transforming growth factor-beta3 inhibitor, useful for detecting or treating preeclampsia in pregnant women.  
 XX Example 4; Page 22; 59pp; English.  
 XX AAV63225-26 represent phosphorothioate oligonucleotides directed against nucleic acid encoding human transforming growth factor-beta 2 (TGF-beta2). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclampsia in pregnant women or choriocarcinomas  
 XX Sequence 16 BP; 5 A; 4 C; 4 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1217 CATGCACACTACTGTGTG 1232  
 Db 16 CATGCACACTACTGTGTG 1

PA (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
 XX Caniggia I, Post M, Lye S;  
 XX WPI; 1998-520837/44.  
 DR Regulation of trophoblast invasion - by, e.g. transforming growth factor-beta3 inhibitor, useful for detecting or treating preeclampsia in pregnant women.  
 XX Example 4; Page 22; 59pp; English.  
 XX AAV63225-26 represent phosphorothioate oligonucleotides directed against nucleic acid encoding human transforming growth factor-beta 2 (TGF-beta2). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclampsia in pregnant women or choriocarcinomas  
 XX Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 0.4%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1217 CATGCACACTACTGTGTG 1232  
 Db 1 CATGCACACTACTGTGTG 16  
 RESULT 329  
 AAV48957/c  
 ID AAV48957 standard; DNA; 16 BP.  
 XX AAV48957;  
 XX 15-OCT-1998 (first entry)  
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-28.  
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX EP856579-A1.  
 XX 05-AUG-1998.  
 PD 31-JAN-1997; 97EP-00101531.  
 XX 31-JAN-1997; 97EP-00101531.  
 PR (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA Schlingensiepen K, Brysch W;  
 PI WPI; 1998-400910/35.  
 XX Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in culture.  
 XX Claim 10; Fig 8a; 286pp; English.  
 XX AAV48930-49007 represent antisense oligonucleotides directed against

CC transforming growth factor-beta2 (TGF-beta2). Of these, only  
 CC oligonucleotides AAV49930-67 resulted in significant reduction in TGF-  
 CC beta 2 protein expression, while oligonucleotides AAV49968-49007 had  
 CC little effect. The oligonucleotides exemplify the invention. The  
 CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 CC which contain at most 8 nucleotides that can each form three hydrogen  
 CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 CC form three H-bonds each to four consecutive cytosines; do not contain two  
 CC sequences of three consecutive nucleotides each able to form three H-  
 CC bonds to three consecutive cytosines, and the ratio between residues able  
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or  
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 CC keratinocytes). The oligonucleotides can also be used to analyse function  
 CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 CC stimulating the immune system  
 XX  
 SQ Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2156 GCAGGATAATTGCTGC 2171  
 Db 16 GCAGGATAATTGCTGC 1

RESULT 330  
 AA265460/c  
 ID AA265460 standard; DNA; 16 BP.

XX AA265460;  
 XX 30-MAR-2000 (first entry)  
 XX  
 XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-20.

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; ss;  
 KW atherosclerosis.

XX Unidentified.

XX WO9963975-A2.

XX 16-DEC-1999.

XX 10-JUN-1999; 99WO-EP004013.

XX 10-JUN-1998; 98EP-00110709.

PR 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

PI WPI; 2000-097470/08.

XX Composition containing immune stimulant and inhibitor of agent that  
 PT adversely affects the immune response, for treating cancers and  
 PT infections.

XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
 CC used in the invention. The invention relates to a composition which

CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor  
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes  
 CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
 CC syndrome and the formation of atherosclerotic plaque  
 XX  
 SQ Sequence 16 BP; 5 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TGTGACGAGTAATTGC 2168  
 Db 16 TGTGACGAGTAATTGC 1

RESULT 331  
 AA265458/c  
 ID AA265458 standard; DNA; 16 BP.

XX AA265458;

XX 30-MAR-2000 (first entry)

XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-18.

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; ss;  
 KW atherosclerosis.

XX Unidentified.

XX WO9963975-A2.

XX 16-DEC-1999.

XX 10-JUN-1999; 99WO-EP004013.

XX 10-JUN-1998; 98EP-00110709.

PR 25-JUL-1998; 98EP-00113974.

XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen K, Schlingensiepen R, Brysch W;

PI WPI; 2000-097470/08.

XX Composition containing immune stimulant and inhibitor of agent that  
 PT adversely affects the immune response, for treating cancers and  
 PT infections.

XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
 CC used in the invention. The invention relates to a composition which  
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor

CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes  
 CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
 CC syndrome and the formation of atherosclerotic plaque  
 XX  
 SQ Sequence 16 BP; 2 A; 3 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2020 AGTCCTAGGAAAAA 2035  
 Db 16 AGTCCTAGGAAAAA 1

RESULT 332  
 AAZ65461/C  
 ID AAZ65461 standard; DNA; 16 BP.  
 AC AAZ65461;  
 XX  
 DT 30-MAR-2000 (first entry)  
 XX  
 DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-21.  
 XX  
 KW Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
 KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
 KW glomerulonephritis; acute respiratory distress syndrome; ss;  
 KW atherosclerosis.  
 XX  
 OS Unidentified.  
 XX  
 FN WO9963975-A2.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 10-JUN-1999; 99WO-EP004013.  
 XX  
 PR 10-JUN-1998; 98EP-00110709.  
 PR 25-JUL-1998; 98EP-00113974.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Schlingensiepen R, Brysch W;  
 XX  
 DR WPI; 2000-097470/08.  
 XX  
 PT Composition containing immune stimulant and inhibitor of agent that  
 PT adversely affects the immune response, for treating cancers and  
 PT infections.  
 XX  
 PS Claim 5; Fig 1; 30pp; English.  
 XX  
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
 CC used in the invention. The invention relates to a composition which  
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
 CC transforming growth factor TGF-beta, vascular endothelial growth factor  
 CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
 CC that adversely affects the immune response. The composition also includes

CC at least one stimulant that positively affects the immune response. This  
 CC oligonucleotide is an example of an inhibitor that is used in the  
 CC composition. The composition is used as an immunostimulant for the  
 CC treatment of neoplasms and infections, particularly hyperproliferation;  
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
 CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
 CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative  
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
 CC syndrome and the formation of atherosclerotic plaque  
 XX  
 SQ Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2156 GCAGGATAATTCGTGC 2171  
 Db 16 GCAGGATAATTCGTGC 1

RESULT 333  
 AAZ00479  
 ID AAZ00479 standard; DNA; 17 BP.  
 AC AAZ00479;  
 XX  
 DT 06-OCT-1999 (first entry)  
 XX  
 DE Human thioredoxin DNA binding antisense oligonucleotide 2602.  
 XX  
 KW Thioredoxin; thioredoxin reductase; human; antisense; primer; metastasis;  
 KW cytostatic; tumour growth inhibitor; detection; nuclease resistant;  
 KW phosphorothioate linkage; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9938963-A1.  
 XX  
 PD 05-AUG-1999.  
 XX  
 PF 29-JAN-1999; 99WO-CA000077.  
 XX  
 PR 30-JAN-1998; 98US-0073196P.  
 XX  
 PA (GENE-) GENESENSE TECHNOLOGIES INC.  
 XX  
 PI Wright JA, Young AH, Lee YS;  
 XX  
 DR WPI; 1999-469328/39.  
 XX  
 PT Antisense oligonucleotides against thioredoxin and thioredoxin reductase  
 PT genes, useful for inhibiting tumor growth and metastasis.  
 XX  
 PS Claim 1; Page 18; 88pp; English.  
 XX  
 CC This invention describes novel antisense oligonucleotides against  
 CC thioredoxin and thioredoxin reductase gene which have cytostatic activity  
 CC and are useful for inhibiting tumour growth and metastasis in mammals.  
 CC They may also be used as hybridization probes to detect the presence of  
 CC the thioredoxin and thioredoxin reductase mRNAs in mammalian cells. They  
 CC may also be used as molecular weight markers. The antisense  
 CC oligonucleotides are nuclease resistant due to the presence of  
 CC phosphorothioate internucleotide linkages. AAZ00478-Z00503 represent  
 CC oligonucleotide primers capable of binding to human thioredoxin mRNA  
 XX  
 SQ Sequence 17 BP; 7 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

|                       |   |                 |                    |           |            |  |  |
|-----------------------|---|-----------------|--------------------|-----------|------------|--|--|
| Query Match           |   | 0.4%;           | Score 16;          | DB 1;     | Length 17; |  |  |
| Best Local Similarity |   | 100.0%;         | Pred. No. 1.5e+02; |           |            |  |  |
| Matches 16;           |   | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0;    |  |  |
| QY                    | 2209 GATGGAATGGATCCA 2224   |                 |                    |           |            |  |  |
| DB                    | 1 GATGGAATGGATCCA 16  |                 |                    |           |            |  |  |
| RESULT 334            |   |                 |                    |           |            |  |  |
| AAZ65500/c            |   |                 |                    |           |            |  |  |
| ID                    | AAZ65500 standard; DNA; 17 BP.  |                 |                    |           |            |  |  |
| XX                    | AC AAZ65500;  |                 |                    |           |            |  |  |
| XX                    | AC AAZ65500;  |                 |                    |           |            |  |  |
| DT                    | 30-MAR-2000 (first entry)   |                 |                    |           |            |  |  |
| XX                    | Immunosuppressant inhibitor oligonucleotide TGF-beta2-98-3.               |                 |                    |           |            |  |  |
| DE                    | Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;   |                 |                    |           |            |  |  |
| XX                    | vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  |                 |                    |           |            |  |  |
| KW                    | prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; |                 |                    |           |            |  |  |
| KW                    | monocyte chemoattractic protein-1; MCP-1; ulcerative colitis; diabetes;   |                 |                    |           |            |  |  |
| KW                    | glomerulonephritis; acute respiratory distress syndrome; ss;              |                 |                    |           |            |  |  |
| KW                    | atherosclerosis.  |                 |                    |           |            |  |  |
| XX                    | Unidentified.   |                 |                    |           |            |  |  |
| OS                    | WO9963975-A2.   |                 |                    |           |            |  |  |
| XX                    | 16-DEC-1999.  |                 |                    |           |            |  |  |
| PD                    | 10-JUN-1999; 99WO-EP004013.   |                 |                    |           |            |  |  |
| PF                    | 10-JUN-1998; 98EP-00110709.   |                 |                    |           |            |  |  |
| XX                    | 25-JUL-1998; 98EP-00113974.   |                 |                    |           |            |  |  |
| PR                    | (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.                          |                 |                    |           |            |  |  |
| XX                    | Schlingensiepen K, Schlingensiepen R, Brysch W;                           |                 |                    |           |            |  |  |
| PI                    | WPI; 2000-097470/08.  |                 |                    |           |            |  |  |
| XX                    | Composition containing immune stimulant and inhibitor of agent that       |                 |                    |           |            |  |  |
| PT                    | adversely affects the immune response, for treating cancers and           |                 |                    |           |            |  |  |
| PT                    | infections.   |                 |                    |           |            |  |  |
| XX                    | Claim 10; Fig 1; 30pp; English.   |                 |                    |           |            |  |  |
| PS                    | This sequence is an immunosuppressant inhibitor oligonucleotide, which is |                 |                    |           |            |  |  |
| XX                    | used in the invention. The invention relates to a composition which       |                 |                    |           |            |  |  |
| CC                    | contains at least one inhibitor (less than 100 kD) of a substance (e.g.   |                 |                    |           |            |  |  |
| CC                    | transforming growth factor TGF-beta, vascular endothelial growth factor   |                 |                    |           |            |  |  |
| CC                    | VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)    |                 |                    |           |            |  |  |
| CC                    | that adversely affects the immune response. The composition also includes |                 |                    |           |            |  |  |
| CC                    | at least one stimulant that positively affects the immune response. This  |                 |                    |           |            |  |  |
| CC                    | oligonucleotide is an example of an inhibitor that is used in the         |                 |                    |           |            |  |  |
| CC                    | composition. The composition is used as an immunostimulant for the        |                 |                    |           |            |  |  |
| CC                    | treatment of neoplasms and infections, particularly hyperproliferation;   |                 |                    |           |            |  |  |
| CC                    | leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,   |                 |                    |           |            |  |  |
| CC                    | colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,   |                 |                    |           |            |  |  |
| CC                    | breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  |                 |                    |           |            |  |  |
| CC                    | malignant melanoma, brain tumours and sarcomas. The oligonucleotides,     |                 |                    |           |            |  |  |
| CC                    | most of which are directed against TGFbeta or VEGF, are inhibitors of     |                 |                    |           |            |  |  |
| CC                    | monocyte chemoattractic protein-1 (MCP-1) and are useful as anti-         |                 |                    |           |            |  |  |
| CC                    | inflammatories for treating e.g. asthma, Crohn's disease, ulcerative      |                 |                    |           |            |  |  |
| CC                    | colitis, diabetes, glomerulonephritis, acute respiratory distress         |                 |                    |           |            |  |  |
| CC                    | syndrome and the formation of atherosclerotic plaque                      |                 |                    |           |            |  |  |
| XX                    | Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;                         |                 |                    |           |            |  |  |
| SQ                    | Query Match   | 0.4%;           | Score 16;          | DB 1;     | Length 17; |  |  |
| Best Local Similarity |   | 100.0%;         | Pred. No. 1.5e+02; |           |            |  |  |
| Matches 16;           |   | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0;    |  |  |
| QY                    | 424 AGGCAGCAGCGCGGC 439   |                 |                    |           |            |  |  |
| DB                    | 1 AGGCAGCAGCGCGGC 16  |                 |                    |           |            |  |  |
| RESULT 335            |   |                 |                    |           |            |  |  |
| ABZ59896              |   |                 |                    |           |            |  |  |
| ID                    | ABZ59896 standard; RNA; 17 BP.  |                 |                    |           |            |  |  |
| XX                    | AC ABZ59896;  |                 |                    |           |            |  |  |
| XX                    | AC ABZ59896;  |                 |                    |           |            |  |  |
| DT                    | 21-MAR-2003 (first entry)   |                 |                    |           |            |  |  |
| XX                    | Human K-Ras DNazyme substrate #8.   |                 |                    |           |            |  |  |
| DE                    | Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;               |                 |                    |           |            |  |  |
| XX                    | enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;         |                 |                    |           |            |  |  |
| KW                    | anti-rheumatic; cancer; AIDS; ss.   |                 |                    |           |            |  |  |
| OS                    | Homo sapiens.   |                 |                    |           |            |  |  |
| XX                    | WO200297114-A2.   |                 |                    |           |            |  |  |
| PN                    | 05-DEC-2002.  |                 |                    |           |            |  |  |
| XX                    | 29-MAY-2002; 2002WO-US016840.   |                 |                    |           |            |  |  |
| PF                    | 29-MAY-2001; 2001US-0294140P.   |                 |                    |           |            |  |  |
| XX                    | 06-JUN-2001; 2001US-0296249P.   |                 |                    |           |            |  |  |
| PR                    | 10-SEP-2001; 2001US-0318471P.   |                 |                    |           |            |  |  |
| XX                    | (RIBO-) RIBOZYME PHARM INC.   |                 |                    |           |            |  |  |
| PA                    | Moswiggen J;  |                 |                    |           |            |  |  |
| XX                    | WPI; 2003-140484/13.  |                 |                    |           |            |  |  |
| DR                    | Novel short interfering RNA and enzymatic nucleic acid useful for         |                 |                    |           |            |  |  |
| XX                    | treating cancer, modulates the expression of a nucleic acid encoding      |                 |                    |           |            |  |  |
| PT                    | HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.          |                 |                    |           |            |  |  |
| PT                    | HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.          |                 |                    |           |            |  |  |
| XX                    | Claim 58; Page 85; 185pp; English.  |                 |                    |           |            |  |  |
| PS                    | The invention relates to a novel short interfering RNA (siRNA) nucleic    |                 |                    |           |            |  |  |
| XX                    | acid molecule or an enzymatic nucleic acid molecule, that modulates       |                 |                    |           |            |  |  |
| CC                    | expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, |                 |                    |           |            |  |  |
| CC                    | human immunodeficiency virus (HIV) or a component of HIV. The nucleic     |                 |                    |           |            |  |  |
| CC                    | acid molecule of the invention has cytosstatic, anti-HIV, and anti-       |                 |                    |           |            |  |  |
| CC                    | rheumatic activity. The nucleic acid molecules are useful for reducing    |                 |                    |           |            |  |  |
| CC                    | HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are     |                 |                    |           |            |  |  |
| CC                    | also useful for treating breast, ovarian, colorectal, lung, prostate,     |                 |                    |           |            |  |  |
| CC                    | bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences |                 |                    |           |            |  |  |
| CC                    | shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,   |                 |                    |           |            |  |  |
| CC                    | ABZ66530 - ABZ66585 represent substrate/target sequences for the human    |                 |                    |           |            |  |  |
| CC                    | ribozymes of the invention  |                 |                    |           |            |  |  |
| XX                    | Sequence 17 BP; 3 A; 5 C; 9 G; 0 T; 0 U; 0 Other;                         |                 |                    |           |            |  |  |
| SQ                    | Query Match   | 0.4%;           | Score 16;          | DB 1;     | Length 17; |  |  |
| Best Local Similarity |   | 100.0%;         | Pred. No. 1.5e+02; |           |            |  |  |
| Matches 16;           |   | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0;    |  |  |
| QY                    | 424 AGGCAGCAGCGCGGC 439   |                 |                    |           |            |  |  |
| DB                    | 1 AGGCAGCAGCGCGGC 16  |                 |                    |           |            |  |  |
| RESULT 336            |   |                 |                    |           |            |  |  |
| ADL49410/C            |   |                 |                    |           |            |  |  |
| ID                    | ADL49410 standard; RNA; 17 BP.  |                 |                    |           |            |  |  |
| XX                    | ADL49410 standard; RNA; 17 BP.  |                 |                    |           |            |  |  |

```

AC ADL49410;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #524.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
FN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 2943; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 0 C; 0 G; 0 T; 14 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
DB 17 TTTAAAAA 2
RESULT 337
ADL49411/c
ID ADL49411 standard; RNA; 17 BP.
XX

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AC ADL49411;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PKR substrate sequence #525.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
KW substrate; ds.
XX
OS Unidentified.
XX
FN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;
XX WPI; 2003-058513/05.
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 59; SEQ ID NO 2944; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human PKR
CC substrate sequence.
XX
SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2573 TTTAAAAA 2588
DB 16 TTTAAAAA 1
RESULT 338
ADL49411/c
ID ADL49411 standard; RNA; 18 BP.
XX

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AC AAQ38707;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-JUL-1993 (first entry)  
 XX  
 DE First chimeric primer for adding poly A tails.  
 XX  
 KW oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;  
 KW treatment; diagnosis; testing; assay; Candida; papillomavirus;  
 KW cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;  
 KW liver disease; human immunodeficiency virus; herpes simplex virus; HSV;  
 KW human immunodeficiency virus; HIV; AIDS; influenza virus;  
 KW genetic disease; genetic abnormalities.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9305182-A1.  
 XX  
 PD 18-MAR-1993.  
 XX  
 PF 04-SEP-1992; 92WO-US007489.  
 XX  
 PR 05-SEP-1991; 91US-00755485.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bruce TW;  
 XX  
 DT WPI; 1993-101001/12.  
 XX  
 PT Determn. of oligonucleotide(s) with specific activity for a bio:molecule  
 PT - for use in therapeutics, diagnostics and research reagents.  
 XX  
 PS Disclosure; Page 27; 61pp; English.  
 XX  
 CC This sequence was used as a PCR primer in order to add a polyA tail to  
 CC the 3' end of the highest specific activity selected oligonucleotide in  
 CC order to form a first strand. The primer is comprised of a 5' known  
 CC sequence and a 3' polynucleotide portion corresp. to the polynucleotide  
 CC tail of the first strand. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2803 AAAAAAAAAAACATC 2818  
 DB 17 AAAAAAAAAAACATC 2  
 RESULT 339  
 AAT96107/c  
 ID AAT96107 standard; DNA; 18 BP.  
 XX  
 AC AAT96107;  
 XX  
 DT 31-MAR-1998 (first entry)  
 XX  
 DE First chimeric primer.  
 XX  
 KW Determination; oligonucleotide; specific activity; therapy;  
 KW target biomolecule; randomised oligonucleotide; diagnosis; research; PCR;  
 KW chimeric; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5686242-A.  
 XX  
 PD 11-NOV-1997.  
 XX  
 PF 27-OCT-1994; 94US-00330000.

XX  
 PR 05-SEP-1991; 91US-00755485.  
 PR 04-SEP-1992; 92WO-US007489.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Lima WF, Bruce TW;  
 XX  
 DR WPI; 1997-558135/51.  
 XX  
 PT Determination of oligo-nucleotide with specific activity for target bio-  
 PT molecule - using set of randomised oligo-nucleotide(s).  
 XX  
 PS Disclosure; Col 27-28; 22pp; English.  
 XX  
 CC The present sequence was used in the development of a method of  
 CC determining an oligonucleotide having specific activity for a target  
 CC biomolecule. The method comprises assaying a set of randomised  
 CC oligonucleotides for activity against a target biomolecule, separating  
 CC active from inactive oligonucleotides and recovering, amplifying and  
 CC determining the nucleic acid sequence of the active oligonucleotides. The  
 CC oligonucleotides can be used for therapeutic, diagnostic and research  
 CC purposes  
 XX  
 SQ Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2803 AAAAAAAAAAACATC 2818  
 DB 17 AAAAAAAAAAACATC 2  
 RESULT 340  
 AAZ88678/c  
 ID AAZ88678 standard; DNA; 18 BP.  
 XX  
 AC AAZ88678;  
 XX  
 DT 11-MAY-2000 (first entry)  
 XX  
 DE Chimeric primer #1.  
 XX  
 KW Primer; detection; diagnosis; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US6022691-A.  
 XX  
 PD 08-FEB-2000.  
 XX  
 PF 07-NOV-1997; 97US-00965908.  
 XX  
 PR 05-SEP-1991; 91US-00755485.  
 PR 04-SEP-1992; 92WO-US007489.  
 PR 27-OCT-1994; 94US-00330000.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Lima WF, Bruce TW;  
 XX  
 DR WPI; 2000-170669/15.  
 XX  
 PT Assay for a chemical or drug in a sample comprises detecting binding of  
 PT an oligonucleotide selected from a set of randomized oligonucleotides.  
 XX  
 PS Disclosure; Col 27-28; 20pp; English.  
 XX  
 CC This invention describes a novel method (I) for specifically detecting a  
 CC chemical or drug in a sample comprises contacting the sample with an  
 CC oligonucleotide having specific activity for a target biomolecule and

CC detecting the presence or absence of binding where the presence of  
 CC binding indicates the presence of the chemical or drug in the sample. The  
 CC oligonucleotide is identified by: (a) assaying a prepared set of  
 CC randomized oligonucleotides for activity against a target biomolecule;  
 CC (b) separating active from inactive oligonucleotides; (c) recovering the  
 CC active oligonucleotides; and (d) characterizing the recovered  
 CC oligonucleotides by microanalytical structure determination. The method  
 CC can be used for diagnostic or research purposes  
 XX  
 SQ Sequence 18 BP; 1 A; 0 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2803 AAAAAAAAAAACATC 2818  
 Db 17 AAAAAAAAAAACATC 2

RESULT 341  
 ADL95318/C  
 ID ADL95318 standard; DNA; 18 BP.  
 XX  
 AC ADL95318;  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Anti-proliferative oligonucleotide #9.  
 XX  
 KW ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;  
 KW cancer; malignant tumour.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 modified\_base 8  
 /\*tag= a  
 /mod\_base= OTHER  
 /note= "Optionally 32-P labelled"  
 XX US2004067197-A1.  
 XX  
 XX 08-APR-2004.  
 XX  
 XX 02-FEB-2001; 2001US-00775479.  
 XX  
 XX 26-NOV-1997; 97WO-CA000892.  
 XX 24-MAY-1999; 99US-00318106.  
 XX (LECL/) LECLERC G.  
 XX (MART/) MARTEL R.  
 XX  
 XX Leclerc G, Martel R;  
 XX  
 XX WPI; 2004-314974/29.

XX New anti-proliferative substance comprising a radiolabeled DNA carrier,  
 PT useful for preventing or treating uncontrolled cellular proliferation  
 PT e.g. restenosis, cancer or malignant tumors.  
 XX  
 XX Claim 13; SEQ ID NO 9; 28pp; English.

CC The invention relates to an anti-proliferative substance for preventing  
 CC uncontrolled cellular proliferation comprising a radiolabelled DNA  
 CC carrier, where a radioisotope is located internally within the DNA  
 CC sequence, at 5' end or at 3' end, and the radiolabelled DNA carrier  
 CC penetrates the cell membrane and is retained intracellularly for a time  
 CC sufficient for the radio-isotope to effect a dose therapy. The carrier in  
 CC the anti-proliferative substance is an oligonucleotide, which is linear  
 CC or a plasmid, which is circular. The plasmid is of viral or bacterial  
 CC origin. The oligonucleotide is a double- or a single-stranded DNA  
 CC sequence, which is conjugated with an antibody for cell-specific

CC delivery. The oligonucleotide is also conjugated to a stent surface,  
 CC cholesterol, oleic acid, linoleic acid, IgGalpha, antibody, IgGbeta,  
 CC cytokines or growth factors. The anti-proliferative substance is useful  
 CC for preventing or treating uncontrolled cellular proliferation. The  
 CC uncontrolled cell proliferation is a restenosis following angioplasty, or  
 CC cancer or a malignant tumour. The present sequence represents an  
 CC oligonucleotide carrier used in the invention.

SQ Sequence 18 BP; 3 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAAAAAAAAAA 2588  
 Db 18 TTTAAAAAAAAAAAAA 3

RESULT 342  
 AAZ11781  
 ID AAZ11781 standard; DNA; 19 BP.  
 XX  
 AC AAZ11781;  
 DT 23-NOV-1999 (first entry)  
 XX  
 DE Oligonucleotide primer JB659.  
 XX  
 KW internal transcribed spacer; ITS; ribosomal RNA; fungal pathogen; PCR;  
 KW primer; detection; plant disease; crop protection; ss.  
 XX  
 OS Synthetic.  
 OS Pyrenophora tritici-repentis.

XX  
 PN WO9942609-A1.  
 XX  
 PD 26-AUG-1999.  
 XX  
 PF 18-FEB-1999; 99WO-EP001058.  
 XX  
 PR 20-FEB-1998; 98US-00026601.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Beck JU;  
 XX  
 DR WPI; 1999-527487/44.

XX New internal transcribed spacer DNA from fungal pathogens, used as  
 PT sources of primers and probes for pathogen detection.  
 XX  
 PS Claim 13; Page 18; 40pp; English.

XX This primer can be used in the amplification-based detection of a fungal  
 CC internal transcribed spacer (ITS) DNA sequence. This sequence was derived  
 CC from the ITS sequences, specifically from the regions of the ITS which  
 CC exhibit the greatest difference among the fungal pathotypes. This allows  
 CC the identification of specific pathogens and provides a method for  
 CC detecting them

SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3190 GAAGCTTCATGACGC 3205  
 Db 1 GAAGCTTCATGACGC 16

```
RESULT 343
ADF31846
XX ADF31846 standard; RNA; 19 BP.
AC ADF31846;
XX
XX
DT 12-FEB-2004 (first entry)
DE Human IGF-1R siNA lower strand, SEQ ID NO:511.
XX
XX RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW proliferative disease; restenosis; polycystic kidney disease;
KW inflammatory disease; allergic disease; autoimmune disease;
KW transplant rejection; cytostatic; vasotropic; nephrotropic;
KW antiinflammatory; antiallergic; immunosuppressive; human;
KW insulin-like growth factor 1 receptor; IGF-1R; ss.
XX
OS Homo sapiens.
XX
XX WO2003070911-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005044.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Chowrira B;
XX
XX WPI; 2003-721691/68.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer , downregulates expression of the insulin-like growth
PT factor-1 receptor gene.
XX
XX Example 3; SEQ ID NO 511; 147pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human insulin-like growth factor 1
CC receptor (IGF-1R) gene by RNA interference. The siNAs may or may not
CC comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA), double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the IGF-1R gene in cells, tissue explants or organisms
CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC treatment of a variety of conditions. They may be used for treating
CC cancer and other proliferative diseases (e.g., restenosis and polycystic
CC kidney disease), inflammatory and/or allergic diseases, autoimmune
CC diseases and transplant rejection. The siNAs are also useful for drug
CC screening, diagnosis, therapeutic target identification and validation,
CC genetic engineering, pharmacogenomics, studying gene function, and gene
CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
CC represents the lower strand of a human IGF-1R-targeted double-stranded
CC siNA.
```

```
XX
SQ Sequence 19 BP; 1 A; 15 C; 1 G; 0 T; 2 U; 0 Other;
Query Match 0.4%; Score 16; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 972 TCCTCCCCCACCCTCCG 987
Db 4 UCCCCCCCCCCTCCG 19
RESULT 344
ADF31569/c
ID ADF31569 standard; RNA; 19 BP.
XX
XX ADF31569;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human IGF-1R transcript target sequence/siNA upper strand, SEQ ID NO:234.
XX
XX RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; cancer;
KW proliferative disease; restenosis; polycystic kidney disease;
KW inflammatory disease; allergic disease; autoimmune disease;
KW transplant rejection; cytostatic; vasotropic; nephrotropic;
KW antiinflammatory; antiallergic; immunosuppressive; human;
KW insulin-like growth factor 1 receptor; IGF-1R; target sequence; ss.
XX
OS Homo sapiens.
XX
XX WO2003070911-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005044.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Beigelman L, Chowrira B;
XX
XX WPI; 2003-721691/68.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer , downregulates expression of the insulin-like growth
PT factor-1 receptor gene.
XX
XX Example 3; SEQ ID NO 234; 147pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human insulin-like growth factor 1
CC receptor (IGF-1R) gene by RNA interference. The siNAs may or may not
CC comprise ribonucleotides and may be double or single stranded. They
CC further comprise sense and antisense regions, or alternatively are
CC assembled from a sense oligonucleotide and an antisense oligonucleotide.
CC Specifically, the siNAs include short interfering RNA (siRNA), double-
CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs
CC can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the IGF-1R gene in cells, tissue explants or organisms
CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the
CC treatment of a variety of conditions. They may be used for treating
CC cancer and other proliferative diseases (e.g., restenosis and polycystic
CC kidney disease), inflammatory and/or allergic diseases, autoimmune
CC diseases and transplant rejection. The siNAs are also useful for drug
CC screening, diagnosis, therapeutic target identification and validation,
CC genetic engineering, pharmacogenomics, studying gene function, and gene
CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
CC represents the lower strand of a human IGF-1R-targeted double-stranded
CC siNA.
```

CC of siNA; and vectors that express siNA. The siNAs are used to modulate  
CC expression of the IGF-1R gene in cells, tissue explants or organisms  
CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the  
CC treatment of a variety of conditions. They may be used for treating  
CC cancer and other proliferative diseases (e.g., restenosis and polycystic  
CC kidney disease), inflammatory and/or allergic diseases, autoimmune  
CC diseases and transplant rejection. The siNAs are also useful for drug  
CC screening, diagnosis, therapeutic target identification and validation,  
CC genetic engineering, pharmacogenomics, studying gene function, and gene  
CC mapping (e.g., of single nucleotide polymorphisms). The present sequence  
CC represents the upper strand of a human IGF-1R-targeted double-stranded  
CC siNA, which is identical to the IGF-1R transcript target sequence.  
SQ Sequence 19 BP; 2 A; 1 C; 15 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 TCCCCCCCCCACC CGC 987  
Db 16 TCCCCCCCCCACC CGC 1

RESULT 345  
ABD24924  
ID ABD24924 standard; DNA; 19 BP.

AC ABD24924;

XX 29-JUL-2004 (first entry)

XX A1095492-derived oligonucleotide SEQ ID 3936.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
XX analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense  
XX oligonucleotide containing less percentage of adenosine, targeted to  
XX nucleic acids associated with lung airway or lung dysfunction, and  
XX bronchodilating agent.

XX Claim 15; SEQ ID NO 3936; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,  
XX comprising oligonucleotides, effective for alleviating  
XX bronchoconstriction, respiratory tract inflammation, allergies and  
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
XX surfactant depletion or hyposecretion, when administered to a mammal. The  
XX oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX

SQ Sequence 19 BP; 16 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA AAAAAA 2588  
Db 1 TTTAAAAA AAAAAA 16

RESULT 346

AAQ75580/c

ID AAQ75580 standard; DNA; 20 BP.

XX AAQ75580;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)  
XX and using the aggregate of mRNAs as the template for each reverse  
XX transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in sepearate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2573 TTTAAAAA 2588  
 DB 20 TTTAAAAA 5  
 RESULT 347  
 AAC63692  
 ID AAC63692 standard; DNA; 20 BP.  
 XX  
 AC AAC63692;  
 DT 13-FEB-2001 (first entry)  
 XX  
 DE Rat P2X<sub>7</sub>/P2Z PCR primer #4.  
 XX  
 KW Rat; P2X<sub>7</sub>; neuroprotective; nootropic; antiinflammatory; antirheumatic;  
 KW antiarthritic; antibacterial; antiviral; antiallergic; cytostatic;  
 KW cardiac; cerebroprotective; immunosuppressive; P2Z; purinergic receptor;  
 KW nervous system disorder; chronic inflammation; Alzheimer's disease;  
 KW rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection;  
 KW haematopoietic system disorder; immune response; autoimmune disorder;  
 KW allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;  
 KW tuberculosis; PCR primer; ss.  
 XX  
 OS Rattus sp.  
 XX  
 PN US6133434-A.  
 XX  
 PD 17-OCT-2000.  
 XX  
 PF 28-APR-1997; 97US-00842079.  
 XX  
 PR 28-APR-1997; 97US-00842079.  
 XX  
 PA (GLAXO) GLAXO GROUP LTD.  
 XX  
 PI Buell GN, Kawashima E, Surprenant A;  
 XX  
 DR WPI; 2001-006153/01.  
 XX  
 PT Mammalian purinergic receptor (P2X<sub>7</sub>) useful for screening for modulators  
 PT which are useful for treating arthritic, respiratory disorders and  
 PT neurodegenerative disorders, and to generate receptors specific  
 PT antibodies.  
 PS  
 SS Example 1; Col 8; 40pp; English.  
 CC  
 CC The present invention relates to rat and human purinergic receptor  
 CC P2X<sub>7</sub>/P2Z (AAC63692-C63694). The P2X<sub>7</sub> coding sequences can be used to  
 CC treat disorders of the nervous system, particularly diseases with a  
 CC component of chronic inflammation, such as Alzheimer's disease, diseases  
 CC involving acute or chronic inflammation such as rheumatoid arthritis,  
 CC amyloidosis, bacterial, viral and other microbial infections, disorders  
 CC of the haematopoietic system and immune response such as autoimmune  
 CC disorders, allergies and lymphoproliferative disorders, diseases  
 CC involving apoptotic cell death, such as cardiac and cerebral ischaemia  
 CC and microbial infections, particularly tuberculosis. The present sequence  
 CC is a PCR primer used to isolate the rat P2X<sub>7</sub> coding sequence  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2102 GTCCAGCCGCGGAAG 2117  
 DB 1 GTCCAGCCGCGGAAG 16  
 RESULT 348  
 AAC82917/c  
 ID AAC82917 standard; DNA; 20 BP.  
 XX  
 AC AAC82917;  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Human S-9 derived oligonucleotide #1.  
 XX  
 KW Recognition system; screening; identification; pharmaceutical; toxin;  
 KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;  
 KW herbicide; fungicide; pesticide; beta-actin; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE19923966-A1.  
 XX  
 PD 30-NOV-2000.  
 XX  
 PF 25-MAY-1999; 99DE-01023966.  
 XX  
 PR 25-MAY-1999; 99DE-01023966.  
 XX  
 PA (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.  
 XX  
 PI Boekenkamp D, Hoppe H, Burgstaller P;  
 XX  
 DR WPI; 2001-050938/07.  
 XX  
 PT Recognition system, e.g. for identifying nucleic acids, comprises at  
 PT least one recognition unit comprising a region with a defined structure  
 PT adjacent to a region with a randomized structure.  
 XX  
 PS Example; Fig 1; 9pp; German.  
 XX  
 CC This invention describes a novel recognition system comprising at least 1  
 CC recognition unit bound to a support, each recognition unit comprising a  
 CC region A with a defined structure adjacent to a region B with a  
 CC randomized structure. The recognition system is useful for screening,  
 CC identifying, or characterizing at least 1 component of a sample,  
 CC especially nucleic acids and/or proteins, and for screening for and/or  
 CC identifying cellular or synthetic binding partners, preferably proteins,  
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,  
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
 CC teratogens, herbicides, fungicides or pesticides  
 XX  
 SQ Sequence 20 BP; 3 A; 2 C; 2 G; 13 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2573 TTTAAAAA 2588  
 DB 16 TTTAAAAA 1  
 RESULT 349  
 AAC82918/c  
 ID AAC82918 standard; DNA; 20 BP.  
 XX  
 AC AAC82918;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX



CC region A with a defined structure adjacent to a region B with a  
 CC randomized structure. The recognition system is useful for screening,  
 CC identifying, or characterizing at least 1 component of a sample,  
 CC especially nucleic acids and/or proteins, and for screening for and/or  
 CC identifying cellular or synthetic binding partners, preferably proteins,  
 CC peptides, nucleic acids, chemical agents, preferably organic compounds,  
 CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,  
 CC teratogens, herbicides, fungicides or pesticides  
 XX  
 SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2573 TTTAAAAA 2588  
 Db 16 TTTAAAAA 1  
 RESULT 352  
 ADA09834  
 ID ADA09834 standard; DNA; 20 BP.  
 AC ADA09834;  
 XX  
 DT 06-NOV-2003 (first entry)  
 DE Antisense nested PCR primer #2 for amplification of rat P2X7 (P2Z).  
 XX  
 KW PCR; ss; primer; permeabilizing activity; P2X7 receptor; P2Z receptor;  
 KW receptor; ATP; antigen presenting cell; T lymphocyte;  
 KW mitogenic stimulation; multinucleated giant cell; adenosine triphosphate;  
 KW 3'-O-(4-benzoyl)benzoyl ATP; BzATP; fluorescent dye; propidium iodide;  
 KW nootropic; neuroprotective; immunosuppressive; cerebroprotective;  
 KW vasotropic; arthritic disorder; respiratory disorder;  
 KW neurodegenerative disease; Alzheimer's disease; inflammation;  
 KW rheumatoid arthritis; amyloidosis; infection; tuberculosis;  
 KW haematopoietic system; immune response; allergy;  
 KW lymphoproliferative disorder; apoptosis; ischaemia; rat;  
 KW autoimmune disorder.  
 XX  
 OS Rattus sp.  
 XX  
 PN US6509163-B1.  
 XX  
 PD 21-JAN-2003.  
 XX  
 PF 15-AUG-2000; 2000US-00638857.  
 XX  
 PR 28-APR-1997; 97US-00842079.  
 XX  
 PA (GLAXO) GLAXO GROUP LTD.  
 XX  
 PI Buell GN, Surprenant A, Kawashima E;  
 XX  
 DR WPI; 2003-502654/47.  
 XX  
 XX  
 PT Screening of compound for its ability to modulate permeabilizing activity  
 PT of mammalian receptor useful for treating e.g. arthritis, and alzheimer's  
 PT disease.  
 PS  
 PS Example 1; SEQ ID NO 4; 43pp; English.  
 XX  
 CC The invention discloses a method for screening a compound for its ability  
 CC to modulate the permeabilizing activity of a mammalian P2X7 (P2Z)  
 CC receptor. The P2Z receptor is a cell surface receptor for ATP and has  
 CC been implicated in the lysis of antigen presenting cells by cytotoxic T  
 CC lymphocytes, in the mitogenic stimulation of human T lymphocytes, as well  
 CC as in the formation of multinucleated giant cells. The preferred agonist  
 CC is adenosine triphosphate (ATP) or 3'-O-(4-benzoyl)benzoyl ATP (BzATP)  
 CC and the preferred method comprises monitoring the uptake into the cell of  
 CC a detectable molecule, preferably a fluorescent dye (e.g. propidium

CC iodide). The inventive method is useful for screening a compound for its  
 CC ability to modulate the permeabilizing activity of a mammalian P2X7  
 CC receptor useful for treatment of arthritic and respiratory disorders and  
 CC neurodegenerative diseases. It is particularly useful in the treatment of  
 CC Alzheimer's disease, diseases involving acute or chronic inflammation  
 CC including rheumatoid arthritis, amyloidosis, bacterial, viral and other  
 CC microbial infections, e.g. tuberculosis, disorders of the haematopoietic  
 CC system and immune response, including autoimmune disorders, allergies and  
 CC lymphoproliferative disorders, diseases involving apoptotic cell death,  
 CC such as cardiac and cerebral ischaemia. The sequence presented is a  
 CC nested PCR primer used for the amplification of rat P2X7 cDNA.  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2102 GTCCAGCCGCGGAAG 2117  
 Db 1 GTCCAGCCGCGGAAG 16  
 RESULT 353  
 ABZ91658  
 ID ABZ91658 standard; DNA; 20 BP.  
 AC ABZ91658;  
 XX  
 DT 17-OCT-2003 (first entry)  
 DE Human oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIC-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 6900; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive, and  
 CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588  
Dy 3 TTTAAAAA 18

RESULT 354  
ABZ98155/c  
ID ABZ98155 standard; DNA; 20 BP.

XX AC ABZ98155;

XX DT 17-OCT-2003 (first entry)

XX DE Human CD23 + A1261 oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 13397; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 306 CCAGGAGCGGTGTG 321  
Dy 20 CCAGGAGCGGTGTG 5

RESULT 355

ABZ89703

ID ABZ89703 standard; DNA; 20 BP.

XX AC ABZ89703;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4945; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a



CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2588  
 DB 2 TTTAAAAA 17

RESULT 356  
 ABZ88813  
 ID ABZ88813 standard; DNA; 20 BP.

XX AC ABZ88813;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; de.

XX OS Homo sapiens.

XX XX WO200285308-A2.

XX PN 31-OCT-2002.

XX PD 23-APR-2002; 2002WO-US013135.

XX PF 24-APR-2001; 2001US-0286137P.

XX PR (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX XX WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4055; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2573 TTTAAAAA 2588  
 DB 4 TTTAAAAA 19

RESULT 357  
 ABZ88694  
 ID ABZ88694 standard; DNA; 20 BP.

XX AC ABZ88694;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; de.

XX OS Homo sapiens.

XX XX WO200285308-A2.

XX PN 31-OCT-2002.

XX PD 23-APR-2002; 2002WO-US013135.

XX PF 24-APR-2001; 2001US-0286137P.

XX PR (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;

XX XX WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 3936; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588

Db 1 TTTAAAAA 16

RESULT 358

ABD25043

ID ABD25043 standard; DNA; 20 BP.

XX

AC ABD25043;

XX

DT 29-JUL-2004 (first entry)

XX

DE A1128305-derived oligonucleotide SEQ ID 4055.

XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

OS

XX WO200285309-A2.

PN

XX 31-OCT-2002.

XX

XX 23-APR-2002; 2002WO-US013143.

XX

XX 24-APR-2001; 2001US-0286036P.

PR

XX (EPIG-) EPIGENESIS PHARM INC.

XX

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

PI

XX WPI; 2003-093058/08.

XX

XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.

XX

XX Claim 15; SEQ ID NO 4055; 763pp; English.

PS

XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2573 TTTAAAAA 2588

Db 4 TTTAAAAA 19

RESULT 359

ABD31186/c

ID ABD31186 standard; DNA; 20 BP.

XX

AC ABD31186;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human CD23-derived oligonucleotide SEQ ID 13397.

XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.

XX

OS Homo sapiens.

XX

XX WO200285309-A2.

XX

XX 31-OCT-2002.

XX

XX 23-APR-2002; 2002WO-US013143.

XX

XX 24-APR-2001; 2001US-0286036P.

XX

XX (EPIG-) EPIGENESIS PHARM INC.

XX

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

PI

XX WPI; 2003-093058/08.

XX

XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
PS Claim 15; SEQ ID NO 13397; 763pp; English.  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 0.4%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 306 CCAGGAGCGCGTGTG 321  
DB 20 CCAGGAGCGCGTGTG 5  
RESULT 360  
ABD27888  
ID ABD27888 standard; DNA; 20 BP.  
XX  
AC ABD27888;  
XX  
XX 29-JUL-2004 (first entry)  
DE AA258396-derived oligonucleotide SEQ ID 6900.  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX pulmonary transplantation rejection; ss; primer.  
XX  
OS Homo sapiens.  
XX  
XX WO200285309-A2.  
XX  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013143.

XX  
PR 24-APR-2001; 2001US-0286036P.  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-093058/08.  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
PS Claim 15; SEQ ID NO 6900; 763pp; English.  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer,  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 0.4%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2573 TTTAAAAA 2588  
DB 3 TTTAAAAA 18  
RESULT 361  
ADJ60020/c  
ID ADJ60020 standard; DNA; 20 BP.  
XX  
XX ADJ60020;  
AC  
XX 06-MAY-2004 (first entry)  
DT  
DE Oligonucleotide associated to CD23-X04772 #14.  
XX  
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
XX airway inflammation; allergy; asthma; impeded respiration;  
XX cystic fibrosis; acute respiratory distress syndrome;  
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;

KW ss.  
 XX Homo sapiens.  
 XX WO2004011613-A2.  
 XX 05-FEB-2004.  
 XX  
 XX 25-JUL-2003; 2003WO-US0233509.  
 XX  
 XX 29-JUL-2002; 2002US-0399076P.  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 XX NYCE JW, Tang L, Sandraasagra A, Aguilar D, Miller S;  
 XX Shahabuddin S, Lu H, Cong H;  
 XX WPI; 2004-203534/19.  
 XX  
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.  
 XX initiation codons and introns of respiratory disease-relevant genes e.g.,  
 XX CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
 XX disease e.g., asthma.  
 XX  
 XX Claim 2; SEQ ID NO 876; 85pp; English.  
 XX  
 XX The present invention relates to an oligonucleotide anti-sense to e.g.,  
 XX initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
 XX end of nucleic acid target comprising gene(s) chosen from e.g.  
 XX interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
 XX oligonucleotide and optionally surfactant operatively linked to the  
 XX oligonucleotide. The method is useful for preventing or treating a  
 XX respiratory or lung disease, which involves administering to the airways  
 XX of a subject an effective amount of an inhibitor. The oligonucleotide is  
 XX useful for production of a medicament for the prevention and/or treatment  
 XX of a respiratory or lung disease. The respiratory or lung disease is  
 XX chosen from airway inflammation, allergy(ies), asthma, impeded  
 XX respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
 XX (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
 XX (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
 XX obstruction. The present sequence represents an oligonucleotide of the  
 XX invention.  
 XX  
 XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 306 CCAGGAGCGCGTGTG 321  
 Db 20 CCAGGAGCGCGTGTG 5  
 RESULT 362  
 ADL58072/c  
 ID ADL58072 standard; DNA; 20 BP.  
 XX  
 XX ADL58072;  
 XX  
 XX 03-JUN-2004 (first entry)  
 XX  
 XX Human ESM-1 antisense oligonucleotide seqid 321.  
 XX  
 XX cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;  
 XX gene therapy; endothelial specific molecule-1; ESM-1;  
 XX ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
 XX angiogenic disorder; immunological disorder; cardiovascular disorder;  
 XX neurological disorder; antisense technology; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers

FT modified\_base 1..20  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone. All cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 XX  
 XX WO2004021978-A2.  
 XX  
 XX 19-MAR-2004.  
 XX  
 XX 19-AUG-2003; 2003WO-US025833.  
 XX  
 XX 19-AUG-2002; 2002US-0404495P.  
 XX  
 XX (PHAA ) PHARMACIA CORP.  
 XX  
 XX Weinstein EJ, Griggs DW;  
 XX WPI; 2004-248358/23.  
 XX  
 XX New antisense compound, having a sequence targeted to a nucleic acid  
 XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 XX composition for treating e.g., diabetes, cancer or cardiovascular  
 XX disorder.  
 XX  
 XX Claim 3; SEQ ID NO 321; 555pp; English.  
 XX  
 XX The invention describes a new antisense compound, having a sequence  
 XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 XX specific molecule-1 (ESM-1), that specifically hybridises with the  
 XX nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 XX composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 XX treating an animal having a disease or condition associated with ESM-1.  
 XX The compound is useful for preparing a composition for treating diabetes,  
 XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,  
 XX cardiovascular or neurological disorder. This sequence represents an  
 XX antisense oligonucleotide that can be used to modulate expression of  
 XX endothelial specific molecule-1 (ESM-1).  
 XX  
 XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 362 TGGCGCGCTGGAGCAA 377  
 Db 17 TGGCGCGCTGGAGCAA 2  
 RESULT 363  
 ADL58071/c  
 ID ADL58071 standard; DNA; 20 BP.  
 XX  
 XX ADL58071;  
 XX  
 XX 03-JUN-2004 (first entry)  
 XX  
 XX Human ESM-1 antisense oligonucleotide seqid 320.  
 XX  
 XX cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective;  
 XX gene therapy; endothelial specific molecule-1; ESM-1;  
 XX ESM-1 related disorder; diabetes; cancer; ischaemia; reperfusion injury;  
 XX angiogenic disorder; immunological disorder; cardiovascular disorder;  
 XX neurological disorder; antisense technology; ss.

XX Homo sapiens.  
 OS Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= phosphorothioate backbone. All cytidine  
 FT residues are 5-methylcytidines"  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-methoxyethyl (2'-MOE) nucleotides"  
 XX WO2004021978-A2.  
 XX 18-MAR-2004.  
 XX 19-AUG-2003; 2003WO-US025833.  
 XX 19-AUG-2002; 2002US-0404495P.  
 XX (PHAA ) PHARMACIA CORP.  
 XX Weinstein EJ, Griggs DW;  
 XX WPI; 2004-248358/23.  
 XX New antiseense compound, having a sequence targeted to a nucleic acid  
 XX encoding endothelial specific molecule-1 (ESM-1), useful for preparing a  
 XX composition for treating e.g., diabetes, cancer or cardiovascular  
 XX disorder.  
 XX Claim 3; SEQ ID NO 320; 555pp; English.  
 XX The invention describes a new antiseense compound, having a sequence  
 XX comprising 8-30 bp targeted to a nucleic acid encoding endothelial  
 XX specific molecule-1 (ESM-1), that specifically hybridises with the  
 XX nucleic acid ESM-1 and inhibits its expression. Also described are: a  
 XX composition; inhibiting the expression of ESM-1 in cells or tissues; and  
 XX treating an animal having a disease or condition associated with ESM-1.  
 XX The compound is useful for preparing a composition for treating diabetes,  
 XX cancer, ischaemia or reperfusion injury, or angiogenic, immunological,  
 XX cardiovascular or neurological disorder. This sequence represents an  
 XX antiseense oligonucleotide that can be used to modulate expression of  
 XX endothelial specific molecule-1 (ESM-1).  
 XX Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.4%; Score 16; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 362 TGCGCCGCTGGAGCAA 377  
 DB 16 TGCGCCGCTGGAGCAA 1  
 RESULT 364  
 ID ADO45510/C  
 XX ADO45510 standard; DNA; 20 BP.  
 AC ADO45510;  
 XX  
 XX 15-JUL-2004 (first entry)  
 DT Human oligonucleotide #876.  
 XX  
 XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;

KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;  
 KW asthma; lung allergy; inflammation; inflammatory disease;  
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
 KW acute respiratory distress syndrome; pulmonary hypertension;  
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.  
 XX Homo sapiens.  
 XX US2004049022-A1.  
 XX 11-MAR-2004.  
 XX 25-JUL-2003; 2003US-00627930.  
 XX 23-APR-2002; 2002WO-US013135.  
 XX 23-APR-2002; 2002WO-US013143.  
 XX (NYCE/) NYCE J W.  
 XX (SAND/) SANDRASAGRA A.  
 XX (TANG/) TANG L.  
 XX (AGUI/) AGUILAR D.  
 XX (MILL/) MILLER S.  
 XX (SHAH/) SHAHABUDDIN S.  
 XX (LUHH/) LU H.  
 XX (CONG/) CONG H.  
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;  
 XX Shahabuddin S, Lu H, Cong H;  
 XX WPI; 2004-293804/27.  
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.  
 XX initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,  
 XX RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
 XX asthma.  
 XX Claim 2; SEQ ID NO 876; 174pp; English.  
 XX The invention relates to oligonucleotides anti-sense to an initiation  
 XX codon, coding region, 5' or 3' intron-exon junction, intron or region  
 XX with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
 XX chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
 XX -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
 XX tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
 XX also relates to a method of screening a candidate compound that binds to  
 XX one or more nucleic acid target(s) or expressed product(s), for the  
 XX prevention and/or treatment of a respiratory or lung disease. The  
 XX oligonucleotides are useful for reducing or inhibiting expression of a  
 XX gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
 XX CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
 XX tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 XX useful for preventing or treating a respiratory or lung disease. The  
 XX respiratory or lung disease is associated with hyper-responsiveness to  
 XX and/or increased levels of, adenosine and/or levels of adenosine A  
 XX receptor(s), and/or asthma and/or lung allergies associated with  
 XX inflammation or an inflammatory disease. The respiratory or lung disease  
 XX is chosen from airway inflammation, allergy, asthma, impeded respiration,  
 XX cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 XX allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 XX hypertension, lung inflammation, bronchitis, airway obstruction or  
 XX bronchoconstriction. This sequence represents an oligonucleotide of the  
 XX invention.  
 XX  
 XX SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 0.4%; Score 16; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 CCAGGAGCGGTGTTG 321

|            |   |
|------------|---|
| ID         | ADH34300 standard; DNA; 24 BP.  |
| AC         | ADH34300;   |
| XX         |   |
| DT         | 11-MAR-2004 (first entry)   |
| DE         | Hairpin oligonucleotide.  |
| NW         | Nucleoside analogue; oligonucleotide synthesis; antisense therapy;        |
| KW         | antigene method; hairpin oligonucleotide; ss.                             |
| OS         | Synthetic.  |
| FH         | Key Location/Qualifiers   |
| FT         | stem_loop 1..24   |
| XX         | /*tag= a  |
| PN         | WO2003068795-A1.  |
| PD         | 21-AUG-2003.  |
| PF         | 13-FEB-2003; 2003WO-JP001485.   |
| PR         | 13-FEB-2002; 2002JP-00035706.   |
| PA         | (IMAN/) IMANISHI T.   |
| PI         | Imanishi T, Obika S;  |
| DR         | WPI; 2003-689651/65.  |
| XX         | New nucleoside analogs for producing oligonucleotide analogs useful e.g.  |
| PT         | as antisense compounds.   |
| PS         | Example 2; Page 48; 74pp; Japanese.                                       |
| CC         | The invention relates to nucleoside analogues and their salts. The        |
| CC         | invention also encompasses oligonucleotides and their salts comprising at |
| CC         | least one nucleoside analogue of the invention. The nucleoside analogues  |
| CC         | are produced by reducing an nucleoside azide derivative and optionally    |
| CC         | further interconverting, or by reacting a nucleoside derivative with      |
| CC         | formaldehyde and optionally deprotecting and/or interconverting. The      |
| CC         | nucleoside analogues can be used for producing oligonucleotides useful as |
| CC         | antisense compounds and in antigenic methods. The present sequence        |
| CC         | represents a hairpin oligonucleotide used in an example of the invention. |
| SQ         | Sequence 24 BP; 10 A; 4 C; 0 G; 10 T; 0 U; 0 Other;                       |
| QY         | Query Match 0.4%; Score 16; DB 1; Length 24;                              |
| DB         | Best Local Similarity 79.2%; Pred. No. 3.5e+02;                           |
| DB         | Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;               |
| QY         | 2731 AAAAAGAAAACATCTTTT 2754  |
| DB         | 24 AAAAAGAAAAGGGTTTTTTT 1   |
| RESULT 367 |   |
| AAH28312/c |   |
| ID         | AAH28312 standard; RNA; 25 BP.  |
| AC         | AAH28312;   |
| XX         |   |
| DT         | 05-SEP-2001 (first entry)   |
| DE         | 3' untranslated region sequence from TGF-beta gene.                       |
| XX         | mRNA protein complex; tumour development; cell aging; death;              |
| KW         | ribonomic profile; RNA-binding protein; ss.                               |
| OS         | Unidentified.   |
| FN         | WO200148480-A1.   |

  

|            |   |                    |
|------------|---|--------------------|
| Db         |   | 20 CCAGGCGGTGTTG 5 |
| RESULT 365 |   |                    |
| AAX59725/c |   |                    |
| ID         | AAX59725 standard; DNA; 24 BP.  |                    |
| AC         | AAX59725;   |                    |
| XX         |   |                    |
| DT         | 22-JUL-1999 (first entry)   |                    |
| DE         | DNA target used for the modified oligodeoxyribonucleotides.               |                    |
| NW         | Oligodeoxyribonucleotide; intersubunit linkage;                           |                    |
| KW         | phosphoramidate intersubunit; antisense activity; nuclease resistant;     |                    |
| KW         | in-vitro cell growth inhibition assay; infection;                         |                    |
| KW         | smooth muscle cell proliferation disorder; inflammatory process;          |                    |
| KW         | genetic disorder; cancer; ss.   |                    |
| OS         | Synthetic.  |                    |
| XX         |   |                    |
| PN         | WO9525814-A1.   |                    |
| XX         |   |                    |
| PD         | 28-SEP-1995.  |                    |
| XX         |   |                    |
| PF         | 20-MAR-1995; 95WO-US003575.   |                    |
| PR         | 18-MAR-1994; 94US-00210505.   |                    |
| PR         | 18-MAR-1994; 94US-00214599.   |                    |
| XX         |   |                    |
| PA         | (LYNX-) LYNX THERAPEUTICS INC.  |                    |
| XX         |   |                    |
| PI         | Gryaznov SM, Schultz RG, Chen J;  |                    |
| DR         | WPI; 1995-344627/44.  |                    |
| XX         |   |                    |
| PT         | Oligo(nucleotide N3'-P5' phosphoramidate(s) - have improved resistance    |                    |
| PT         | toward phosphodiesterase digestion, and form stable duplexes with DNA and |                    |
| PT         | RNA strands.  |                    |
| XX         |   |                    |
| PS         | Disclosure; Page 61; 101pp; English.                                      |                    |
| XX         |   |                    |
| CC         | The specification describes oligodeoxyribonucleotides having contiguous   |                    |
| CC         | nucleoside subunits joined by intersubunit linkages, where at least 3     |                    |
| CC         | contiguous subunits are joined by phosphoramidate intersubunits. The      |                    |
| CC         | oligodeoxyribonucleotides has a sequence of nucleoside subunits effective |                    |
| CC         | to form a duplex with a target nucleic acid molecule. The                 |                    |
| CC         | oligodeoxyribonucleotides are more resistant to nuclease digestion and    |                    |
| CC         | have improved RNA and dsDNA hybridisation characteristics, relative to    |                    |
| CC         | oligonucleotides not containing N3'-P5' phosphoramidate linkages. They    |                    |
| CC         | also have excellent antisense activity against complementary mRNA targets |                    |
| CC         | in in-vitro cell growth inhibition assays. They also exhibit low          |                    |
| CC         | cytotoxicity. They may be used in diagnostic and therapeutic              |                    |
| CC         | applications, e.g., in combatting infectious agents such as bacteria,     |                    |
| CC         | viruses, etc. or in treatment of smooth muscle cell proliferation         |                    |
| CC         | disorders, inflammatory processes, certain genetic disorders, cancers,    |                    |
| CC         | etc. . The present sequence represents a target for the oligonucleotides  |                    |
| CC         | of the invention  |                    |
| SQ         | Sequence 24 BP; 10 A; 4 C; 0 G; 10 T; 0 U; 0 Other;                       |                    |
| QY         | Query Match 0.4%; Score 16; DB 1; Length 24;                              |                    |
| DB         | Best Local Similarity 79.2%; Pred. No. 3.5e+02;                           |                    |
| DB         | Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;               |                    |
| QY         | 2731 AAAAAGAAAACATCTTTT 2754  |                    |
| DB         | 24 AAAAAGAAAAGGGTTTTTTT 1   |                    |
| RESULT 366 |   |                    |
| ADH34300/c |   |                    |





XX Schlingensiepen K, Brysch W;  
XX WPI; 1998-400910/35.  
XX  
XX Preparation of antisense oligonucleotide(s) which lack long runs of  
XX consecutive guanosine or inosine - and have specific ratio of residues  
XX able to form two or three hydrogen bonds, have greater activity and  
XX reduced toxicity, used therapeutically or to modulate growth of cells in  
XX culture.  
XX  
XX Claim 10; Fig 8a; 286pp; English.  
XX  
XX AA48930-49007 represent antisense oligonucleotides directed against  
XX transforming growth factor-beta2 (TGF-beta2). Of these, only  
XX oligonucleotides AA48930-67 resulted in significant reduction in TGF-  
XX beta 2 protein expression, while oligonucleotides AA48968-49007 had  
XX little effect. The oligonucleotides exemplify the invention. The  
XX specification describes oligonucleotides that contain 8-30 nucleotides,  
XX which contain at most 8 nucleotides that can each form three hydrogen  
XX bonds to cytosine; do not contain four consecutive nucleotides able to  
XX form three H-bonds each to four consecutive cytosines; do not contain two  
XX sequences of three consecutive nucleotides each able to form three H-  
XX bonds to three consecutive cytosines, and the ratio between residues able  
XX to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
XX = 0.33-0.72. The oligonucleotides are used to modulate expression of  
XX genes, particularly the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or  
XX beta 2 to control proliferation of primary cell cultures (e.g. bone  
XX marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
XX keratinocytes). The oligonucleotides can also be used to analyse function  
XX of proteins (by altering their expression or activity) and  
XX therapeutically, e.g. in cases of cancer or (targeting TGF) for  
XX stimulating the immune system

SQ Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAATCGAC 1538  
Db 19 GGAGGTTTACAAATAGAC 1

RESULT 370  
AAZ65447/C  
ID AAZ65447 standard; DNA; 19 BP.  
XX  
XX AAZ65447;

XX 30-MAR-2000 (first entry)  
XX  
XX Immunosuppressant inhibitor oligonucleotide TGF-beta2-7.

XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
XX vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
XX prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
XX monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
XX glomerulonephritis; acute respiratory distress syndrome; ss;  
XX atherosclerosis.

XX Unidentified.

XX WO963975-A2.

XX 16-DEC-1999.

XX 10-JUN-1999; 99WO-EP004013.

XX 10-JUN-1998; 98EP-00110709.

XX 25-JUL-1998; 98EP-00113974.

PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX Schlingensiepen K, Schlingensiepen R, Brysch W;  
PI WPI; 2000-097470/08.  
XX  
XX Composition containing immune stimulant and inhibitor of agent that  
XX adversely affects the immune response, for treating cancers and  
XX infections.  
XX  
XX Claim 5; Fig 1; 30pp; English.

XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
XX used in the invention. The invention relates to a composition which  
XX contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
XX transforming growth factor TGF-beta, vascular endothelial growth factor  
XX VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
XX that adversely affects the immune response. The composition also includes  
XX at least one stimulant that positively affects the immune response. This  
XX oligonucleotide is an example of an inhibitor that is used in the  
XX composition. The composition is used as an immunostimulant for the  
XX treatment of neoplasms and infections, particularly hyperproliferation;  
XX leukaemia; (non-Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
XX colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
XX breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
XX malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
XX most of which are directed against TGFbeta or VEGF, are inhibitors of  
XX monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
XX inflammatory for treating e.g. asthma, Crohn's disease, ulcerative  
XX colitis, diabetes, glomerulonephritis, acute respiratory distress  
XX syndrome and the formation of atherosclerotic plaque  
XX  
XX Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1520 GGAGGTTTATAAATCGAC 1538  
Db 19 GGAGGTTTACAAATAGAC 1

RESULT 371  
AAA86481/C  
ID AAA86481 standard; DNA; 19 BP.  
XX  
XX AAA86481;

XX 04-DEC-2000 (first entry)  
XX  
XX PCBA HH ribozyme binding site #213.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX Mammalia.

XX WO200032765-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US028772.

XX 04-DEC-1998; 98US-0110954P.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
XX RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,



PT PCNA and Cyclin B1.  
 PS Disclosure; Page 108; 109pp; English.  
 XX  
 CC The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
 CC Representative examples of ribozyme recognition sites are given in CC AAA82415 to AAA86787. The ribozyme of the invention is useful for CC inhibiting restenosis by introduction of the ribozyme into cells. The CC ribozyme is resistant to endonuclease activity and hence is efficient in CC restenosis treatment  
 XX  
 SQ Sequence 19 BP; 11 A; 2 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3591 TTGGACTTTTCTTTTAA 3609  
 Db 19 TTGGACTTTTCTTTTAA 1  
 RESULT 372  
 AAF99013  
 ID AAF99013 standard; DNA; 19 BP.  
 AC AAF99013;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #129.  
 XX  
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200122972-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Schetter C, Vollmer J;  
 XX  
 DR WPI; 2001-273485/28.  
 XX  
 PT Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 PS Claim 101; Page 41; 338pp; English.  
 XX  
 CC The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone  
 CC  
 SQ Sequence 19 BP; 11 A; 2 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone  
 XX  
 SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 615 GCGCGCGCGCACGACGCG 633  
 Db 1 GCGCGCGCGCGCGCGCG 19  
 RESULT 373  
 AAF99013/C  
 ID AAF99013 standard; DNA; 19 BP.  
 XX  
 AC AAF99013;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #129.  
 XX  
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200122972-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Schetter C, Vollmer J;  
 XX  
 DR WPI; 2001-273485/28.  
 XX  
 PT Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 PS Claim 101; Page 41; 338pp; English.  
 XX  
 CC The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone  
 CC  
 SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;

```

Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGGCGCGCAGCAGCGC 634
Db 19 CGCGGCGCGCGCGCGCGC 1

RESULT 374
AAC83562/c
ID AAC83562 standard; DNA; 19 BP.
XX
AC AAC83562;
XX
DT 28-FEB-2001 (first entry)
XX
DE DNA synthesis method linker/primer sequence SEQ ID NO: 1.
XX
KW DNA synthesis; directional complementary DNA library; linker; PCR primer;
KW ss.
XX
OS Synthetic.
XX
PN US6143531-A.
XX
PD 07-NOV-2000.
XX
PF 22-JUL-1997; 97US-00899029.
XX
PR 19-SEP-1988; 88US-00246567.
PR 02-MAY-1991; 91US-00700066.
PR 23-NOV-1992; 92US-00981931.
PR 02-SEP-1993; 93US-00116049.
XX
PA (STRA-) STRATAGENE.
XX
PI Hansen CJ, Huse WD;
XX
DR WPI; 2001-006435/01.
XX
PT Double stranded DNA synthesis with specific orientation comprises
PT synthesizing a first strand of DNA complementary to a selected DNA or RNA
PT template and synthesizing second strand complementary to first one.
XX
PS Example 1; Fig 1; 14pp; English.
XX
CC The present invention describes an improved method of DNA synthesis which
CC provides double stranded DNA where the predetermined orientation of the
CC sequence is preserved. This can be used in the construction of
CC complementary DNA and directional DNA libraries
XX
SQ Sequence 19 BP; 1 A; 2 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATTGGAG 2594
Db 19 AAAAAAAAAAAACTCGAG 1

RESULT 375
AAH61643/c
ID AAH61643 standard; DNA; 19 BP.
XX
AC AAH61643;
XX
DT 10-SEP-2001 (first entry)
XX
DE PCNA HH ribozyme binding site SEQ ID NO:4067.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytosatic;
KW antipsoialtic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 367; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoialtic,
CC dermatological, cytosatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 11 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3591 TTTCGACTTTTCTTTTAA 3609
Db 19 TTTCGACTTTTCTTTTAA 1

RESULT 376
ABS77654
ID ABS77654 standard; DNA; 19 BP.
XX
AC ABS77654;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #138.

```

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200253141-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 XX 14-DEC-2001; 2001WO-US048458.  
 XX  
 PR 14-DEC-2000; 2000US-0255534P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 XX  
 PI Bratzler RL;  
 XX  
 DR WPI; 2002-566690/60.  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX  
 PS Claim 2; Page 22; 276pp; English.  
 XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 615 GCGCGCGCGCAGCAGCG 633  
 DB 1 GCGCGCGCGCGCGCGCG 19  
 RESULT 377  
 ABS77654/c  
 ID ABS77654 standard; DNA; 19 BP.  
 XX  
 AC ABS77654;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #138.  
 XX  
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophiliac joint;

KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 OS Synthetic.  
 XX  
 PN WO200253141-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 XX 14-DEC-2001; 2001WO-US048458.  
 XX  
 PR 14-DEC-2000; 2000US-0255534P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 XX  
 PI Bratzler RL;  
 XX  
 DR WPI; 2002-566690/60.  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX  
 PS Claim 2; Page 22; 276pp; English.  
 XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 616 CGCGCGCGCAGCAGCGC 634  
 DB 19 CGCGCGCGCGCGCGCGC 1  
 RESULT 378  
 ABL38943  
 ID ABL38943 standard; DNA; 19 BP.  
 XX  
 AC ABL38943;  
 XX  
 DT 16-APR-2002 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid SEQ ID NO: 342.  
 XX  
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; ss.  
 OS Synthetic.  
 XX  
 PN WO200197843-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 22-JUN-2001; 2001WO-US020154.  
 XX  
 XX 22-JUN-2000; 2000US-0213346P.  
 PR

PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Weiner G, Hartmann G;  
XX WPI; 2002-154611/20.  
XX  
XX  
PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
XX  
PS Disclosure; Page 182; 312pp; English.  
XX  
XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;  
Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 615 GCGGCGCGCGCACGCGCG 633  
DB 1 GCGGCGCGCGCGCGCGCG 19  
RESULT 379  
ABL38943/C  
ID ABL38943 standard; DNA; 19 BP.  
XX  
XX ABL38943;  
XX  
XX 16-APR-2002 (first entry)  
XX Immunostimulatory nucleic acid SEQ ID NO: 342.  
DE  
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.  
XX  
XX Synthetic.  
XX  
XX WO200197843-A2.  
XX  
XX 27-DEC-2001.  
XX  
XX 22-JUN-2001; 2001WO-US020154.  
XX  
XX 22-JUN-2000; 2000US-0213346P.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Weiner G, Hartmann G;  
XX WPI; 2002-154611/20.  
XX  
XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX

PS Disclosure; Page 182; 312pp; English.  
XX  
XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;  
Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 616 GCGGCGCGCGCACGCGCGC 634  
DB 19 GCGGCGCGCGCGCGCGCGC 1  
RESULT 380  
ACD99445  
ID ACD99445 standard; DNA; 19 BP.  
XX  
XX ACD99445;  
XX  
XX 25-SEP-2003 (first entry)  
XX Immunostimulatory nucleic acid #131.  
DE  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
XX Synthetic.  
XX  
XX US2003050268-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 29-MAR-2002; 2002US-00112653.  
XX  
XX 29-MAR-2001; 2001US-0279642P.  
XX  
XX (KRIE/) KRIEG A M.  
XX PA (BERG/) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
XX  
XX WPI; 2003-521815/49.  
XX  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX Disclosure; Page 12; 229pp; English.  
XX  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.

CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 633  
Db 1 GCGCGCGCGCGCGCGCG 19

RESULT 381  
ACD99445/c  
ID ACD99445 standard; DNA; 19 BP.

XX  
AC ACD99445;

XX  
DT 25-SEP-2003 (first entry)

XX  
DE Immunostimulatory nucleic acid #131.

XX Immunostimulatory; antiinflammatory; dermatological; antipeoriatic;  
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

OS Synthetic.

XX  
PN US2003050268-A1.

XX  
PD 13-MAR-2003.

PF 29-MAR-2002; 2002US-00112653.

XX  
PR 29-MAR-2001; 2001US-0279642P.

XX  
PA (KRIE/) KRIEG A M.

XX  
PA (BERG/) BERG D J.

XX  
PI Krieg AM, Berg DJ;

XX  
DR WPI; 2003-521815/49.

XX  
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.

XX  
PS Disclosure; Page 12; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid

XX  
SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 616 CGCGCGCGCACGCGCGC 634  
Db 19 CGCGCGCGCGCGCGCGC 1

RESULT 382  
ADB36515

ID ADB36515 standard; DNA; 19 BP.

XX  
AC ADB36515;

XX  
DT 04-DEC-2003 (first entry)

XX  
DE Immunostimulatory nucleic acid #129.

XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.

XX  
OS Synthetic.

XX  
PN US2003087848-A1.

XX  
PD 08-MAY-2003.

XX  
PF 02-FEB-2001; 2001US-00776479.

XX  
PR 03-FEB-2000; 2000US-0179991P.

XX  
PA (BRAT/) BRATZLER R L.

XX  
PA (PETE/) PETERSEN D M.

XX  
PA (FOUR/) FOURON Y.

XX  
PI Bratzler RL, Petersen DM, Fouron Y;

XX  
DR WPI; 2003-657977/62.

XX  
PT Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX  
PS Disclosure; Page 7; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.

XX  
SQ Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 615 GCGCGCGCGCACGCGCG 633

Db 1 GCGCGCGCGCGCGCGCG 19

RESULT 383

ADB36515/c

ID ADB36515 standard; DNA; 19 BP.

XX  
AC ADB36515;

XX  
DT 04-DEC-2003 (first entry)

XX  
DE Immunostimulatory nucleic acid #129.

XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.

XX  
OS Synthetic.

XX  
PN US2003087848-A1.

XX  
PD 08-MAY-2003.

XX  
PF 02-FEB-2001; 2001US-00776479.

XX

```
PR 03-FEB-2000; 2000US-0179991P.
XX (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
XX Bratzler RL, Petersen DM, Fouron Y;
PI WPI; 2003-657977/62.
XX
XX WPI; 2003-657977/62.
XX
XX Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX Disclosure; Page 7; 221pp; English.
XX
XX The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
XX Sequence 19 BP; 0 A; 9 C; 10 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 616 CGCGCGCGCGCAGCAGCGGC 634
Db 19 CGCGCGCGCGCGCGCGCGC 1
RESULT 384
ADP42503
ID ADD42503 standard; DNA; 19 BP.
XX
XX ADD42503;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human infertility associated primer SEQ ID 364.
XX
XX primer; male infertility; infertility-associated mutation;
XX azoospermia factor; Y-chromosome;
XX cystic fibrosis transmembrane conductance regulator; CFTR;
XX Kallmann syndrome; KAL1; androgen resistance; steroid 21-hydroxylase;
XX CYP21; microarray; quantitative trait locus; in vitro fertilization;
XX oligospermia; ss.
XX
XX Homo sapiens.
XX
XX WO2003050299-A2.
XX
XX 19-JUN-2003.
XX
XX 10-DEC-2002; 2002WO-EF013995.
XX
XX 10-DEC-2001; 2001DE-01060563.
XX
XX (OGHA-) OGHAM GMBH.
XX
XX Cullen P, Seedorf U;
PI WPI; 2003-505402/47.
XX
XX Investigating male genetic infertility, useful for diagnosis e.g. for
PT assessing suitability for in vitro fertilization, based on multifactorial
PT analysis of infertility-related mutations.
XX
XX Claim 13; SEQ ID NO 365; 110pp; German.
XX
XX This invention describes a novel method for investigating genetic
CC
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CC infertility or predisposition in males. The method involves selecting at
CC least two infertility-associated mutations which are recessive or
CC intermediate that are associated with infertility in the heterozygous
CC state and/or only in the homozygous state. Preferably at least one
CC azoospermia factor is detected which may be lost by microdeletions in
CC intervals 5 or 6 of the Y-chromosome. Also any of several hundred
CC mutations, listed, present in the cystic fibrosis transmembrane
CC conductance regulator (CFTR), Kallmann syndrome (KAL1), androgen
CC resistance (AR) or steroid 21-hydroxylase (CYP21) genes may be detected.
CC Probes for the mutated genes and/or native nucleic acid, or their
CC complementary strands, are fixed to a carrier, particularly as a
CC microarray, then tested for hybridization with oligonucleotides from or
CC synthesized from, a patient sample and hybridization detected.
CC Multifactorial analysis is by standard statistical methods, particularly
CC the quantitative trait locus method. The method is used to diagnose
CC inherited male infertility or predisposition to its, especially in
CC conjunction with in vitro fertilization programs, e.g. for assessing
CC subjects with oligospermia for possible application of the
CC intracytoplasmic sperm injection method. Analysis of many mutations
CC improves diagnosis of the genetic basis of male infertility, including
CC polygenic origins (complex interactions between different heterozygotic
CC mutations). A chip for analyzing genetic infertility in males comprises
CC oligonucleotides that represent known mutations (nonsense or missense,
CC insertions, allelic variants deletions or rearrangements) in the cystic
CC fibrosis transmembrane conductance regulator, Kallmann syndrome, androgen
CC resistance and steroid 21-hydroxylase genes. ADD42140-ADD42633 represent
CC oligonucleotides used in the microarray described in the method of the
CC invention. NOTE: there are no SEQ ID's 133, 472 or 473 represented in the
CC SEQ ID list of the specification.
XX
XX Sequence 19 BP; 6 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3162 TCAAAGCCCCGACGAAACAC 3180
Db 1 TCACGTGCCCGACGAAACAC 19
RESULT 385
ADP50074
ID ADF50074 standard; RNA; 19 BP.
XX
XX ADF50074;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human BCL2 siNA lower sequence SEQ ID NO:802.
XX
XX ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
XX cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
XX autoimmune disease; viral infection; HIV.
XX
XX Homo sapiens.
XX
XX WO2003070969-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-US004908.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX
XX 11-MAR-2002; 2002US-0363124P.
XX
XX 06-JUN-2002; 2002US-0386782P.
XX
XX 18-JUL-2002; 2002US-0396905P.
XX
XX 29-AUG-2002; 2002US-0406784P.
XX
XX 05-SEP-2002; 2002US-0408378P.
XX
XX 09-SEP-2002; 2002US-0409293P.
XX
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
```

XX Mcswiggen J, Beigelman L;  
 XX WPI; 2003-712622/67.  
 XX New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of cancer or autoimmune disease, downregulates expression of  
 PT the BCL2 gene.  
 PS Example 3; SEQ ID NO 802; 148pp; English.  
 XX The invention relates to a novel short interfering nucleic acid (siNA)  
 CC that downregulates expression of the BCL2 gene by RNA interference. A  
 CC siNA of the invention has cytostatic, immunosuppressive, virucide, and  
 CC anti-HIV activity. The siNA are useful for modulation (inhibition) of  
 CC expression or activity of BCL2 by RNA interference. siNA are used to  
 CC modulate expression of BCL2 genes, in cells, tissue explants or  
 CC organisms, e.g. for treating cancer, autoimmune diseases and viral  
 CC infections (including by HIV) but also for drug screening, diagnosis,  
 CC target identification and validation, genetic engineering,  
 CC pharmacogenomics, studying gene function and gene mapping (e.g. of single  
 CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143  
 CC represent siNA of the invention.  
 XX SQ Sequence 19 BP; 7 A; 2 C; 5 G; 0 T; 5 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 68.4%; Pred. No. 2.2e+02;  
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 3748 AATGACATGAGCTACTCG 3766  
 Db 1 AAUGAAAGCUGCUACUGG 19  
 |||||:|||||:|||||  
 1 AAUGAAAGCUGCUACUGG 19  
 RESULT 386  
 ADF49399  
 ID ADF49399 standard; RNA; 19 BP.  
 XX ADF49399;  
 XX 12-FEB-2004 (first entry)  
 XX Human BCL2 siNA upper sequence SEQ ID NO:127.  
 DE ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;  
 KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;  
 KW autoimmune disease; viral infection; HIV.  
 XX Homo sapiens.  
 XX WO2003070969-A2.  
 XX 28-AUG-2003.  
 XX 18-FEB-2003; 2003WO-US004908.  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 18-JUL-2002; 2002US-0396905P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA Mcswiggen J, Beigelman L;  
 XX WPI; 2003-712622/67.  
 XX New short interfering nucleic acid, useful e.g. for treatment and

PT diagnosis of cancer or autoimmune disease, downregulates expression of  
 PT the BCL2 gene.  
 XX Example 3; SEQ ID NO 127; 148pp; English.  
 XX The invention relates to a novel short interfering nucleic acid (siNA)  
 CC that downregulates expression of the BCL2 gene by RNA interference. A  
 CC siNA of the invention has cytostatic, immunosuppressive, virucide, and  
 CC anti-HIV activity. The siNA are useful for modulation (inhibition) of  
 CC expression or activity of BCL2 by RNA interference. siNA are used to  
 CC modulate expression of BCL2 genes, in cells, tissue explants or  
 CC organisms, e.g. for treating cancer, autoimmune diseases and viral  
 CC infections (including by HIV) but also for drug screening, diagnosis,  
 CC target identification and validation, genetic engineering,  
 CC pharmacogenomics, studying gene function and gene mapping (e.g. of single  
 CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143  
 CC represent siNA of the invention.  
 XX SQ Sequence 19 BP; 7 A; 2 C; 5 G; 0 T; 5 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 68.4%; Pred. No. 2.2e+02;  
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 4248 TCCAGCTGATTAAAAA 4266  
 Db 1 UGCAGGCGUUAAGAAAA 19  
 :|||||:|||||  
 1 UGCAGGCGUUAAGAAAA 19  
 RESULT 387  
 ADF49660/c  
 ID ADF49660 standard; RNA; 19 BP.  
 XX ADF49660;  
 XX 12-FEB-2004 (first entry)  
 XX Human BCL2 siNA lower sequence SEQ ID NO:388.  
 DE ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;  
 KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;  
 KW autoimmune disease; viral infection; HIV.  
 XX Homo sapiens.  
 XX WO2003070969-A2.  
 XX 28-AUG-2003.  
 XX 18-FEB-2003; 2003WO-US004908.  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 18-JUL-2002; 2002US-0396905P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA Mcswiggen J, Beigelman L;  
 XX WPI; 2003-712622/67.  
 XX New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of cancer or autoimmune disease, downregulates expression of  
 PT the BCL2 gene.  
 XX Example 3; SEQ ID NO 388; 148pp; English.  
 XX The invention relates to a novel short interfering nucleic acid (siNA)

CC that downregulates expression of the BCL2 gene by RNA interference. A  
 CC siNA of the invention has cytostatic, immunosuppressive, virucide, and  
 CC anti-HIV activity. The siNA are useful for modulation (inhibition) of  
 CC expression or activity of BCL2 by RNA interference. siNA are used to  
 CC modulate expression of BCL2 genes, in cells, tissue explants or  
 CC organisms, e.g. for treating cancer, autoimmune diseases and viral  
 CC infections (including by HIV) but also for drug screening, diagnosis,  
 CC target identification and validation, genetic engineering,  
 CC pharmacogenomics, studying gene function and gene mapping, (e.g. of single  
 CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143  
 CC represent siNA of the invention.

SQ Sequence 19 BP; 5 A; 5 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3748 AATGACATGAGCTACCTGG 3766  
 ||||| ||||| ||||| |||||  
 Db 19 AATGAATGAGCTATCTGG 1

RESULT 388  
 ADF49813/C  
 ID ADF49813 standard; RNA; 19 BP.  
 XX  
 AC ADF49813;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human BCL2 siNA upper sequence SEQ ID NO:541.  
 XX  
 KW ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;  
 KW cytostatic; immunosuppressive; virucide; anti-HIV; cancer;  
 KW autoimmune disease; viral infection; HIV.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003070969-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 18-FEB-2003; 2003WO-US0004908.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 18-JUL-2002; 2002US-0396905P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J, Beigelman L;  
 XX  
 DR WPI; 2003-712622/67.  
 XX  
 PT New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of cancer or autoimmune disease, downregulates expression of  
 PT the BCL2 gene.  
 XX  
 PS Example 3; SEQ ID NO 541; 148pp; English.  
 XX

CC The invention relates to a novel short interfering nucleic acid (siNA)  
 CC that downregulates expression of the BCL2 gene by RNA interference. A  
 CC siNA of the invention has cytostatic, immunosuppressive, virucide, and  
 CC anti-HIV activity. The siNA are useful for modulation (inhibition) of  
 CC expression or activity of BCL2 by RNA interference. siNA are used to  
 CC modulate expression of BCL2 genes, in cells, tissue explants or  
 CC organisms, e.g. for treating cancer, autoimmune diseases and viral

CC infections (including by HIV) but also for drug screening, diagnosis,  
 CC target identification and validation, genetic engineering,  
 CC pharmacogenomics, studying gene function and gene mapping (e.g. of single  
 CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143  
 CC represent siNA of the invention.

SQ Sequence 19 BP; 5 A; 5 C; 2 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4248 TGCAGGCTGATTAATAAAA 4266  
 ||||| ||||| ||||| |||||  
 Db 19 TGCAGGCTGTTTAAAGAAA 1

RESULT 389  
 ADF31627/C  
 ID ADF31627 standard; RNA; 19 BP.  
 XX  
 AC ADF31627;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human IGF-1R siNA lower strand, SEQ ID NO:292.  
 XX  
 KW RNA interference; short interfering nucleic acid; siNA;  
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;  
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;  
 KW drug screening; diagnosis; therapeutic target identification;  
 KW pharmacogenomics; gene function analysis; gene mapping; cancer;  
 KW proliferative disease; restenosis; polycystic kidney disease;  
 KW inflammatory disease; allergic disease; autoimmune disease;  
 KW transplant rejection; cytostatic; vasotropic; nephrotropic;  
 KW antiinflammatory; antiallergic; immunosuppressive; human;  
 KW insulin-like growth factor 1 receptor; IGF-1R; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003070911-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US0005044.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Mcswiggen J, Beigelman L, Chowrira B;  
 XX  
 DR WPI; 2003-721691/68.  
 XX  
 PT New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of cancer, downregulates expression of the insulin-like growth  
 PT factor-1 receptor gene.  
 XX  
 PS Example 3; SEQ ID NO 292; 147pp; English.  
 XX

CC The invention relates to short interfering nucleic acids (siNA) which  
 CC downregulate expression of the human insulin-like growth factor 1  
 CC receptor (IGF-1R) gene by RNA interference. The siNAs may or may not  
 CC comprise ribonucleotides and may be double or single stranded. They  
 CC further comprise sense and antisense regions, or alternatively are  
 CC assembled from a sense oligonucleotide and an antisense oligonucleotide.  
 CC Specifically, the siNAs include short interfering RNA (siRNA), double-



CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs  
 CC can be unmodified or chemically modified, can contain  
 CC deoxyribonucleotides, and can be chemically synthesised, expressed from a  
 CC vector or enzymatically synthesised. The invention also relates to kits  
 CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes  
 CC of siNA; and vectors that express siNA. The siNAs are used to modulate  
 CC expression of the IGF-1R gene in cells, tissue explants or organisms  
 CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the  
 CC treatment of a variety of conditions. They may be used for treating  
 CC cancer and other proliferative diseases (e.g., restenosis and polycystic  
 CC kidney disease), inflammatory and/or allergic diseases, autoimmune  
 CC diseases and transplant rejection. The siNAs are also useful for drug  
 CC screening, diagnosis, therapeutic target identification and validation,  
 CC genetic engineering, pharmacogenomics, studying gene function, and gene  
 CC mapping (e.g., of single nucleotide polymorphisms). The present sequence  
 CC represents the lower strand of a human IGF-1R-targeted double-stranded  
 CC siNA.

XX Sequence 19 BP; 3 A; 3 C; 11 G; 0 T; 2 U; 0 Other;  
 SQ Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2332 CCGAAGCTTCCGCTTCCCC 2350  
 Db 19 CCGCAGCTACCGCTTCCCC 1  
 ||| |||| ||||| |||||

RESULT 390  
 ADF31350  
 ID ADF31350 standard; RNA; 19 BP.  
 AC ADF31350;  
 XX  
 XX 12-FEB-2004 (first entry)  
 DT Human IGF-1R transcript target sequence/siNA upper strand, SEQ ID NO:15.  
 DE  
 DE RNA interference; short interfering nucleic acid; siNA;  
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;  
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;  
 KW drug screening; diagnosis; therapeutic target identification;  
 KW pharmacogenomics; gene function analysis; gene mapping; cancer;  
 KW proliferative disease; restenosis; polycystic kidney disease;  
 KW inflammatory disease; allergic disease; autoimmune disease;  
 KW transplant rejection; cytostatic; vasotropic; nephrotropic;  
 KW antiinflammatory; antiallergic; immunosuppressive; human;  
 KW insulin-like growth factor 1 receptor; IGF-1R; target sequence; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2003070911-A2.  
 PN  
 XX  
 XX 28-AUG-2003.  
 PD  
 XX  
 XX 20-FEB-2003; 2003WO-US005044.  
 PF  
 XX  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR  
 XX 11-MAR-2002; 2002US-0363124P.  
 PR  
 XX 06-JUN-2002; 2002US-0386782P.  
 PR  
 XX 29-AUG-2002; 2002US-0406784P.  
 PR  
 XX 05-SEP-2002; 2002US-0408378P.  
 PR  
 XX 09-SEP-2002; 2002US-0409293P.  
 PR  
 XX 15-JAN-2003; 2003US-0440129P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX  
 XX Mcswiggen J, Beigelman L, Chowrira B;  
 PI  
 XX WPI; 2003-721691/68.  
 DR  
 XX  
 XX New short interfering nucleic acid, useful e.g. for treatment and

PT diagnosis of cancer, downregulates expression of the insulin-like growth  
 PT factor-1 receptor gene.  
 XX  
 XX Example 3; SEQ ID NO 15; 147pp; English.  
 PS  
 XX The invention relates to short interfering nucleic acids (siNA) which  
 CC downregulate expression of the human insulin-like growth factor 1  
 CC receptor (IGF-1R) gene by RNA interference. The siNAs may or may not  
 CC comprise ribonucleotides and may be double or single stranded. They  
 CC further comprise sense and antisense regions, or alternatively are  
 CC assembled from a sense oligonucleotide and an antisense oligonucleotide.  
 CC Specifically, the siNAs include short interfering RNA (siRNA), double-  
 CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs  
 CC can be unmodified or chemically modified, can contain  
 CC deoxyribonucleotides, and can be chemically synthesised, expressed from a  
 CC vector or enzymatically synthesised. The invention also relates to kits  
 CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes  
 CC of siNA; and vectors that express siNA. The siNAs are used to modulate  
 CC expression of the IGF-1R gene in cells, tissue explants or organisms  
 CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the  
 CC treatment of a variety of conditions. They may be used for treating  
 CC cancer and other proliferative diseases (e.g., restenosis and polycystic  
 CC kidney disease), inflammatory and/or allergic diseases, autoimmune  
 CC diseases and transplant rejection. The siNAs are also useful for drug  
 CC screening, diagnosis, therapeutic target identification and validation,  
 CC genetic engineering, pharmacogenomics, studying gene function, and gene  
 CC mapping (e.g., of single nucleotide polymorphisms). The present sequence  
 CC represents the upper strand of a human IGF-1R-targeted double-stranded  
 CC siNA, which is identical to the IGF-1R transcript target sequence.

XX  
 SQ Sequence 19 BP; 2 A; 11 C; 3 G; 0 T; 3 U; 0 Other;  
 Query Match 0.4%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 73.7%; Pred. No. 2.2e+02;  
 Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2332 CCGAAGCTTCCGCTTCCCC 2350  
 Db 1 CCGCAGCUACCGUCCCC 19  
 ||| |||| ||||| |||||

RESULT 391  
 ADQ14537/c  
 ID ADQ14537 standard; RNA; 22 BP.  
 XX ADQ14537;  
 AC ADQ14537;  
 XX  
 XX 23-SEP-2004 (first entry)  
 DT TGF beta 2 3'-UTR consensus sequence SEQ ID NO:32.  
 XX  
 XX TGF beta 2 3'-UTR consensus sequence SEQ ID NO:32.  
 DE  
 XX metabolic state; mRNA protein complex; mRNA complex; RNA binding protein;  
 KW mRNA complex-associated protein; mRNA complex-associated protein;  
 KW mRNA target; protein target; physiological pathway;  
 KW TGF beta 2 3'-UTR consensus sequence; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX WO2004057032-A1.  
 PN  
 XX  
 XX 08-JUL-2004.  
 PD  
 XX  
 XX 04-DEC-2003; 2003WO-US038475.  
 PF  
 XX  
 XX 04-DEC-2002; 2002US-00309788.  
 PR  
 XX  
 XX (RIBO-) RIBONOMICS INC.  
 PA  
 XX  
 XX Keene JD, Tenenbaum SA, Carson CC, Phelps WC;  
 PI  
 XX WPI; 2004-525445/50.  
 DR  
 XX  
 XX Assessing the metabolic state of a cell comprises isolating at least one

PT mRNP complex comprising at least one RNA binding protein, and at least  
PT one mRNA or at least one mRNP complex-associated protein.  
PS Example 4; SEQ ID NO 32; 86pp; English.  
XX  
CC The present invention describes a method for assessing the metabolic  
CC state of a cell. The method comprises isolating at least one mRNP complex  
CC having at least one RNA binding protein, and at least one mRNA or at  
CC least one mRNP complex-associated protein, and determining the expression  
CC level of the mRNA or mRNP complex-associated protein, where the level of  
CC expression of the at least one mRNA or the at least one mRNP complex-  
CC associated protein is indicative of the metabolic state of the cell. The  
CC method can be used for assessing the metabolic state in a cell, and for  
CC identifying and evaluating mRNA and protein targets associated with mRNP  
CC complexes and implicated in the expression of proteins involved in common  
CC physiological pathways. The present sequence represents a TGF beta 2 3'-  
CC UTR consensus sequence, which is used in an example from the present  
CC invention.  
XX  
SQ Sequence 22 BP; 2 A; 1 C; 2 G; 0 T; 17 U; 0 Other;  
Query Match 0.4%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.3e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2578 AAAAAAAAAATTGGAGAAAAA 2599  
DB 22 AAAAAAAAACTTAAGAAAAA 1  
RESULT 392  
AA63947  
ID AAX63947 standard; RNA; 17 BP.  
XX  
AC AAX63947;  
XX  
DT 20-JUL-1999 (first entry)  
DE Rabbit stromelysin hammerhead target SEQ ID NO:579.  
XX  
KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
KW diagnosis; ss.  
XX  
OS Oryctolagus cuniculus.  
XX  
PN WO9618736-A2.  
XX  
PD 20-JUN-1996.  
XX  
PF 22-NOV-1995; 95WO-US015516.  
XX  
PR 13-DEC-1994; 94US-00354920.  
PR 23-DEC-1994; 94US-00363253.  
PR 23-DEC-1994; 94US-00363254.  
PR 17-FEB-1995; 95US-00390850.  
PR 20-APR-1995; 95US-00426124.  
PR 02-MAY-1995; 95US-00432874.  
PR 04-MAY-1995; 95US-00434509.  
PR 07-JUL-1995; 95US-0000951P.  
PR 07-JUL-1995; 95US-0000974P.  
PR 07-AUG-1995; 95US-00512861.  
PR 05-OCT-1995; 95US-00541365.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Beigelman J, Stinchcomb DT, Jarvis T, Draper K, Pavco P;  
PI McSwiggen L, Gustafson J, Usman N, Wincott F, Matulic-Adamic J;  
PI Karpeisky A, Thompson JD, Modak A, Burgin A;  
XX WPI; 1996-300653/30.

XX  
PT Enzymatic nucleic acid molecules having a hammer-head motif - used for  
PT the treatment of arthritis, induction of graft tolerance or treatment of  
PT auto-immune diseases.  
XX  
PS Example 1; Page 155; 307pp; English.  
XX  
CC The present invention describes a novel enzymatic nucleic acid (ENA)  
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
CC : (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
CC can inhibit collagenase and stromelysin production in the synovial  
CC membrane of joints for the treatment or prevention of arthritis,  
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
CC be used to treat antigen presenting cells of a donor to induce tolerance  
CC in a recipient to an alloantigen of a donor. They can also be used for  
CC enhancing graft tolerance or for treating autoimmune disease, and for  
CC treating allergies and other inflammatory conditions. The ENA's can also  
CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
CC stromelysin without introducing the non-specific effects upon gene  
CC expression which accompany treatment with retinoids and dexamethasone.  
CC The concentration of ribozyme required to affect a therapeutic treatment  
CC is lower than that required of antisense molecules, and is highly  
CC specific. The present sequence is used in the exemplification of the  
CC present invention  
XX  
SQ Sequence 17 BP; 5 A; 1 C; 2 G; 0 T; 9 U; 0 Other;  
Query Match 0.4%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 41.2%; Pred. No. 1.9e+02;  
Matches 7; Conservative 9; Mismatches 1; Indels 0; Gaps 0;  
QY 1032 TTTTCTTTTAAAGGA 1048  
DB 1 UUUUCAUUUUUAAAGGA 17  
RESULT 393  
AA63948  
ID AAX63948 standard; RNA; 17 BP.  
XX  
AC AAX63948;  
XX  
DT 20-JUL-1999 (first entry)  
DE Rabbit stromelysin hammerhead target SEQ ID NO:580.  
XX  
KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
KW diagnosis; ss.  
XX  
OS Oryctolagus cuniculus.  
XX  
PN WO9618736-A2.  
XX  
PD 20-JUN-1996.  
XX  
PF 22-NOV-1995; 95WO-US015516.  
XX  
PR 13-DEC-1994; 94US-00354920.  
PR 23-DEC-1994; 94US-00363253.  
PR 23-DEC-1994; 94US-00363254.  
PR 17-FEB-1995; 95US-00390850.  
PR 20-APR-1995; 95US-00426124.  
PR 02-MAY-1995; 95US-00432874.  
PR 04-MAY-1995; 95US-00434509.  
PR 07-JUL-1995; 95US-0000951P.  
PR 07-JUL-1995; 95US-0000974P.  
PR 07-AUG-1995; 95US-00512861.  
PR 05-OCT-1995; 95US-00541365.  
XX

|                       |   |
|-----------------------|---|
| PA                    | (RIBO-) RIBOZYME PHARM INC.   |
| XX                    |   |
| PI                    | Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;                  |
| PI                    | McSwiggen J, Gustofson J, Usman N, Wincott F, Matulich-Adamic J;          |
| PI                    | Karpeisky A, Thompson JD, Modak A, Burgin A;                              |
| XX                    |   |
| DR                    | WPI; 1996-300653/30.  |
| XX                    |   |
| XX                    | Enzymatic nucleic acid molecules having a hammer-head motif - used for    |
| PT                    | the treatment of arthritis, induction of graft tolerance or treatment of  |
| PT                    | auto-immune diseases.   |
| XX                    |   |
| PS                    | Example 1; Page 155; 307pp; English.                                      |
| XX                    |   |
| CC                    | The present invention describes a novel enzymatic nucleic acid (ENA)      |
| CC                    | having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues |
| CC                    | ; (ii) a 2'-C-allv modification at position 4 of the ENA; (iii) at least  |
| CC                    | ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  |
| CC                    | can inhibit collagenase and stromelysin production in the synovial        |
| CC                    | membrane of joints for the treatment or prevention of arthritis,          |
| CC                    | particularly osteoarthritis or rheumatoid arthritis. The ENA's can also   |
| CC                    | be used to treat antigen presenting cells of a donor to induce tolerance  |
| CC                    | in a recipient to an alloantigen of a donor. They can also be used for    |
| CC                    | enhancing graft tolerance or for treating autoimmune disease, and for     |
| CC                    | treating allergies and other inflammatory conditions. The ENA's can also  |
| CC                    | be used in diagnosis. Ribozyme therapy impacts on the expression of       |
| CC                    | stromelysin without introducing the non-specific effects upon gene        |
| CC                    | expression which accompany treatment with retinoids and dexamethasone.    |
| CC                    | The concentration of ribozyme required to affect a therapeutic treatment  |
| CC                    | is lower than that required of antisense molecules, and is highly         |
| CC                    | specific. The present sequence is used in the exemplification of the      |
| CC                    | present invention   |
| XX                    |   |
| SQ                    | Sequence 17 BP; 6 A; 1 C; 2 G; 0 T; 8 U; 0 Other;                         |
|                       |   |
| Query Match           | 0.4%; Score 15.4; DB 1; Length 17;  |
| Best Local Similarity | 47.1%; Pred. No. 1.9e+02;   |
| Matches               | 8; Conservative 8; Mismatches 1; Indels 0; Gaps 0;                        |
|                       |   |
| QY                    | 1033 TTCTTTTTTTAAAGGAA 1049   |
|                       |   |
| DB                    | 1 UUUCUUUUUUAAGGAA 17   |
|                       |   |
| RESULT 394            |   |
| AAV93710              |   |
| ID                    | AAV93710 standard; RNA; 17 BP.  |
| XX                    |   |
| AC                    | AAV93710;   |
| XX                    |   |
| DT                    | 18-FEB-1999 (first entry)   |
| XX                    |   |
| DE                    | Human B-raf substrate nucleotide position 2457.                           |
| XX                    |   |
| KW                    | Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;        |
| KW                    | target; substrate; catalyst; modulation; expression; Raf gene; delivery;  |
| KW                    | screening; identification; synthesis; deprotection; purification; cancer; |
| KW                    | inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;   |
| KW                    | restenosis; rheumatoid arthritis; ss.                                     |
| XX                    |   |
| OS                    | Homo sapiens.   |
| PN                    | WO9850530-A2.   |
| XX                    |   |
| PD                    | 12-NOV-1998.  |
| XX                    |   |
| Pf                    | 05-MAY-1998; 98WO-US009249.   |
| XX                    |   |
| PR                    | 09-MAY-1997; 97US-0046059P.   |
| PR                    | 03-JUN-1997; 97US-0049002P.   |
| PR                    | 03-JUL-1997; 97US-0051718P.   |
| PR                    | 22-AUG-1997; 97US-0056808P.   |
| PR                    | 02-OCT-1997; 97US-0061321P.   |
|                       |   |
| PR                    | 02-OCT-1997; 97US-0061324P.   |
| PR                    | 05-NOV-1997; 97US-0064866P.   |
| XX                    |   |
| XX                    | 19-DEC-1997; 97US-0068212P.   |
| PA                    | (RIBO-) RIBOZYME PHARM INC.   |
| XX                    |   |
| PI                    | Jarvis T, Matulich-Adamic J, Reynolds M, Kisich K, Bellon L;              |
| PI                    | Ferry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;                |
| PI                    | Thompson J, Workman CT, Beaudry A, Sweedler D;                            |
| XX                    |   |
| XX                    | WPI; 1999-009494/01.  |
| XX                    |   |
| PT                    | Identifying new catalytic nucleic acid that modulates selected processes  |
| PT                    | - especially ribozymes that cleave Raf RNA for treating cancer,           |
| PT                    | restenosis, and also new ribozymes and modified nucleoside triphosphates  |
| PT                    | used as antiviral agents and synthons.                                    |
| XX                    |   |
| PS                    | Claim 177; Page 172; 259pp; English.                                      |
| XX                    |   |
| CC                    | A method has been developed for the identification of a nucleic acid      |
| CC                    | capable of modulating a process in a biological system. The method        |
| CC                    | comprises: (a) introducing into the system a random library of nucleic    |
| CC                    | acid catalysts (NAC) having a substrate binding domain (SBD), comprising  |
| CC                    | a random sequence, and a catalytic domain (CD); and (b) identifying NAC   |
| CC                    | in systems where modulation has occurred and/or determining the sequence  |
| CC                    | of at least part of the SBDs in such systems. Nucleic acid molecules with |
| CC                    | endonuclease activity and catalytic activity, from the present invention, |
| CC                    | are used to modulate gene expression in plant and mammalian cells and to  |
| CC                    | cleave target nucleic acid, particularly for treating systemic diseases   |
| CC                    | caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic |
| CC                    | ascites and infection. They may also be used to detect genetic drift and  |
| CC                    | mutations in diseased cells and to determine c-raf RNA. Specifically NACS |
| CC                    | with RNA-cleaving activity that modulate expression of the Raf gene, are  |
| CC                    | used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or   |
| CC                    | generally any condition associated with the level of c-raf. Introduction  |
| CC                    | of sugar/phosphate modifications increases stability against nuclease and |
| CC                    | activity. AAV90922 to AAV93877 represent NACS that can be used in the     |
| CC                    | method, specifically for modulating the expression of a Raf gene          |
| XX                    |   |
| SQ                    | Sequence 17 BP; 2 A; 2 C; 2 G; 0 T; 11 U; 0 Other;                        |
|                       |   |
| Query Match           | 0.4%; Score 15.4; DB 1; Length 17;  |
| Best Local Similarity | 29.4%; Pred. No. 1.9e+02;   |
| Matches               | 5; Conservative 11; Mismatches 1; Indels 0; Gaps 0;                       |
|                       |   |
| QY                    | 2743 TCCTTTTTTTTTTAAAGG 2759  |
|                       |   |
| DB                    | 1 UCUCUUUUUUUUUUAAGG 17   |
|                       |   |
| RESULT 395            |   |
| AAZ65512/c            |   |
| ID                    | AAZ65512 standard; DNA; 17 BP.  |
| XX                    |   |
| AC                    | AAZ65512;   |
| XX                    |   |
| DT                    | 30-MAR-2000 (first entry)   |
| XX                    |   |
| DE                    | Immunosuppressant'inhibitor oligonucleotide TGF-beta-23-2268.             |
| XX                    |   |
| KW                    | Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;   |
| KW                    | vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  |
| KW                    | prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; |
| KW                    | monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;      |
| KW                    | glomerulonephritis; acute respiratory distress syndrome; ss;              |
| KW                    | atherosclerosis.  |
| XX                    |   |
| OS                    | Unidentified.   |
| XX                    |   |
| PN                    | WO9963975-A2.   |
| XX                    |   |
| PD                    | 16-DEC-1999.  |
| XX                    |   |

```
PF 10-JUN-1999; 99WO-EP004013.
XX
XX 10-JUN-1998; 98EP-00110709.
XX 25-JUN-1998; 98EP-00113974.
XX
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX Schlingensiepen K, Schlingensiepen R, Brysch W;
XX
XX WPI; 2000-097470/08.
XX
XX Composition containing immune stimulant and inhibitor of agent that
XX adversely affects the immune response, for treating cancers and
XX infections.
XX
XX Claim 10; Fig 1; 30pp; English.
XX
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is
XX used in the invention. The invention relates to a composition which
XX contains at least one inhibitor (less than 100 kD) of a substance (e.g.
XX transforming growth factor TGF-beta, vascular endothelial growth factor
XX VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)
XX that adversely affects the immune response. The composition also includes
XX at least one stimulant that positively affects the immune response. This
XX oligonucleotide is an example of an inhibitor that is used in the
XX composition. The composition is used as an immunostimulant for the
XX treatment of neoplasms and infections, particularly hyperproliferation;
XX leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
XX colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
XX breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
XX malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
XX most of which are directed against TGFbeta or VEGF, are inhibitors of
XX monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
XX inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
XX colitis, diabetes, glomerulonephritis, acute respiratory distress
XX syndrome and the formation of atherosclerotic plaque
XX
XX Sequence 17 BP; 5 A; 4 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. NO. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2349 CCTGTGCTGTGTGCCA 2365
DB 17 CCTGTGCTGTGTGCCA 1
RESULT 396
ABZ59897
ID ABZ59897 standard; RNA; 17 BP.
XX
XX ABZ59897;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human K-Ras DNazyme substrate #9.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0296140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 58; Page 85; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59899 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
XX Sequence 17 BP; 3 A; 6 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. NO. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 427 CAGCAGCGCGCGCTGCA 443
DB 1 CAGCAGCGCGCGCGCA 17
RESULT 397
ADI49626/c
ID ADI49626 standard; DNA; 17 BP.
XX
XX ADI49626;
XX
XX 15-APR-2004 (first entry)
XX
XX Human tumour suppression/reversion-related DNA sequence SeqID2129.
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
XX primer; PCR; gene chip; antisense; viral disease; tumour;
XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX Homo sapiens.
XX
XX WO2003025177-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004523.
XX
XX 17-SEP-2001; 2001FR-00011980.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313354/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumours and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; SEQ ID NO 2129; 30pp; French.
```

XX This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration.  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publicdpct\_sequences  
 XX  
 SQ Sequence 17 BP; 11 A; 1 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3598 TTTTCTTTTAAATGATC 3614  
 Db 17 TTTCTTTTAAATGATC 1  
 RESULT 398  
 ADL49413/C  
 ID ADL49413 standard; RNA; 17 BP.  
 XX  
 AC ADL49413;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human PKR substrate sequence #527.  
 XX  
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
 KW protein kinase PKR; cerebrovascular accident;  
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
 KW substrate; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200281628-A2.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 03-APR-2002; 2002WO-US010512.  
 XX  
 PR 05-APR-2001; 2001US-00827395.  
 PR 29-MAY-2001; 2001US-0294412P.  
 PR 28-AUG-2001; 2001US-0315315P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;  
 XX  
 DR WPI; 2003-058513/05.  
 XX  
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite  
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
 XX  
 PS Claim 59; SEQ ID NO 2946; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
 CC that down regulate the expression or inhibit the function of a receptor  
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
 CC invention are useful for treating: cerebrovascular accident, central  
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
 CC nucleic acids of the invention are also useful for down-regulating the  
 CC expression of a target gene and as a diagnostic tool to examine genetic  
 CC drifts and mutations within diseased cells or to detect the presence of a  
 CC target RNA in a cell. The present RNA sequence represents a human PKR  
 CC substrate sequence.  
 XX  
 SQ Sequence 17 BP; 4 A; 1 C; 1 G; 0 T; 11 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2570 GTCTTTAAAAA 2586  
 Db 17 GTCTTTAAAAA 1  
 RESULT 399  
 ADL49412/C  
 ID ADL49412 standard; RNA; 17 BP.  
 XX  
 AC ADL49412;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human PKR substrate sequence #526.  
 XX  
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
 KW protein kinase PKR; cerebrovascular accident;  
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
 KW substrate; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200281628-A2.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 03-APR-2002; 2002WO-US010512.  
 XX  
 PR 05-APR-2001; 2001US-00827395.  
 PR 29-MAY-2001; 2001US-0294412P.  
 PR 28-AUG-2001; 2001US-0315315P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;  
 XX  
 DR WPI; 2003-058513/05.  
 XX  
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite  
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
 XX  
 PS Claim 59; SEQ ID NO 2945; 317pp; English.

XX CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
 CC that down regulate the expression or inhibit the function of a receptor  
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
 CC invention are useful for treating: cerebrovascular accident, central  
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
 CC nucleic acids of the invention are also useful for down-regulating the  
 CC expression of a target gene and as a diagnostic tool to examine genetic  
 CC drifts and mutations within diseased cells or to detect the presence of a  
 CC target RNA in a cell. The present RNA sequence represents a human PKR  
 CC substrate sequence.

XX SQ Sequence 17 BP; 4 A; 0 C; 1 G; 0 T; 12 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2571 TGTTTAAAAA 2587  
 DB 17 TCTTTAAAAA 1

RESULT 400  
 AAQ78463/c  
 ID AAQ78463 standard; DNA; 18 BP.  
 XX AAQ78463;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 27-JUN-1995 (first entry)  
 DE TGF-beta gene phosphorothioate antisense oligonucleotide.  
 XX  
 XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
 KW immunosuppression; oligonucleotide; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9425588-A2.  
 XX  
 XX 10-NOV-1994.  
 XX  
 XX 29-APR-1994; 94WO-EP001362.  
 XX  
 XX 30-APR-1993; 93EP-00107089.  
 PR 13-MAY-1993; 93EP-00107849.  
 XX  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
 PI Bogdahn U;  
 XX  
 XX WPI; 1994-358266/44.  
 DR  
 XX New transforming growth factor beta anti:sense oligo:nucleotide(s) - for  
 PT treating immunosuppression, tumours, etc.  
 XX  
 XX Claim 6; Page 56; 74pp; English.  
 PS  
 XX The antisense oligonucleotides are useful in the treatment of tumours in  
 CC which expression of TGF-beta is of relevance for pathogenicity and/or  
 CC inhibition of pathological angiogenesis. They are used especially for the  
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous

CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
 CC of skin carcinogenesis, and treatment of oesophageal and gastric  
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESSEQ files  
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
 CC beta 1. The sequences given in GENESSEQ files AAQ78408-78487 are antisense  
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 18 BP; 6 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2136 GCCTACTGCTTTAGAAA 2152  
 DB 17 GCCTATTGCTTTAGAAA 1

RESULT 401  
 AAZ57445/c  
 ID AAZ57445 standard; DNA; 18 BP.  
 XX AAZ57445;  
 AC  
 XX 10-APR-2000 (first entry)  
 DT  
 XX  
 DE Phosphorothioate oligonucleotide SEQ ID NO:4.  
 XX  
 XX Phosphorothioate; antisense oligonucleotide; triester oligonucleotide;  
 KW bioversible phosphate blocking group; therapeutic; diagnosis; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..18  
 FT /\*tag= a  
 FT /note= "phosphorothioate linkages"  
 XX  
 XX WO9964434-A1.  
 XX  
 XX 16-DEC-1999.  
 PD  
 XX  
 XX 10-JUN-1999; 99WO-US013141.  
 PF  
 XX 11-JUN-1998; 98US-00095822.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX Manoharan M, Guzaev A;  
 PI  
 XX WPI; 2000-116518/10.  
 DR  
 XX Oligonucleotide bioversible phosphate esters used as, e.g. research  
 PT agents.  
 XX  
 XX Example 5; Page 35; 61pp; English.  
 PS  
 XX The present invention describes oligonucleotides containing bioversible  
 CC phosphate ester groups and their mimetics. The oligonucleotides are of  
 CC value in therapeutics, diagnostics, and as research reagents. The  
 CC compound from the present invention may be used in control of hereditary,  
 CC metabolic, and/or cellular processes in any organism utilising DNA-RNA  
 CC transcription and/or RNA-protein translation. These organisms include  
 CC prokaryotic and eukaryotic unicellular and multicellular organisms;  
 CC including bacteria, yeasts, protozoa, algae, and all plants and higher  
 CC animal forms, including warm blooded animals, particularly humans; also  
 CC organelle sub-cellular translation and transcription processes. The new  
 CC synthetic process provides pre-oligonucleotides, i.e., oligonucleotides  
 CC blocked at phosphate groups by bioversible groups which can be cleaved  
 CC by intracellular and intercellular enzymes to generate an active or  
 CC oligonucleotide, as for prodrugs and drugs. By careful selection of

CC protecting groups, deprotection of nucleobases and partial deprotection  
 CC of phosphate linkages can be achieved in the reaction sequence. Suggested  
 CC specific groups include S-pivaloylmercaptethyl (SPME) and  
 CC cyanoethylcarbonyl (CEOC) groups. Spacer molecules include diglycolyl  
 CC (COCH<sub>2</sub>2OCH<sub>2</sub>2CO) and its analogue with a catechol bisresidue replacing the  
 CC oxygen atom (1,2-phenylenedioxy-diacetic acid). The present sequence  
 CC represents a phosphorothioate oligonucleotide used in the exemplification  
 CC of the present invention  
 XX  
 SQ Sequence 18 BP; 2 A; 5 C; 0 G; 11 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2578 AAAAAAAAAAATGGAG 2594  
 DB 18 AAAAAAAAAAATGGGG 2  
 RESULT 402  
 ABL57541/c  
 ID ABL57541 standard; DNA; 18 BP.  
 XX  
 AC ABL57541;  
 XX  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Nucleic acid probe f.  
 XX  
 XX Concentration; quantification; mutation detection; polymorphic;  
 KW polymerase chain reaction; PCR; probe; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN EP1046717-A2.  
 XX  
 PD 25-OCT-2000.  
 XX  
 PF 20-APR-2000; 2000EP-00108643.  
 XX  
 PR 20-APR-1999; 99JP-00111601.  
 XX  
 XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
 PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
 PA (KANK-) KANKYO ENG CO LTD.  
 XX  
 PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
 PI Koyama O, Furusho K;  
 XX  
 DR WPI; 2000-657765/64.  
 XX  
 PT Determining the concentration of a target nucleic acid, useful e.g. for  
 PT detecting genetic mutations, comprises using a fluorescently labeled  
 PT probe in which emission is reduced by binding to the target nucleic acid.  
 XX  
 PS Example 5; Page 21; 55pp; English.  
 XX  
 CC The invention relates to the determination of the concentration of a  
 CC nucleic acid target, using a fluorescently labeled probe which produces  
 CC reduced fluorescence emission when hybridised to the target nucleic acid.  
 CC The method comprises measuring the reduction in emission caused by  
 CC hybridisation. The new method is particularly used to quantify target  
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
 CC quantifying microbial cells in co-cultures or symbiotic systems, for  
 CC detecting gene mutations or polymorphisms, and for analysing melting  
 CC curves of target nucleic acids to determine a Tm value. Methods of the  
 CC invention allow target nucleic acids to be quantified quickly, easily and  
 CC accurately. Particularly there is no need to remove unbound probe, and no  
 CC materials are introduced that inhibit amplification by Taq polymerase (so  
 CC conventional PCR conditions can be used). The specificity of PCR is kept  
 CC high (amplification of primer dimers is delayed), and the limit of  
 CC quantitation is reduced. Complex probes are not needed, and amplification

CC can be monitored in real time. The working graph for data analysis  
 CC (automatically generated by a computer) has a higher correlation  
 CC coefficient than conventional graphs so more accurate quantitation is  
 CC possible. The current sequence represents a nucleic acid probe of the  
 CC invention that was used for investigating the base selectivity of a  
 CC target nucleic acid  
 XX  
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1161 TATATATATTTTCTT 1177  
 DB 17 TATATATTTTCTT 1  
 RESULT 403  
 ABA97626/c  
 ID ABA97626 standard; DNA; 18 BP.  
 XX  
 AC ABA97626;  
 XX  
 DT 11-APR-2002 (first entry)  
 XX  
 DE Probe f.  
 XX  
 XX ss; fluorochrome; nucleic acid probe; fluorescence.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2001286300-A.  
 XX  
 PD 16-OCT-2001.  
 XX  
 PF 20-APR-2000; 2000JP-00120097.  
 XX  
 PR 20-APR-1999; 99JP-00111601.  
 PR 24-AUG-1999; 99JP-00236666.  
 PR 30-AUG-1999; 99JP-00242693.  
 PR 01-FEB-2000; 2000JP-00028896.  
 XX  
 XX (BIOI-) BIOINDUSTRY KYOKAI SH.  
 PA (KANK-) KANKYO ENG KK.  
 PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.  
 XX  
 DR WPI; 2002-134193/18,  
 XX  
 PT Measurement of nucleic acids, using a nucleic acid probe and analysis of  
 PT the obtained data.  
 XX  
 PS Example 5; Page 17; 34pp; Japanese.  
 XX  
 CC This invention relates to a method for measuring nucleic acids using a  
 CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe  
 CC decreases the fluorescence of the fluorochrome when hybridised with a  
 CC target nucleic acid, the decrease in the fluorescence is measured. The  
 CC method can be used for measuring a target nucleic acid  
 XX  
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1153 TTCTTTTATATATAT 1169  
 DB 18 TTCTTTTATATATAT 2  
 RESULT 404  
 ABA97628/c

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ID  ABA97628 standard; DNA; 18 BP.
XX
AC  ABA97628;
XX
DT  11-APR-2002 (first entry)
XX
DE  Probe h.
XX
KW  ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS  Unidentified.
XX
PN  JP2001286300-A.
XX
PD  16-OCT-2001.
XX
PF  20-APR-2000; 2000JP-00120097.
XX
PR  20-APR-1999; 99JP-00111601.
PR  24-AUG-1999; 99JP-00236666.
PR  30-AUG-1999; 99JP-00242693.
PR  01-FEB-2000; 2000JP-00028896.
XX
XX  (BIOI-) BIOINDUSTRY KYOKAI SH.
PA  (KANK-) KANKYO ENG KK.
PA  (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIJUTSU SOGO KEN.
XX
XX  WPI; 2002-134193/18.
XX
XX  Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT  the obtained data.
XX
XX  Example 5; Page 17; 34pp; Japanese.
XX
XX  This invention relates to a method for measuring nucleic acids using a
CC  nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC  decreases the fluorescence of the fluorochrome when hybridised with a
CC  target nucleic acid, the decrease in the fluorescence is measured. The
CC  method can be used for measuring a target nucleic acid
XX
XX  Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
SQ
    Query Match      0.4%; Score 15.4; DB 1; Length 18;
    Best Local Similarity 94.1%; Pred. No. 2.2e+02;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1152 TTCTTTTATATATA 1168
    ||| ||||| |||||
Db  17 TTTTATATATATA 1

RESULT 405
ABL95901/c
ID  ABL95901 standard; DNA; 18 BP.
XX
AC  ABL95901;
XX
DT  19-JUN-2002 (first entry)
XX
DE  Probe h for assaying nucleic acids.
XX
KW  Probe; polymorphism detection; mutation detection; disease diagnosis;
KW  microbial identification; ss.
XX
OS  Unidentified.
XX
PN  WO200208414-A1.
XX
PD  31-JAN-2002.
XX
PF  27-JUN-2001; 2001WO-IB001147.
XX
PR  27-JUN-2000; 2000JP-00193133.
PR  03-AUG-2000; 2000JP-00236115.
PR  26-SEP-2000; 2000JP-00292483.
XX
XX  (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA  (KANK-) KANKYO ENG CO LTD.
XX
XX  Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI  Yokomaku T;
XX
XX  WPI; 2002-195876/25.
DR
XX

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PR  03-AUG-2000; 2000JP-00236115.
PR  26-SEP-2000; 2000JP-00292483.
XX
XX  (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA  (KANK-) KANKYO ENG CO LTD.
XX
XX  Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI  Yokomaku T;
XX
XX  WPI; 2002-195876/25.
DR
XX
XX  Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT  their polymorphism and mutation, particularly useful in science and
PT  medicine for e.g. analytical applications, disease diagnosis and
PT  microbial identification.
XX
XX  Example 12; Page 60; 152pp; Japanese.
XX
XX  The present invention relates to nucleic acid probes, which are useful
CC  for assaying nucleic acids by hybridising with a target nucleic acid, in
CC  which a single-stranded oligonucleotide is labelled with a fluorescent
CC  substance and a quencher in a manner that the fluorescence intensity of
CC  the hybridisation reaction system is increased after completion of the
CC  hybridisation but no stem loop structure is formed. The probes are useful
CC  for assaying nucleic acids and their polymorphism and mutation.
CC  particularly useful for e.g. analytical applications, disease diagnosis
CC  and microbial identification. The present sequence was used to illustrate
CC  the invention
XX
XX  Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
SQ
    Query Match      0.4%; Score 15.4; DB 1; Length 18;
    Best Local Similarity 94.1%; Pred. No. 2.2e+02;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1152 TTCTTTTATATATA 1168
    ||| ||||| |||||
Db  17 TTTTATATATATA 1

RESULT 406
ABL95899/c
ID  ABL95899 standard; DNA; 18 BP.
XX
AC  ABL95899;
XX
DT  19-JUN-2002 (first entry)
XX
DE  Probe f for assaying nucleic acids.
XX
KW  Probe; polymorphism detection; mutation detection; disease diagnosis;
KW  microbial identification; ss.
XX
OS  Unidentified.
XX
PN  WO200208414-A1.
XX
PD  31-JAN-2002.
XX
PF  27-JUN-2001; 2001WO-IB001147.
XX
PR  27-JUN-2000; 2000JP-00193133.
PR  03-AUG-2000; 2000JP-00236115.
PR  26-SEP-2000; 2000JP-00292483.
XX
XX  (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA  (KANK-) KANKYO ENG CO LTD.
XX
XX  Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI  Yokomaku T;
XX
XX  WPI; 2002-195876/25.
DR
XX

```



PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
 PT their polymorphism and mutation, particularly useful in science and  
 PT medicine for e.g. analytical applications, disease diagnosis and  
 PT microbial identification.

PS Example 12; Page 60; 152pp; Japanese.

XX The present invention relates to nucleic acid probes, which are useful  
 CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
 CC which a single-stranded oligonucleotide is labelled with a fluorescent  
 CC substance and a quencher in a manner that the fluorescence intensity of  
 CC the hybridisation reaction system is increased after completion of the  
 CC hybridisation but no stem loop structure is formed. The probes are useful  
 CC for assaying nucleic acids and their polymorphism and mutation,  
 CC particularly useful for e.g. analytical applications, disease diagnosis  
 CC and microbial identification. The present sequence was used to illustrate  
 CC the invention

XX Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1161 TATATATATTTTCTT 1177  
 DB 17 TATATATTTTCTT 1

RESULT 407  
 ABL9598/C  
 ID ABL9598 standard; DNA; 18 BP.

XX ABL95898;

DT 19-JUN-2002 (first entry)

XX Probe d for assaying nucleic acids.

DE Probe; polymorphism detection; mutation detection; disease diagnosis;  
 KW microbial identification; ss.

XX Unidentified.

OS WO200208414-A1.

PN 31-JAN-2002.

PD 27-JUN-2001; 2001WO-IB001147.

XX 27-JUN-2000; 2000JP-00193133.

PR 03-AUG-2000; 2000JP-00236115.

PR 26-SEP-2000; 2000JP-00292483.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (KANK-) KANKYO ENG CO LTD.

XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;

PI Yokomaku T;

XX WPI; 2002-195876/25.

DR Fluorescently-labeled nucleic acid probes for assaying nucleic acids and

XX their polymorphism and mutation, particularly useful in science and

PT medicine for e.g. analytical applications, disease diagnosis and

PT microbial identification.

PS Example 12; Page 60; 152pp; Japanese.

XX The present invention relates to nucleic acid probes, which are useful

CC for assaying nucleic acids by hybridising with a target nucleic acid, in

CC the hybridisation reaction system is increased after completion of the  
 CC hybridisation but no stem loop structure is formed. The probes are useful  
 CC for assaying nucleic acids and their polymorphism and mutation,  
 CC particularly useful for e.g. analytical applications, disease diagnosis  
 CC and microbial identification. The present sequence was used to illustrate  
 CC the invention

XX Sequence 18 BP; 14 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1152 TTCTTTTATATATA 1168  
 DB 17 TTTTATATATATA 1

RESULT 408  
 ABZ10862/C  
 ID ABZ10862 standard; DNA; 18 BP.

XX ABZ10862;

DT 16-JAN-2003 (first entry)

XX Haematopoietic cell proliferation disorder related oligonucleotide #1002.

DE Human; haematopoietic cell proliferation disorder; cytostatic;  
 KW Gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
 KW cytosine methylation state; probe; primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO200277272-A2.

XX 03-OCT-2002.

XX 26-MAR-2002; 2002WO-EP003401.

XX 26-MAR-2001; 2001US-0278333P.

XX (EPITG-) EPIGENOMICS AG.

XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;

PI Olek A, Piepenbrock C, Adorian P, Grabs G, Lesche R, Leu E;

PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;

PI Schwoppe I, Ziebarth H;

XX WPI; 2003-018942/01.

XX Detecting and differentiating between hematopoietic cell proliferative

PT disorders, comprises contacting a target nucleic acid with a reagent that  
 PT distinguishes between methylated and non-methylated CpG dinucleotides.  
 XX Claim 15; Page 67; 117pp; English.

XX The present invention describes a method for detecting and  
 CC differentiating between haematopoietic cell proliferative disorders  
 CC associated with at least 1 gene and/or their regulatory regions in a  
 CC subject. The method comprises contacting a target nucleic acid in a  
 CC biological sample obtained from the subject with at least 1 reagent,  
 CC which distinguishes between methylated and non-methylated CpG  
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
 CC represent specifically claimed nucleotide sequences from the present  
 CC invention. Oligonucleotides from the present invention can be used: for  
 CC differentiating between healthy haematopoietic cells and proliferative  
 CC disorder haematopoietic cells; for differentiating between acute  
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
 CC determining the cytosine methylation state and/or single nucleotide  
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
 CC related sequences and their complements; and as primers for the

CC amplification of haematopoietic cell proliferation disorder related DNA  
 CC sequences. The nucleotide sequences from the present invention can also  
 CC be used for detecting a predisposition to, differentiation between  
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
 CC haematopoietic cell proliferation disorders. The present method enables a  
 CC highly specific classification of haematopoietic cell proliferative  
 CC disorders allowing for improved and informed treatment of patients  
 XX  
 SQ Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;  
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2807 AAAAAAACATCAAAAC 2823  
 ||||| ||||| |||||  
 Db 18 AAAAAAACACCAAAAC 2

RESULT 409  
 AAV40352  
 ID AAV40352 standard; DNA; 19 BP.

XX AAV40352;

DT 27-AUG-2003 (revised)  
 DT 14-OCT-1998 (first entry)

DE Maize oligonucleotide marker S48F.

XX Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;  
 KW polymorphic site; corn; gramineae species; ss.

XX Synthetic.  
 OS Zea.

XX W09830717-A2.

XX 16-JUL-1998.

XX 02-DEC-1997; 97WO-EP0071134.

XX 02-DEC-1996; 96US-0032069P.

XX (BIOC-) BIOCEM SA.

XX Murigneux A;

XX WPI; 1998-399160/34.

PT Vegetal sequences including single nucleotide polymorphism - useful, e.g.  
 PT to determine polymorphisms in plants, determine strain in plant breeding  
 PT and to correlate polymorphisms with phenotypic traits.

XX Example 2; Page 9; 32pp; English.

XX The present invention describes a nucleic acid segment comprising at  
 CC least 10 contiguous nucleotides from a vegetal sequence including a  
 CC polymorphic site which is a single nucleotide polymorphism (SNP), or the  
 CC complement of the segment. Also described are: (1) an allele-specific  
 CC oligonucleotides hybridizing to segment, or their complements; and (2) a  
 CC method of analysing nucleic acids from a subject, by determining if a  
 CC base is occupying any one (or a set) of polymorphic sites in 261  
 CC sequences derived from six maize lines (see AAV47701 to AAV47961). The  
 CC segments are useful in fingerprint analysis in plants to determine which  
 CC polymorphisms are present, which strain a plant belongs to and to  
 CC distinguish between strains. The polymorphisms may correlate with  
 CC phenotypic traits (e.g. plant growth rate or crop yield), and the  
 CC segments are useful to determine the presence/absence of specific  
 CC polymorphisms correlating with the existence/absence of particular  
 CC traits. The segments are also useful in marker assisted back-cross  
 CC techniques to select plants with a higher percentage of recurrent parent  
 CC in a back-cross population. Segments incorporate SNPs which occur more

CC frequently than other polymorphism types and are therefore more likely to  
 CC be located close to genetic loci of interest; different forms of  
 CC characterised SNPs are also often easier to detect than other  
 CC polymorphism types. AAV40304 to AAV40369 are used in an example from the  
 CC present invention as markers and PCR primers. (Updated on 27-AUG-2003 to  
 CC correct OS field.)  
 XX

SQ Sequence 19 BP; 7 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3090 AGGGGGAAGGAGTTCAT 3106  
 ||||| ||||| |||||  
 Db 2 AGGGGGAAGAGGTTCAT 18

RESULT 410  
 AAA72748/c  
 ID AAA72748 standard; DNA; 19 BP.

XX AAA72748;

XX 11-DEC-2000 (first entry)

DE PCR primer WB242 for bkt:npt construct fragment amplification.

XX Transgenic plant; potato; lepidopteran resistance; delta endotoxin;  
 KW hornworm; pesticide; PCR primer; ss.

XX Bacillus thuringiensis.

XX US6100456-A.

XX 08-AUG-2000.

XX 16-MAR-1992; 92US-00851509.

XX 16-MAR-1992; 92US-00851509.

XX (UNMS ) UNIV MICHIGAN STATE.

XX Sticklen MB, Cheng J;

XX WPI; 2000-542452/49.

PT New transgenic potato (Solanum tuberosum) plants resistant to  
 PT lepidopteran insects comprise 5-10 copies of DNA encoding Bacillus  
 PT thuringiensis endotoxin, for reducing synthetic pesticides in protecting  
 PT potato crops.

XX Example 1; Col 5; 17pp; English.

XX A transformed potato (Solanum tuberosum) plant comprising 5-10 copies of  
 CC a DNA, which encodes a Bacillus thuringiensis endotoxin integrated into  
 CC the plant genome, has resistance to lepidopteran insects. The DNA encodes  
 CC the B. thuringiensis variety Kustaki (b.k.t.) HD-73 delta endotoxin  
 CC (represented by sequence AAA72746). The potato plants are transformed  
 CC using a vector containing the endotoxin gene fragment and neomycin  
 CC phosphotransferase II (NPT II) in a translational fusion. The transgenic  
 CC potato plants with higher endotoxin expression are more resistant to  
 CC lepidopteran insects e.g. hornworms, hence these transgenic plants are  
 CC particularly useful in reducing the amount of synthetic pesticides used  
 CC in protecting potato crops worldwide, and for producing lepidopteran  
 CC insect resistant potato varieties. The present sequence represents a PCR  
 CC primer used to amplify a fragment of the HD-73 endotoxin and NPT II  
 CC construct. The PCR product is used in the construction of the transgenic  
 CC plant of the invention

SQ Sequence 19 BP; 6 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;

```
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2612 GTTCAACATTTTGCAA 2628
DB 19 GTTCAACATTTTGCAA 3

RESULT 411
AAA85943/c
ID AAA85943 standard; DNA; 19 BP.
XX AC AAA85943;
XX DT 04-DEC-2000 (first entry)
XX DE Cdc 25 hs ribozyme binding site #51.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX DE Cdc 25 hs ribozyme binding site #51.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX WPI; 2000-412314/35.
XX DE New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX PS Disclosure; Page 100; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX SQ Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAA 940
DB 17 CCAGGAGAAAAA 1

RESULT 412
AAA85940/c
ID AAA85940 standard; DNA; 19 BP.
XX AC AAA85940;
XX DT 04-DEC-2000 (first entry)
XX DE Cdc 25 hs ribozyme binding site #48.
XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAA 940
DB 17 CCAGGAGAAAAA 1

RESULT 413
AAZ70263
ID AAZ70263 standard; DNA; 19 BP.
XX AC AAZ70263;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker upstream amplification primer SEQ ID NO:4619.
XX KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX OS Homo sapiens.
XX PN WO954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;
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XX WPI; 2000-013267/01.  
 DR Novel biallelic markers used to construct a high density disequilibrium  
 XX map of the human genome.  
 PT  
 XX  
 PS Claim 8; Page 1216; 2745pp; English.  
 XX  
 CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention  
 XX  
 XX Sequence 19 BP; 5 A; 2 C; 5 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3126 GTTGTATAGCACTAAG 3142  
 |||||  
 DB 2 GTTGTATAGCACTAAG 18

RESULT 414  
 AAZ29275  
 ID AAZ29275 standard; DNA; 19 BP.  
 XX  
 AC AAZ29275;  
 XX  
 DT 28-FEB-2000 (first entry)  
 XX  
 DE Antisense nucleotide of sALG-2LP CDNA 3'UTR.  
 XX  
 KW Antisense nucleotide; sALG-2LP 3'UTR; programmed cell death; sALG-2LP;  
 KW monkey apoptosis linked gene-2 like protein; apoptosis;  
 KW Alzheimer's disease; Parkinson's disease; Lewy diffuse body disease;  
 KW multiple sclerosis; proliferative disorder;  
 KW amyotrophic lateral sclerosis; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9961459-A1.  
 PN  
 XX  
 PD 02-DEC-1999.  
 XX  
 XX 13-MAY-1999; 99WO-US010581.  
 PF  
 XX 26-MAY-1998; 98US-00084749.  
 PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Curtis RAJ;  
 PI  
 XX WPI; 2000-086701/07.  
 DR  
 XX Genes useful for treating neurodegenerative disorders characterized by  
 XX deregulated programmed cell death, such as Alzheimer's disease, multiple  
 XX sclerosis and Parkinson's disease.  
 PT  
 PS Disclosure; Page 23; 108pp; English.  
 XX

CC The present sequence is the antisense nucleotide to the 3'UTR region of  
 CC monkey apoptosis linked gene-2 like protein (sALG-2LP) which modulates  
 CC programmed cell death. This nucleotide when administered to a subject or  
 CC generated in situ hybridises with cellular mRNA or genomic DNA encoding  
 CC sALG-2LP to inhibit expression of the protein by inhibiting transcription  
 CC or translation. sALG-2LP proteins are used for identifying compounds  
 CC modulating the activity of a protein involved in apoptosis which may provide  
 CC novel therapeutic approaches for treatment of disorders characterised by  
 CC deregulated programmed cell death, e.g. Alzheimer's disease, Parkinson's  
 CC and other Lewy diffuse body diseases, multiple sclerosis, amyotrophic  
 CC lateral sclerosis, proliferative disorders etc  
 XX  
 XX Sequence 19 BP; 5 A; 7 C; 4 G; 3 T; 0 U; 0 Other;  
 SQ

Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 158 CAACCCATCTGCGGAGA 174  
 |||||  
 DB 3 CAACCCATCTGCGGAGA 19

RESULT 415  
 AAA71584/c  
 ID AAA71584 standard; DNA; 19 BP.  
 XX  
 AC AAA71584;  
 XX  
 DT 11-DEC-2000 (first entry)  
 XX  
 DE Human MPROT13 forward PCR primer.  
 XX  
 KW MPROT13; human; metalloprotease; gene therapy; respiratory disease;  
 KW arthritis; thrombosis; diabetes; cancer; inflammatory disorder;  
 KW osteoporosis; cardiovascular disorder; neurodegenerative disease;  
 KW central nervous system disorder; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200044913-A1.  
 PN  
 XX  
 PD 03-AUG-2000.  
 XX  
 XX 17-JAN-2000; 2000WO-EP000344.  
 PF  
 XX 28-JAN-1999; 99GB-00001947.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 XX Southan CD, Palmer L, Zhu Y, Li X;  
 PI  
 XX WPI; 2000-505980/45.  
 DR  
 XX New metalloprotease (MPROT)13 polypeptides and polynucleotides, used to  
 XX treat arthritis, diabetes, respiratory disorders, cancer, inflammation,  
 XX and neurodegenerative disorders.  
 PT  
 XX Example; Page 22; 34pp; English.  
 PS  
 XX This invention describes a novel human metalloprotease (MPROT)13  
 CC polypeptide (I), which can be used for gene therapy. (I) and  
 CC polynucleotides encoding it can be used to treat arthritis, respiratory  
 CC disease, thrombosis, diabetes, cancer, inflammatory disorders,  
 CC osteoporosis, cardiovascular disorders, neurodegenerative diseases, and  
 CC central nervous system disorders. Modulators of (I) can be used to treat  
 CC conditions associated with MPROT13 imbalance. (I) can also be used in  
 CC diagnostic assays to detect diseases associated with inappropriate  
 CC MPROT13 activity, or levels. The polynucleotides can be used as  
 CC hybridization probes for cDNA and genomic DNA and as primers for  
 CC polymerase chain reaction, to isolate full length cDNAs and genomic  
 CC clones of other genes which have high similarity to the polynucleotide

CC sequence encoding (I). This sequence represents a PCR primer used in the  
 CC amplification of the human MPROT13 protein described in the method of the  
 CC invention  
 XX  
 SQ Sequence 19 BP; 2 A; 2 C; 9 G; 6 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1748 AACATCTCCACCAGC 1764  
 Db 18 AACATCTCCAGCCAGC 2  
 RESULT 416  
 AAC89901  
 ID AAC89901 standard; DNA; 19 BP.  
 XX AC AAC89901;  
 XX  
 DT 08-MAR-2001 (first entry)  
 XX  
 DE Oligonucleotide #2 used in a nucleic acid hybridisation assay.  
 XX  
 KW Fluorescence polarisation assay; polyion; binding assay;  
 KW enzyme activity assay; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200072016-A1.  
 PD 30-NOV-2000.  
 XX  
 PF 11-MAY-2000; 2000WO-US013293.  
 XX  
 PR 21-MAY-1999; 99US-00316447.  
 PR 16-JUN-1999; 99US-0139562P.  
 PR 28-SEP-1999; 99US-0156366P.  
 XX  
 PA (CALI-) CALIPER TECHNOLOGIES CORP.  
 XX  
 PI Nikiforov TT;  
 XX  
 DR WPI; 2001-061370/07.  
 XX  
 XT Fluorescence polarization assays using polyions for detecting  
 PT phosphorylation of a phosphorylatable compound, and for identifying the  
 PT presence of a subsequence of nucleotides in a target sequence.  
 XX  
 PS Example 6; Page 38; 82pp; English.  
 XX  
 CC The present invention relates to a fluorescence polarisation assay  
 CC involving polyions. The assay of the present invention is useful for  
 CC identifying the presence of a subsequence of nucleotides in a target  
 CC nucleic acid sequence. In addition, the assay is useful in carrying out a  
 CC variety of binding assays and in assaying for enzymatic activity. The  
 CC present sequence is an oligonucleotide used in a nucleic acid  
 CC hybridisation assay, using the fluorescence polarisation detection assay  
 CC of the present invention  
 XX  
 SQ Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2123 CGCTTTGGATGCTGCT 2139  
 Db 1 CGCTTGGATGCTGCT 17  
 RESULT 417

AAC61102/c  
 ID AAC61102 standard; DNA; 19 BP.  
 XX  
 AC AAC61102;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Cdc25 hs ribozyme binding site SEQ ID NO:3526.  
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;  
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;  
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;  
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
 KW basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;  
 KW sickle cell retinopathy; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200130362-A2.  
 PD 03-MAY-2001.  
 XX  
 PF 26-OCT-2000; 2000WO-US029500.  
 XX  
 PR 26-OCT-1999; 99US-0161532P.  
 XX  
 PA (IMMU-) IMMUSOL INC.  
 XX  
 PI Robbins JM, Tritz R;  
 XX  
 DR WPI; 2001-300427/31.  
 XX  
 XT Treating proliferative skin or eye diseases and scarring, using ribozymes  
 PT that cleave RNA encoding cytokines involved in inflammation, matrix  
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
 XX  
 PS Example 1; Page 328; 408pp; English.  
 XX  
 CC The present invention describes a method for treating a proliferative  
 CC skin or eye disease and scarring. The method involves administering a  
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
 CC dependent kinase, growth factor or a reductase, or administering a  
 CC nucleic acid molecule (II) comprising a promoter operably linked to a  
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,  
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,  
 CC ophthalmological, vulnery, keratolytic and virucide activities, and  
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
 CC also be used for treating proliferative eye diseases such as diabetic  
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
 CC prematurity and retinal detachment, and for treating and preventing  
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
 CC scar. AAC61102/c represents sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 19 BP; 1 A; 3 C; 4 G; 11 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 925 CAGGAGAAAAAACAAC 941  
 Db 19 CAGGAGAAAAAACAAC 3

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RESULT 418
AAH61105/c
ID AAH61105 standard; DNA; 19 BP.
XX
XX
AC AAH61105;
DT
DT 10-SEP-2001 (first entry)
XX
DE Cdc25 hs ribozyme binding site SEQ ID NO:3529.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cycostatic;
KW antipsoptic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antiskilling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200130362-A2.
PN
PN 03-MAY-2001.
PD
PF 26-OCT-2000; 2000WO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
PR
XX (IMMU-) IMMUSOL INC.
PA
XX
XX Robbins JM, Tritz R;
PI
PI WPI; 2001-300427/31.
DR
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 328; 408pp; English.
PS
XX
XX The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoptic,
CC dermatological, cycostatic, antiseborrheic, antidiabetic, antiskilling,
CC ophthalmological, vulnery, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 19 BP; 0 A; 3 C; 4 G; 12 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CCAGGAGAAAAA 940
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Db 17 CCAGGAGAAAAA 1
RESULT 419
ABL41198/c
ID ABL41198 standard; RNA; 19 BP.
XX
XX ABL41198;
AC
DT 12-AUG-2002 (first entry)
XX
XX Human p27 gene polymorphic fragment.
DE
XX Genetic diagnosis; tumour; single nucleotide polymorphism; SNP; human;
KW p27; ds.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH allele 13
FT /*tag= a
FT /note= "SNP of U to C"
XX
XX JP2002095484-A.
PN
XX 02-APR-2002.
PD
PF 26-SEP-2000; 2000JP-00291869.
XX
XX 26-SEP-2000; 2000JP-00291869.
PR
XX (TAKA/) TAKAHASHI H.
XX (OKAN/) OKANO H.
XX (DARN/) DARNELL R B.
PA
XX WPI; 2002-439992/47.
DR
XX
XX Genetic diagnosis or screening of danger of contracting malignant tumors,
PT involves judging single nucleotide polymorphisms.
XX
XX Disclosure; Fig 2; 6pp; Japanese.
PS
XX The invention relates to genetic diagnosis or screening of danger of
CC contracting malignant tumors by judging from the single nucleotide
CC polymorphism of the 79th base at the upstream side of human p27 gene
CC translational region. The method can be used for investigating if a
CC patient is easily contracted by malignant tumours. The present sequence
CC represents a human p27 gene polymorphic fragment
XX
XX Sequence 19 BP; 1 A; 6 C; 10 G; 0 T; 2 U; 0 Other;
SQ
Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 723 AGCCCGGCGCAGCCCG 739
|||||
Db 19 AGCCCGGCGCAGCCCG 3
RESULT 420
ABA97625/c
ID ABA97625 standard; DNA; 19 BP.
XX
XX ABA97625;
AC
XX
XX 11-APR-2002 (first entry)
DT
XX Probe d.
DE
XX ss; fluorochrome; nucleic acid probe; fluorescence.
KW
XX Unidentified.
OS

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XX PN JP2001286300-A.
XX PD 16-OCT-2001.
XX PF 20-APR-2000; 2000JP-00120097.
XX PR 20-APR-1999; 99JP-00111601.
XX PR 24-AUG-1999; 99JP-00236666.
XX PR 30-AUG-1999; 99JP-00242693.
XX PR 01-FEB-2000; 2000JP-00028896.
XX PA (BIOI-) BIOINDUSTRY KYOKAI SH.
XX PA (KANK-) KANKYO ENG KK.
XX PA (KEIZ-) KEIZAI SANGYOUSHO SANGYO GIJUTSU SOGO KEN.
XX DR WPI; 2002-134193/18.
XX MEASUREMENT OF nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX Example 5; Page 17; 34pp; Japanese.
XX This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX Sequence 19 BP; 15 A; 0 C; 0 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1152 TTCTTTTTTATATATA 1168
DB 17 TTTT TTTT TTTT ATATA 1

RESULT 421
ACA62440
ID ACA62440 standard; DNA; 19 BP.
XX ACA62440;
XX 14-AUG-2003 (first entry)
XX HCV core protein frameshift region DNA #2.
XX HCV; hepatitis C infection; RNA frameshift; core protein; p17; virucide;
KW hepatotropic; overlapping open reading frame; p21c; vaccine; ds.
XX Hepatitis C virus.
OS
PN US2002076415-A1.
XX 20-JUN-2002.
XX 14-DEC-2000; 2000US-00736959.
XX 14-DEC-1999; 99US-0170835P.
XX (OUJ/) OU J.
XX (XUZ/) XU Z.
XX Ou J, Xu Z;
PI WPI; 2003-479366/45.
XX Isolated hepatitis C virus (HCV) proteins formed by expression of
PT overlapping open reading frames in the core protein gene sequence through
PT a frame shifting mechanism, useful for vaccinating against, and detecting
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PT HCV infections.
XX Example 5; Fig 6B; 37pp; English.
XX The invention relates to an isolated and purified protein of the
CC hepatitis C virus (HCV) that is formed by expression of an overlapping
CC open reading frame in the core protein gene sequence through an RNA frame
CC shifting mechanism. The protein is termed p17 (the full length, unshifted
CC protein being p21c). Also included are a vaccine (including a DNA
CC vaccine) for immunising a mammal against hepatitis C (producing a
CC protective antibody) comprising at least 1 protein of p17 (or a nucleic
CC acid encoding p17), an anti-viral composition (used to treat hepatitis C)
CC comprising a compound that binds to p17, antibodies directed against an
CC HCV core protein which are elicited by immunising an animal using the
CC partially purified protein p17, a method for analysing an HCV antigen in
CC a sample using the anti-p17 antibodies and detection of anti-HCV
CC antibodies in a sample using the p17 proteins. The HCV p17 and the DNA
CC sequences that encode it may be used as vaccines for immunising patients
CC against HCV infection. The antibodies and the antiviral compound may also
CC be used for treating HCV infections. HCV p17 and the antibodies may also
CC be used in immunoassays for detecting HCV antigens and/or antibodies in
CC samples for the diagnosis of HCV infections. The present sequence
CC represents part of the an HCV core protein DNA from the frameshift region
XX Sequence 19 BP; 15 A; 2 C; 1 G; 1 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 931 AAAAAAAACCAACCT 947
DB 1 AAAAAAAACCAACCT 17

RESULT 422
ADS90818
ID ADS90818 standard; DNA; 19 BP.
XX ADS90818;
XX 18-NOV-2004 (first entry)
XX Oligonucleotide of the invention SEQ ID NO:1834.
XX ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
XX Unidentified.
OS
PN WO2004035803-A2.
XX 29-APR-2004.
XX 01-OCT-2003; 2003WO-EP010881.
XX 01-OCT-2002; 2002DE-01045779.
XX 07-JAN-2003; 2003DE-01000096.
XX 17-APR-2003; 2003DE-01017955.
XX (EPIG-) EPIGENOMICS AG.
XX Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI Nimrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX WPI; 2004-348468/32.
XX Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
XX Disclosure; SEQ ID NO 1834; 104pp; English.
```

XX The invention relates to a novel method for predicting the responsiveness  
 CC of a subject with a cell proliferative disorder of the breast tissues to  
 CC a therapy comprising analysing the methylation pattern of a target  
 CC nucleic acid by contacting at least one of the target nucleic acids in a  
 CC biological sample obtained from the subject prior to or during treatment.  
 CC The method of the invention has cytostatic activity, and may have a use  
 CC in gene therapy. The set of oligonucleotides comprising at least two of  
 CC the oligomers are useful for detecting the cytosine methylation state  
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The  
 CC methods, nucleic acid, oligonucleotide, and kit are useful for the  
 CC treatment, characterisation, classification and/or differentiation, of  
 CC breast cell proliferative disorders. The method is also useful for  
 CC predicting the responsiveness of a subject with a cell proliferative  
 CC disorder of the breast tissues to a therapy. The present sequence is used  
 CC in the exemplification of the invention.

XX SQ Sequence 19 BP; 3 A; 0 C; 5 G; 11 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2959 GTTATTTATTGTTGTT 2975  
 Db 1 GGTATTTATTGTTGTT 17

RESULT 423  
 ADS75429/c  
 ID ADS75429 standard; DNA; 19 BP.  
 XX  
 AC ADS75429;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 XX TAK-1 gene PCR primer K-TRAL3.  
 XX  
 DE ss; primer; antiinflammatory; antiasthmatic; respiratory;  
 KW central nervous system; antiallergic; antiarthritic; antirheumatic;  
 KW antiulcer; gastrointestinal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004083854-A1.  
 XX  
 PD 30-SEP-2004.  
 XX  
 PF 16-MAR-2004; 2004WO-EP002712.  
 XX  
 PR 17-MAR-2003; 2003GB-00006071.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 XX  
 XX Dubois G;  
 XX  
 XX WPI; 2004-728516/71.  
 XX  
 XX Identifying substance which modulates activity of transforming growth  
 PT factor beta-activated kinase 1 (TAK1) useful for treating inflammatory  
 PT diseases, involves combining candidate substance with kinase and  
 PT measuring activity of kinase.  
 XX  
 PS Example 1; Page 11; 17pp; English.  
 XX  
 CC The invention relates to a method of identifying (M1) a substance  
 CC suitable for use in the treatment of an inflammatory disease which  
 CC modulates the activity of transforming growth factor beta-activated  
 CC kinase 1 (TAK1), by combining a candidate substance with the kinase and  
 CC measuring the effect of the candidate substance on the activity of the  
 CC kinase. (M1) is useful for identifying a substance suitable for use in  
 CC the treatment of an inflammatory disease which modulates the activity of

CC TAK1. (II), (III) or (IV) is useful in preparation of a pharmaceutical  
 CC that inhibits the accumulation of leukocytes in a human tissue or in  
 CC preparation of pharmaceutical for the treatment of an inflammatory  
 CC disease. The inflammatory disease is a respiratory disease which is  
 CC asthma, chronic obstructive pulmonary disease, cystic fibrosis,  
 CC adult/acute respiratory distress syndrome or allergic rhinitis. The  
 CC respiratory disease is chronic obstructive pulmonary disease (COPD) (all  
 CC claimed). The substance identified by (M1) is useful for treating  
 CC inflammatory disease such as neutrophil associated inflammatory or  
 CC obstructive airways diseases including COPD, chronic bronchitis and  
 CC emphysema, cystic fibrosis and adult (or acute) respiratory distress  
 CC syndrome (ARDS), rheumatoid arthritis and inflammatory bowel diseases  
 CC such as Crohn's disease and ulcerative colitis. The substance identified  
 CC by (M1) is useful for treating eosinophil-associated inflammatory or  
 CC obstructive airways diseases such as asthma and allergic rhinitis. This  
 CC sequence corresponds to a PCR primer to amplify the TAK1 gene from a  
 CC retroviral insert following selection based on a reduction of ICAM-1  
 CC expression in A549.tTA.G3 cells.

XX SQ Sequence 19 BP; 6 A; 3 C; 10 G; 0 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15.4; DB 1; Length 19;  
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2927 CCTCCCGTCCCTTCCT 2943  
 Db 19 CCTCCCGTCCCTTCCT 3

RESULT 424  
 AAF87713  
 ID AAF87713 standard; DNA; 20 BP.  
 XX  
 AC AAF87713;  
 XX  
 DT 06-JUL-2001 (first entry)  
 XX  
 DE Human glutathione S-transferase pi promoter (GSTP1) PCR primer N-F1.  
 XX  
 KW Human; glutathione S-transferase pi; GSTP1; CpG island; diagnosis;  
 KW hepatic cell proliferative disorder; liver cancer; anticancer;  
 KW tumorigenesis; detection; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200126536-A2.  
 XX  
 PD 19-APR-2001.  
 XX  
 PF 12-OCT-2000; 2000WO-US028427.  
 XX  
 PR 13-OCT-1999; 99US-0159168P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 PA  
 PI Nelson WG, Lin X, Tchou JC, Bakker J;  
 XX  
 XX WPI; 2001-290647/30.  
 DR  
 PT Detecting hepatic cell proliferative disorder useful for detecting  
 PT hepatocellular carcinoma comprises detecting a methylated CpG-containing  
 PT glutathione-S-transferase nucleic acid.  
 XX  
 PS Claim 83; Page 42; 64pp; English.  
 XX  
 CC The present invention describes a method for detecting hepatic cell  
 CC proliferative disorders. The method comprises detecting a methylated CpG-  
 CC containing glutathione-S-transferase (GST) nucleic acid (I) in a hepatic  
 CC specimen or a biological fluid, where a methylated GST nucleic acid is  
 CC indicative of a hepatic cell proliferative disorder. The method can be  
 CC used to diagnose hepatocellular carcinoma, and to monitor progress of its  
 CC treatment. Increasing the level of GST is useful in the treatment of



CC liver cancer, in humans or animals. The method can detect the early  
 CC stages of tumorigenesis in liver cells simply. The present sequence  
 CC represents a PCR primer which is used in the amplification of the human  
 CC glutathione S-transferase pi gene (GSTP1) promoter in an example from the  
 CC present invention for mapping somatic GSTP1 CpG island DNA  
 CC hypermethylation changes by genomic sequencing after bisulfite treatment  
 XX  
 SQ Sequence 20 BP; 4 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 20;  
 Best Local Similarity 94.1%; Pred. No. 2.8e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2742 ATCTTTTCTTTTAAAG 2758  
 |||||  
 Db 4 ATTTTCTTTTAAAG 20

RESULT 425  
 AAV48999/C  
 ID AAV48999 standard; DNA; 15 BP.  
 XX  
 AC AAV48999;  
 XX  
 DT 15-OCT-1998 (first entry)  
 XX  
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-N-32.  
 XX  
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 PN EP856579-A1.  
 XX  
 PD 05-AUG-1998.  
 XX  
 PF 31-JAN-1997; 97EP-00101531.  
 XX  
 PR 31-JAN-1997; 97EP-00101531.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Brysch W;  
 XX  
 DR WPI; 1998-400910/35.  
 XX

XX Preparation of antisense oligo:nucleotide(s) which lack long runs of  
 PT consecutive guanosine or inosine - and have specific ratio of residues  
 PT able to form two or three hydrogen bonds, have greater activity and  
 PT reduced toxicity, used therapeutically or to modulate growth of cells in  
 PT culture.  
 XX  
 PS Example 6; Fig 8b; 286pp; English.  
 XX  
 CC AAV48930-49007 represent antisense oligonucleotides directed against  
 PS transforming growth factor-beta2 (TGF-beta2). Of these, only  
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
 CC little effect. The oligonucleotides exemplify the invention. The  
 CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 CC which contain at most 8 nucleotides that can each form three hydrogen  
 CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 CC form three H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or  
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 CC keratinocytes). The oligonucleotides can also be used to analyse function  
 CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 CC stimulating the immune system

CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 CC stimulating the immune system  
 XX  
 SQ Sequence 15 BP; 6 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1919 TAATAATACATCAT 1933  
 |||||  
 Db 15 TAATAATACATCAT 1

RESULT 426  
 AAV48950/C  
 ID AAV48950 standard; DNA; 15 BP.  
 XX  
 AC AAV48950;  
 XX  
 DT 15-OCT-1998 (first entry)  
 XX  
 DE TGF-beta2 antisense oligonucleotide TGF-beta2-21.  
 XX  
 KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 PN EP856579-A1.  
 XX  
 PD 05-AUG-1998.  
 XX  
 PF 31-JAN-1997; 97EP-00101531.  
 XX  
 PR 31-JAN-1997; 97EP-00101531.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen K, Brysch W;  
 XX  
 DR WPI; 1998-400910/35.  
 XX

XX Preparation of antisense oligo:nucleotide(s) which lack long runs of  
 PT consecutive guanosine or inosine - and have specific ratio of residues  
 PT able to form two or three hydrogen bonds, have greater activity and  
 PT reduced toxicity, used therapeutically or to modulate growth of cells in  
 PT culture.  
 XX  
 PS Claim 10; Fig 8a; 286pp; English.  
 XX  
 CC AAV48930-49007 represent antisense oligonucleotides directed against  
 PS transforming growth factor-beta2 (TGF-beta2). Of these, only  
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
 CC little effect. The oligonucleotides exemplify the invention. The  
 CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 CC which contain at most 8 nucleotides that can each form three hydrogen  
 CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 CC form three H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or  
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 CC keratinocytes). The oligonucleotides can also be used to analyse function  
 CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 CC stimulating the immune system

XX SQ Sequence 15 BP; 4 A; 6 C; 2 G; 3 T; 0 U; 0 Other;  
 Query Match 0.4%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1968 GCAGGTATTGATGGC 1982  
 |||||  
 Db 15 GCAGGTATTGATGGC 1

RESULT 427  
 AAV48951/c  
 ID AAV48951 standard; DNA; 15 BP.  
 XX AC AAV48951;  
 XX DT 15-OCT-1998 (first entry)  
 XX DE TGF-beta2 antisense oligonucleotide TGF-beta2-22.  
 XX KW Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 XX KW modulate; gene expression; ss.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN EP856579-A1.  
 XX PD 05-AUG-1998.  
 XX PF 31-JAN-1997; 97EP-00101531.  
 XX PF 31-JAN-1997; 97EP-00101531.  
 XX PR (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX PA Schlingensiepen K, Brysch W;  
 XX PI WPI; 1998-400910/35.  
 XX DR Preparation of antisense oligo:nucleotide(s) which lack long runs of  
 XX PT consecutive guanosine or inosine - and have specific ratio of residues  
 XX PT able to form two or three hydrogen bonds, have greater activity and  
 XX PT reduced toxicity, used therapeutically or to modulate growth of cells in  
 XX PT culture.  
 XX PS Claim 10; Fig 8a; 286pp; English.

XX CC AAV48930-49007 represent antisense oligonucleotides directed against  
 XX CC transforming growth factor-beta2 (TGF-beta2). Of these, only  
 XX CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
 XX CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
 XX CC little effect. The oligonucleotides exemplify the invention. The  
 XX CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 XX CC which contain at most 8 nucleotides that can each form three hydrogen  
 XX CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 XX CC form three H-bonds each to four consecutive cytosines; do not contain two  
 XX CC sequences of three consecutive nucleotides each able to form three H-  
 XX CC bonds to three consecutive cytosines, and the ratio between residues able  
 XX CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 XX CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 XX CC genes, particularly the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or  
 XX CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 XX CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 XX CC keratinocytes). The oligonucleotides can also be used to analyse function  
 XX CC of proteins (by altering their expression or activity) and  
 XX CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 XX CC stimulating the immune system

XX SQ Sequence 15 BP; 4 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

XX SQ Query Match 0.4%; Score 15; DB 1; Length 15;  
 XX SQ Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 XX SQ Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1971 GGTTATTGATGGCACC 1985  
 |||||  
 Db 15 GGTTATTGATGGCACC 1

RESULT 428  
 AAF53238/c  
 ID AAF53238 standard; DNA; 15 BP.  
 XX AC AAF53238;  
 XX DT 30-MAR-2001 (first entry)  
 XX DE TGF-I oligonucleotide #4198.  
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 XX KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 XX KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
 XX KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 XX KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 XX KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 XX KW hyperneovascular condition; hyperplasia; kidney disease;  
 XX KW neovascular condition of the retina; ss.  
 XX OS Homo sapiens.  
 XX PN WO200078341-A1.  
 XX PD 28-DEC-2000.  
 XX PF 21-JUN-2000; 2000WO-AU000693.  
 XX PF 21-JUN-1999; 99US-0140345P.  
 XX PR (MURD-) MURDOCH CHILDRENS RES INST.  
 XX PA Wraight CJ, Werther GA, Edmondson SR;  
 XX PI WPI; 2001-041421/05.  
 XX DR Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 XX PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 XX PT inhibits or reduces growth factor mediated cell proliferation and/or  
 XX PT inflammation.

XX PS Example 8; Page 88; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of  
 XX CC skin disorders. The method comprises contacting the skin with an  
 XX CC antisense oligonucleotide, (for insulin-like Growth factor [IGF]-1  
 XX CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 XX CC inhibiting or reducing growth factor mediated cell proliferation,  
 XX CC inflammation and/or other disorders. The present sequence is an  
 XX CC oligonucleotide which can be used to design the antisense  
 XX CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 XX CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 XX CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 XX CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 XX CC hyperneovascular condition such as a neovascular condition of the retina,  
 XX CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 XX CC disease, kidney disease, hyperproliferation of the inside of blood  
 XX CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 1 A; 1 C; 12 G; 1 T; 0 U; 0 Other;

XX SQ Query Match 0.4%; Score 15; DB 1; Length 15;  
 XX SQ Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 XX SQ Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 972 TCCCCCCCCACCCCG 986
Db 15 TCCCCCCCCACCCCG 1

RESULT 429
AAF45320/c
ID AAF45320 standard; DNA; 15 BP.
XX
XX
AC AAF45320;
XX
XX 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #159.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 6; Page 35; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 8 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 GGCAGCAGCGCGGC 439
Db 15 GGCAGCAGCGCGGC 1

RESULT 431
AAF60455/c
ID AAF60455 standard; DNA; 15 BP.

```

XX AC AAF60455;  
XX DT 27-APR-2001 (first entry)  
XX DE Oligonucleotide clamp #10.  
XX KW Oligonucleotide clamp; ds.  
XX OS Unidentified.  
XX PN US6180777-B1.  
XX PD 30-JAN-2001.  
XX PF 03-JAN-1997; 97US-00787321.  
XX PR 12-JAN-1996; 96US-0009918P.  
XX PA (FARB ) BAYER CORP.  
XX PI Horn T;  
XX DR WPI; 2001-201911/20.  
XX PT Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothioate groups.  
XX PS Example 5; Col 17-18; 20pp; English.  
XX CC The present invention relates to a method for synthesising a branched or multiply connected macromolecular structure, comprising oligonucleotide clamps (OC). The macromolecular structure is capable of specifically binding to a target molecule, and can therefore be used as probes. At least one OC comprises a target binding sequence that binds specifically and stably with the target molecule, and at least two OCs comprise signal generation moieties capable of generating a detectable signal in the presence of the target molecule. In addition the OCs are connected to one another by thioalkylamino, or thiophosphorylalkylamino bridges. The present sequence is an OC used in the present invention  
XX SQ Sequence 15 BP; 1 A; 2 C; 0 G; 12 T; 0 U; 0 Other;  
Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2800 GTGAAAAAATAAAA 2814  
DB 15 GTGAAAAAATAAAA 1  
RESULT 432  
ID ABK96652/c  
XX AC ABK96652; DNA; 15 BP.  
XX DT 24-SEP-2002 (first entry)  
XX DE Interleukin-3 (IL-3) allele specific oligonucleotide primer #3.  
XX KW Interleukin 3; colony-stimulating factor; IL3; transgenic animal;  
XX KW IL3 isogene; central nervous system disorder; multiple sclerosis;  
XX KW Alzheimer's disease; Parkinson's disease; CNS injury; immune disorder;  
XX KW inflammatory disorder; allele specific oligonucleotide; ASO; PCR; primer;  
XX OS ss.  
XX OS Homo sapiens.  
XX PN WO200244410-A1.  
XX

PD 06-JUN-2002.  
XX 28-NOV-2000; 2000WO-US032381.  
XX PR 28-NOV-2000; 2000WO-US032381.  
XX PA (GENA-) GENAISSANCE PHARM INC.  
XX PI Chew A, Denton RR, Nandabalan K, Stephens JC;  
XX DR WPI; 2002-519590/55.  
XX PT Novel isolated polynucleotide comprising a sequence which is a polymorphic variant for a reference sequence for interleukin 3 gene useful for studying the expression and biological function of the protein.  
XX PS Claim 11; Page 16; 62pp; English.  
XX CC The invention describes an isolated polynucleotide (I) comprising a sequence which is a polymorphic variant for a reference sequence for interleukin 3 (colony-stimulating factor) (IL3) gene or its fragment. (I) is useful for studying the expression and biological function of IL3, as well as in developing drugs targeting the IL3 protein. A transgenic animal is useful for studying expression of IL3 isogenes in vivo, for in vivo screening and testing of drugs targeted against IL3 protein, and for testing the efficacy of therapeutic agents and compounds for diseases of the central nervous system e.g. multiple sclerosis, Alzheimer's disease, Parkinson's disease and CNS injury, and immune or inflammatory disorders. The method described in the invention is useful in developing diagnostic tests and therapeutic treatments for diseases of the central nervous system and immune or inflammatory disorders. This sequence represents an allele specific oligonucleotide primer for detecting polymorphisms in the IL-3 gene  
XX SQ Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 0.4%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 87 CTGAGAGCTGAGCTC 101  
DB 15 CTGAGAGCTGAGCTC 1  
RESULT 433  
ID AAX18370 standard; DNA; 17 BP.  
XX AC AAX18370;  
XX DT 11-MAY-1999 (first entry)  
XX DE RT-PCR primer of the invention SEQ ID 11.  
XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
XX OS Synthetic.  
XX PN JP11032765-A.  
XX PD 09-FEB-1999.  
XX PF 18-JUL-1997; 97JP-00208312.  
XX PR 18-JUL-1997; 97JP-00208312.  
XX PA (TAKI ) TAKARA SHUZO CO LTD.  
XX DR WPI; 1999-183822/16.  
XX PT Peptides having at least two new nucleotides - useful as primers in RT-

PT PCR.  
PS Disclosure; Page 11; 19pp; Japanese.  
XX  
XX This sequence represents a primer of the invention. The invention relates  
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
CC natural number indicating the repetition of alpha; beta, delta = V or N;  
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
CC repetition of gamma, in which thymine expressed by gamma is composed of  
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
CC useful as primers for RT-PCR and determination of base sequences. The new  
CC sequences allow for reproductive and highly efficient analysis of gene  
CC sequences  
XX  
SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2574 TTAATAAAAAAAAAA 2588  
DB 17 TTAATAAAAAAAAAA 3  
  
RESULT 434  
ABT35106/C  
ID ABT35106 standard; DNA; 17 BP.  
XX  
AC ABT35106;  
XX  
XX  
DT 12-JUN-2003 (first entry)  
XX  
DE Tumour suppression related human fukutin oligo SEQ ID No 743.  
XX  
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025175-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 17-SEP-2002; 2002WO-IB004208.  
XX  
PR 17-SEP-2001; 2001PR-00011978.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
DR WPI; 2003-313353/30.  
XX  
XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
PS Disclosure; Page 120; 720pp; French.  
XX  
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one

CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;  
  
Query Match 0.4%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3922 CTGTGTGAACACAGA 3936  
DB 17 CTGTGTGAACACAGA 3  
  
RESULT 435  
ADL49409/C  
ID ADL49409 standard; RNA; 17 BP.  
XX  
AC ADL49409;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human PKR substrate sequence #523.  
XX  
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
KW protein kinase PKR; cerebrovascular accident;  
KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
KW substrate; ds.  
XX  
OS Unidentified.  
XX  
PN WO200281628-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 03-APR-2002; 2002WO-US010512.  
XX  
PR 05-APR-2001; 2001US-00827395.  
PR 29-MAY-2001; 2001US-0294412P.  
PR 28-AUG-2001; 2001US-0315315P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;  
XX  
XX WPI; 2003-058513/05.  
DR  
XX Novel enzymatic nucleic acid that down-regulates expression of neurite  
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
XX  
PS Claim 59; SEQ ID NO 2942; 317pp; English.  
XX  
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
CC that down regulate the expression or inhibit the function of a receptor

CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
 CC invention are useful for treating: cerebrovascular accident, central  
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
 CC ischemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
 CC nucleic acids of the invention are also useful for down-regulating the  
 CC expression of a target gene and as a diagnostic tool to examine genetic  
 CC drifts and mutations within diseased cells or to detect the presence of a  
 CC target RNA in a cell. The present RNA sequence represents a human PKR  
 CC substrate sequence.

XX  
 SQ Sequence 17 BP; 2 A; 1 C; 0 G; 0 T; 14 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAA AAAAAAAAAA 2588  
 Db 17 TTAAAAA AAAAAAAAAA 3

RESULT 436  
 ADP86176  
 ID ADP86176 standard; DNA; 17 BP.  
 XX  
 AC ADP86176;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE CpG immunostimulatory oligonucleotide #47.

XX CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;  
 KW viral infection; bacterial infection; cancer; lymphoma;  
 KW intraepithelial neoplasia; melanoma; neuroblastoma; Hodgkin's lymphoma;  
 KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.

XX Unidentified.

XX Key Location/Qualifiers  
 FH modified\_base 1..17  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"

XX WO2004053104-A2.

XX 24-JUN-2004.

XX 11-DEC-2003; 2003WO-US039775.

XX 11-DEC-2002; 2002US-0432409P.

XX 25-SEP-2003; 2003US-0506108P.

XX (COLE-) COLEY PHARM GROUP INC.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Jurk M, Vollmer J, Uhlmann E;

XX WPI; 2004-487902/46.

XX New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.

XX Example; SEQ ID NO 47; 104pp; English.

XX The invention relates to a class of CpG immunostimulatory

CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that

CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,  
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasias,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.

XX  
 SQ Sequence 17 BP; 11 A; 1 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2572 GTTTAAAAA AAAAAA 2586  
 Db 3 GTTTAAAAA AAAAAA 17

RESULT 437  
 AAT41540  
 ID AAT41540 standard; DNA; 18 BP.

XX  
 AC AAT41540;

XX 24-JUN-1997 (first entry)

XX Human apolipoprotein-J gene exon 8-specific 5' PCR primer.

XX Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;  
 KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;  
 KW diagnosis; ss.

XX Synthetic.

XX WO9632502-A1.

XX 17-OCT-1996.

XX 02-APR-1996; 96WO-US004510.

XX 11-APR-1995; 95US-00420291.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Mayeux R, Tycko B;

XX WPI; 1996-477152/47.

XX New oligonucleotide specific for apolipoprotein-J polymorphisms - used  
 PT to identify patients susceptible to Alzheimer's disease or prostate  
 PT cancer.

XX Example 1; Page 20; 62pp; English.

XX AAT41527-T41541 are exon-specific PCR primers used for the amplification  
 CC of exons 2-8 of the human apolipoprotein-J (ApoJ) gene. The primers were  
 CC used in a method for detecting polymorphisms associated with an allelic  
 CC variation in the ApoJ gene. The oligonucleotide (OG) detects the  
 CC probability of a person developing Alzheimer's disease (AD), preferably  
 CC in patients of African or Hispanic descent. The OG also detects the  
 CC probability of a person developing a cognitive disorder, or a prostatic  
 CC carcinoma. Transgenic mammals expressing an allelic variant of an ApoJ  
 CC gene may be used as a prognostic and diagnostic means for studying AD,  
 CC and to determine the effectiveness of therapeutic drugs

XX Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

```

Query Match      0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3845 CCACAGTGTTCAGC 3859
DB 1 CCACAGTGTTCAGC 15

RESULT 438
AAV54164/c
ID AAV54164 standard; cDNA; 18 BP.
XX AC
XX AAV54164;
DT 21-DEC-1998 (first entry)
XX DE
XX Nucleotide sequence PCR primer 1.
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX OS
XX Synthetic.
XX WO9839437-A1.
PN 11-SEP-1998.
XX PD
XX 05-MAR-1998; 98WO-JP000905.
XX PF
XX 05-MAR-1997; 97JP-00050302.
XX PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA
XX Sakaki Y;
XX PI
XX WPI; 1998-495844/42.
XX DR
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX Example 1; Page 47; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX SQ
Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match      0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2588
DB 18 TTAATAAAAAAAAAA 4

RESULT 439
AAV54164/c
ID AAV54164 standard; cDNA; 18 BP.
XX AC
XX AAV54164;
DT 21-DEC-1998 (first entry)
XX DE
XX RT-PCR primer of the invention SEQ ID 13.
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

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XX OS Synthetic.
XX JP11032765-A.
XX PN
XX 09-FEB-1999.
XX PD
XX 18-JUL-1997; 97JP-00208312.
XX PF
XX 18-JUL-1997; 97JP-00208312.
XX PR
XX (TAKI ) TAKARA SHUZO CO LTD.
XX PA
XX WPI; 1999-183822/16.
XX DR
XX Peptides having at least two new nucleotides - useful as primers in RT-
PT PCR.
XX PS Disclosure; Page 11; 19pp; Japanese.
XX This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX SQ
Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match      0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2588
DB 18 TTAATAAAAAAAAAA 4

RESULT 440
AAZ90646/c
ID AAZ90646 standard; DNA; 18 BP.
XX AC
XX AAZ90646;
XX DT
XX 13-JUN-2000 (first entry)
XX DE
XX Human adipose tissue gene amplifying primer #7.
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS
XX Homo sapiens.
XX PN
XX JP2000037190-A.
XX PD
XX 08-FEB-2000.
XX PF
XX 23-JUL-1998; 98JP-00225228.
XX PR
XX 23-JUL-1998; 98JP-00225228.
XX PA
XX (NISH ) JAPAN TOBACCO INC.
XX DR
XX WPI; 2000-306578/27.
XX PT
XX A physiologically active protein specifically derived from mammal tissue.
XX

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PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
    Query Match      0.4%; Score 15; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 2.5e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAATAAAAAAAAAA 2588
Db 18 TTAATAAAAAAAAAA 4

RESULT 441
ADL95317
ID ADL95317 standard; DNA; 18 BP.
XX
AC ADL95317;
XX
DT 01-JUL-2004 (first entry)
XX
DE Anti-proliferative oligonucleotide #8.
XX
KW ss; anti-proliferative; cellular proliferation; restenosis; angioplasty;
KW cancer; malignant tumour.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 8 /*tag= a
FT /*mod_base= OTHER
FT /*notes= "Optionally 32-P labelled"
XX
PN US2004067197-A1.
XX
PD 08-APR-2004.
XX
PF 02-FEB-2001; 2001US-00775479.
XX
PR 26-NOV-1997; 97WO-CA000892.
PR 24-MAY-1999; 99US-00318106.
XX
PA (LECL/) LECLERC G.
PA (MART/) MARTEL R.
PI Leclerc G, Martel R;
XX
DR WPI; 2004-314974/29.
XX
PT New anti-proliferative substance comprising a radiolabelled DNA carrier,
PT useful for preventing or treating uncontrolled cellular proliferation
PT e.g. restenosis, cancer or malignant tumors.
XX
PS Claim 13; SEQ ID NO 8; 28pp; English.
XX
CC The invention relates to an anti-proliferative substance for preventing
CC uncontrolled cellular proliferation comprising a radiolabelled DNA
CC carrier, where a radioisotope is located internally within the DNA
CC sequence, at 5', end or at 3', end, and the radiolabelled DNA carrier
CC penetrates the cell membrane and is retained intracellularly for a time
CC sufficient for the radio-isotope to effect a dose therapy. The carrier in
CC the anti-proliferative substance is an oligonucleotide, which is linear
CC or a plasmid, which is circular. The plasmid is of viral or bacterial
CC origin. The oligonucleotide is a double- or a single-stranded DNA

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CC sequence, which is conjugated with an antibody for cell-specific
CC delivery. The oligonucleotide is also conjugated to a stent surface,
CC cholesterol, oleic acid, linoleic acid, TGfalpha, antibody, TGFbeta,
CC cytokines or growth factors. The anti-proliferative substance is useful
CC for preventing or treating uncontrolled cellular proliferation. The
CC uncontrolled cell proliferation is a restenosis following angioplasty, or
CC cancer or a malignant tumour. The present sequence represents an
CC oligonucleotide carrier used in the invention.
XX
SQ Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
    Query Match      0.4%; Score 15; DB 1; Length 18;
    Best Local Similarity 100.0%; Pred. No. 2.5e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2576 AAAAAAAAAAAATT 2590
Db 3 AAAAAAAAAAAATT 17

RESULT 442
AAZ32003/C
ID AAZ32003 standard; DNA; 20 BP.
XX
AC AAZ32003;
XX
DT 14-JUN-1999 (first entry)
XX
DE MSH2 gene specific primer.
XX
KW Allele profile; diagnosis; treatment; pharmacogenetic; breast cancer;
KW CFTT; cystic fibrosis; dystrophin; Duchenne muscular dystrophy; p53;
KW Becker muscular dystrophy; Li-Fraumeni syndrome; neurofibromatosis;
KW colorectal cancer; MSH2 gene; MLH1 gene; BRCA1 gene; BRCA2 gene;
KW BAP1 gene; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9906598-A2.
XX
PD 11-FEB-1999.
XX
PF 04-AUG-1998; 98WO-US016574.
XX
PR 04-AUG-1997; 97US-00905772.
PR 22-MAY-1998; 98US-00084471.
XX
PA (ONCO-) ONCORMED INC.
XX
PI Murphy PD;
XX
DR WPI; 1999-153820/13.
XX
PT Determining common functional alleles in a population - useful in the
PT diagnosis of disease associated with allelic heterogeneity.
XX
PS Example 1; Page 24; 78pp; English.
XX
CC The invention relates to methods of determining a functional allele
CC profile of a gene in a population. Functional allele profiles comprise
CC the commonly occurring alleles in a population, and the relative
CC frequencies at which such alleles of a given gene occur. The methods are
CC used to identify and determine the frequency of the functional alleles of
CC genes which display extensive allelic heterogeneity, particularly those
CC implicated in disease or conditions, such as the BRCA1 gene associated
CC with breast cancer, CFTT associated with cystic fibrosis, dystrophin
CC associated with Duchenne muscular dystrophy and Becker muscular
CC dystrophy, and p53 associated with Li-Fraumeni syndrome. The methods can
CC also be employed for diseases where allelic and genetic heterogeneity
CC exist, such as breast cancer, neurofibromatosis, and hereditary non-
CC polyposis colorectal cancer. Identification of functional alleles is
CC necessary for identification of mutations which may be implicated in the
CC disease. Sequences AAZ32001-172 represent primers for determining the

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CC functional allele profiles of various genes. The primers are specific for  
CC genes such as MSH2 gene, MLH1 gene, BRCA1 gene, BRCA2 gene and BAP1 gene  
SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAA 2588  
Db 15 TTAAAAA 1

RESULT 443  
ADA45244/c  
ID ADA45244 standard; DNA; 20 BP.

XX AC ADA45244;

XX DT 20-NOV-2003 (first entry)

XX DE Human MSH2 gene PCR primer #3.

XX KW Functional allele profile; genetic inheritance; haplotype; population;  
KW disease; pharmacogenetic application; selective pressure; human; MSH2;  
KW MLH1; BRCA1; BRCA2; PTEN; BAP1; BARD1; p53; PCR; primer; ss.

XX OS Homo sapiens.

XX PN US2003096236-A1.

XX PD 22-MAY-2003.

XX PF 08-AUG-2001; 2001US-00923327.

XX PR 12-FEB-1996; 96US-00598591.

XX PR 12-FEB-1997; 97US-00798691.

XX PR 04-AUG-1997; 97US-00905772.

XX PR 22-MAY-1998; 98US-00084471.

XX PR 04-AUG-1998; 98US-00129134.

XX PR 14-MAR-2000; 2000US-00524794.

XX PA (ONCO-) ONCORMED INC.

XX PI Murphy PD;

XX WPI; 2003-576875/54.

XX Determining a functional allele profile of a gene in a population by  
PT identifying the nucleotide sequence of a gene of genomic DNA from each of  
PT the individuals with a family history of functional alleles of the gene  
PT of interest.

XX Example 1; Page 9; 28pp; English.

XX The present invention relates to a method for determining a functional  
CC allele profile of a gene in a population. The method comprises  
CC identifying the nucleotide sequence of a gene of interest out of genomic  
CC DNA from each of a population of individuals identified as having a  
CC family history which indicates inheritance of functional alleles of the  
CC gene of interest, and rank ordering the frequency of occurrence of each  
CC haplotype, where the identity of the alleles containing each haplotype  
CC and the determination of their relative frequencies constitutes the  
CC functional allele profile of the gene of interest in the population. The  
CC method is useful for determining functional allele profiles which are  
CC useful in the treatment and diagnosis of diseases, for genetic and  
CC pharmacogenetic applications, and for evaluating the degree to which the  
CC gene(s) are under selective pressure. The present sequence represents a  
CC PCR primer used in the method of the invention.

XX SQ Sequence 20 BP; 3 A; 1 C; 3 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2574 TTAAAAA 2588  
Db 15 TTAAAAA 1

RESULT 444  
ADQ14575/c  
ID ADQ14575 standard; RNA; 23 BP.

XX AC ADQ14575;

XX DT 23-SEP-2004 (first entry)

XX DE TGF beta 2 3'-UTR consensus sequence.

XX KW metabolic state; mRNA protein complex; mRNA complex; RNA binding protein;  
KW mRNA complex-associated protein; mRNA complex-associated protein;  
KW mRNA target; protein target; physiological pathway;  
KW TGF beta 2 3'-UTR consensus sequence; ss.

XX OS Synthetic.

XX PN WO2004057032-A1.

XX PD 08-JUL-2004.

XX PF 04-DEC-2003; 2003WO-US038475.

XX PR 04-DEC-2002; 2002US-00309788.

XX PA (RIBO-) RIBONOMICS INC.

XX PI Keene JD, Tenenbaum SA, Carson CC, Phelps WC;

XX WPI; 2004-525445/50.

XX Assessing the metabolic state of a cell comprises isolating at least one  
PT mRNA complex comprising at least one RNA binding protein, and at least  
PT one mRNA or at least one mRNA complex-associated protein.

XX Example 4; Page 35; 86pp; English.

XX The present invention describes a method for assessing the metabolic  
CC state of a cell. The method comprises isolating at least one mRNA complex  
CC having at least one RNA binding protein, and at least one mRNA or at  
CC least one mRNA complex-associated protein, and determining the expression  
CC level of the mRNA or mRNA complex-associated protein, where the level of  
CC expression of the at least one mRNA or the at least one mRNA complex-  
CC associated protein is indicative of the metabolic state of the cell. The  
CC method can be used for assessing the metabolic state in a cell, and for  
CC identifying and evaluating mRNA and protein targets associated with mRNA  
CC complexes and implicated in the expression of proteins involved in common  
CC physiological pathways. The present sequence represents a TGF beta 2 3'-  
CC UTR consensus sequence, which is used in an example from the present  
CC invention.

XX SQ Sequence 23 BP; 2 A; 1 C; 2 G; 1 T; 16 U; 1 Other;

Query Match 0.4%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2577 AAAAAA 2599  
Db 23 AAAAAA 1

RESULT 445  
AAQ70698

```
ID AAQ70698 standard; DNA; 18 BP.
XX
AC AAQ70698;
XX
XX (INMR ) BIO MERIEUX.
XX
DT 25-MAR-2003 (revised)
DT 15-MAR-1995 (first entry)
XX
XX C-Rich oligonucleotide used to inhibit c-myc transcription.
XX
XX c-myc; upstream region; regulatory element; gene expression; triplex;
KW antisense; inhibition; screening; identification; ss.
XX
XX Synthetic.
XX
XX WO9417086-A1.
XX
XX 04-AUG-1994.
XX
XX 10-JAN-1994; 94WO-US000348.
XX
XX 25-JAN-1993; 93US-00008897.
XX
XX (APOL-) APOLLON INC.
XX
XX Yoon K, Lu M;
XX
XX WPI; 1994-264018/32.
XX
XX Composition for decreasing gene transcription - comprises
PT oligo:nucleotide or deriv. complementary to target gene region.
XX
XX Example 1; Page 28; 71pp; English.
XX
XX A number of oligonucleotides were screened for their ability to inhibit c
CC -myc transcription. They were tested on the substrate molecule described
CC in AAQ70670. This substrate molecule is a nuclease sensitive element
CC which has been shown to bind transcriptional factors, be involved in
CC transcriptional regulation and form H-DNA in vitro. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
XX Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 973 CCCCCCCCACCGGCCCC 990
Db 1 CCCCCCCCCCCCCCCCCC 18
RESULT 446
AAQ57781/C
ID AAQ57781 standard; DNA; 18 BP.
XX
AC AAQ57781;
XX
XX 25-MAR-2003 (revised)
DT 15-AUG-1994 (first entry)
XX
XX M.avium-intracellular complex-specific probe (640-657).
XX
XX Mycobacterium avium-intracellular complex; species specific; detection;
KW polymerase chain reaction; amplification; MAIC; PCR primer; probe;
KW 65kd mycobacterial antigen; ss.
XX
XX Synthetic.
XX
XX EP584023-A1.
XX
XX 23-FEB-1994.
PD
XX 12-AUG-1993; 93EP-00420339.
PF
12-AUG-1992; 92EP-00010094.
XX
XX (INMR ) BIO MERIEUX.
XX
XX Mabilat C, Pechere J;
XX
XX WPI; 1994-058892/08.
XX
XX Mycobacterium DNA fragments - corresp. to 65-kD antigen sequences, and
PT primers and probes for detecting Mycobacterium spp.
XX
XX Claim 14; Page 34; 40pp; French.
XX
XX The region corresponding to nucleotides 438-751 encoding the
CC M.tuberculosis 65kD antigen is highly conserved among mycobacteria. DNA
CC fragments having at least 70 per cent homology to this region and to the
CC corresponding region from other species are claimed. PCR amplification of
CC the appropriate region is performed using oligonucleotides AAQ57768 and
CC AAQ57769 as primers. The primers were designed to be "universal", i.e. to
CC amplify DNA from all Mycobacteria. Oligonucleotide AAQ57781 is a probe
CC specific to species belonging to the Mycobacterium avium-intracellular
CC complex; it hybridises to a species-specific sequence within the
CC amplified region. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 359 CCTTGGCCGCTTGAGCA 376
Db 18 CCTTGGCCGCTTGAGCA 1
RESULT 447
AAQ79242
ID AAQ79242 standard; DNA; 18 BP.
XX
AC AAQ79242;
XX
XX 25-MAR-2003 (revised)
DT 19-JUL-1995 (first entry)
XX
XX Guanosine rich oligonucleotide (sic) used to treat viral infection.
XX
XX Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;
KW infection; herpes simplex virus; human papilloma virus;
KW Epstein-Barr virus; HIV; adenovirus; respiratory syncytial virus;
KW hepatitis B virus; human cytomegalovirus; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 18
FT misc_feature /tag= a
FT /mod_base
FT /note= "Amine moiety attached to this base."
XX
XX WO9425037-A1.
XX
XX 10-NOV-1994.
PD
XX 25-APR-1994; 94WO-US004529.
XX
XX 23-APR-1993; 93US-00053027.
PR
XX 28-OCT-1993; 93US-00145704.
XX
XX (TRIP-) TRIPLEX PHARM CORP.
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Rando RF, Fennewald S, Zendegui JG, Ojwang JO, Hogan ME;
PI
```

XX WPI; 1994-357890/44.  
 XX  
 PT Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used  
 PT to treat viral infections, e.g. herpes-virus and HIV.  
 XX  
 PS Claim 41; Page 66; 101pp; English.  
 XX  
 CC The oligonucleotides (See AAQ79201-52) can be used to treat viral  
 CC infections. The oligonucleotides inhibit viral replication by forming  
 CC guanosine tetrads which form a stabilised 3D structure. Preferred  
 CC oligonucleotides contain at least 2 runs of at least 2 guanosine bases  
 CC and may be capped at the 3' terminus with a modifier selected from  
 CC polyamine, poly-L-lysine, cholesterol and propanolamine. They may also  
 CC have a modified phosphodiester linkage or be modified to contain a  
 CC phosphorothioate linkage. They are used to treat infections with viruses  
 CC such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,  
 CC HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human  
 CC cytomegalovirus. NOTE: This poly C sequence is a claimed sequence and  
 CC given in Table 1 in the specification (Page 14) as a guanosine rich  
 CC oligonucleotide although clearly it is not. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 973 CCCCCCCCCACCGCGCCC 990  
 Db 1 CCCCCCCCCCCCCCCCCC 18  
 RESULT 448  
 AAQ79243  
 ID AAQ79243 standard; DNA; 18 BP.  
 AC AAQ79243;  
 DT 25-MAR-2003 (revised)  
 DT 19-JUL-1995 (first entry)  
 XX  
 DE Guanosine rich oligonucleotide (sic) used to treat viral infection.  
 KW Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;  
 KW infection; herpes simplex virus; human papilloma virus;  
 KW Epstein-Barr virus; HIV, adenovirus; respiratory syncytial virus;  
 KW hepatitis B virus; human cytomegalovirus; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..18  
 FT /\*tag= b  
 FT /note= "Phosphorothioate backbone."  
 FT misc\_feature 18  
 FT /\*tag= a  
 FT /mcd\_base  
 FT /note= "Amine moiety attached to this base."  
 XX  
 PN W09425037-A1.  
 PD 10-NOV-1994.  
 XX  
 PF 25-APR-1994; 94WO-05004529.  
 XX  
 PR 23-APR-1993; 93US-00053027.  
 PR 28-OCT-1993; 93US-00145704.  
 XX  
 PA (TRIP-) TRIPLEX PHARM CORP.  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 XX

PI Rando RF, Fennewald S, Zengdegui JG, Ojwang JO, Hogan ME;  
 XX WPI; 1994-357890/44.  
 XX  
 PT Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used  
 PT to treat viral infections, e.g. herpes-virus and HIV.  
 XX  
 PS Claim 41; Page 67; 101pp; English.  
 XX  
 CC The oligonucleotides (See AAQ79201-52) can be used to treat viral  
 CC infections. The oligonucleotides inhibit viral replication by forming  
 CC guanosine tetrads which form a stabilised 3D structure. Preferred  
 CC oligonucleotides contain at least 2 runs of at least 2 guanosine bases  
 CC and may be capped at the 3' terminus with a modifier selected from  
 CC polyamine, poly-L-lysine, cholesterol and propanolamine. They may also  
 CC have a modified phosphodiester linkage or be modified to contain a  
 CC phosphorothioate linkage. They are used to treat infections with viruses  
 CC such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,  
 CC HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human  
 CC cytomegalovirus. NOTE: This poly C sequence is a claimed sequence and  
 CC given in Table 1 in the specification (Page 14) as a guanosine rich  
 CC oligonucleotide although clearly it is not. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 973 CCCCCCCCCACCGCGCCC 990  
 Db 1 CCCCCCCCCCCCCCCCCC 18  
 RESULT 449  
 AAQ78447/c  
 ID AAQ78447 standard; DNA; 18 BP.  
 AC AAQ78447;  
 DT 25-MAR-2003 (revised)  
 DT 27-JUN-1995 (first entry)  
 XX  
 DE TGF-beta gene phosphorothioate antisense oligonucleotide.  
 KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
 KW immunosuppression; oligonucleotide; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W09425588-A2.  
 XX  
 PD 10-NOV-1994.  
 XX  
 PF 29-APR-1994; 94WO-EP001362.  
 XX  
 PR 30-APR-1993; 93EP-00107089.  
 PR 13-MAY-1993; 93EP-00107849.  
 XX  
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 XX  
 PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
 PI Bogdahn U;  
 XX  
 DR WPI; 1994-358266/44.  
 XX  
 PT New transforming growth factor beta anti-sense oligo:nucleotide(s) - for  
 PT treating immunosuppression, tumours, etc.  
 XX  
 PS Claim 6; Page 51; 74pp; English.

XX The antisense oligonucleotides are useful in the treatment of tumours in  
CC which expression of TGF-beta is of relevance for pathogenicity and/or  
CC inhibition of pathological angiogenesis. They are used especially for the  
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
CC of skin carcinogenesis, and treatment of oesophageal and gastric  
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files  
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense  
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 18 BP; 5 A; 2 C; 5 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1880 AATAAGTTTACATGCC 1897  
DB 18 AATAAGCTTACATGTC 1  
  
RESULT 450  
AAQ78430/c  
ID AAQ78430 standard; DNA; 18 BP.  
XX  
AC AAQ78430;  
XX  
XX 25-MAR-2003 (revised)  
DT 27-JUN-1995 (first entry)  
XX  
DE TGF-beta gene phosphorothioate antisense oligonucleotide.  
XX  
KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
KW immunosuppression; oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
XX WO9425588-A2.  
XX  
XX 10-NOV-1994.  
XX  
XX 29-APR-1994; 94WO-EP001362.  
XX  
XX 30-APR-1993; 93EP-00107089.  
XX  
XX 13-MAY-1993; 93EP-00107849.  
XX  
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
PI Bogdahn U;  
XX  
XX WPI; 1994-358266/44.  
XX  
XX New transforming growth factor beta anti-sense oligo:nucleotide(s) - for  
PT treating immunosuppression, tumours, etc.  
XX  
XX Claim 6; Page 46; 74pp; English.  
XX  
XX The antisense oligonucleotides are useful in the treatment of tumours in  
CC which expression of TGF-beta is of relevance for pathogenicity and/or  
CC inhibition of pathological angiogenesis. They are used especially for the  
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
CC of skin carcinogenesis, and treatment of oesophageal and gastric  
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files  
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense  
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 18 BP; 5 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files  
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense  
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1636 ATGCTTCGAATCTGGTGA 1653  
DB 18 ATGCTTCCAATTTGGTGA 1  
  
RESULT 451  
AAQ78479/c  
ID AAQ78479 standard; DNA; 18 BP.  
XX  
AC AAQ78479;  
XX  
XX 25-MAR-2003 (revised)  
DT 27-JUN-1995 (first entry)  
XX  
DE TGF-beta gene phosphorothioate antisense oligonucleotide.  
XX  
KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
KW immunosuppression; oligonucleotide; ss.  
XX  
OS Synthetic.  
XX  
XX WO9425588-A2.  
XX  
XX 10-NOV-1994.  
XX  
XX 29-APR-1994; 94WO-EP001362.  
XX  
XX 30-APR-1993; 93EP-00107089.  
XX  
XX 13-MAY-1993; 93EP-00107849.  
XX  
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
PI Bogdahn U;  
XX  
XX WPI; 1994-358266/44.  
XX  
XX New transforming growth factor beta anti-sense oligo:nucleotide(s) - for  
PT treating immunosuppression, tumours, etc.  
XX  
XX Claim 6; Page 60; 74pp; English.  
XX  
XX The antisense oligonucleotides are useful in the treatment of tumours in  
CC which expression of TGF-beta is of relevance for pathogenicity and/or  
CC inhibition of pathological angiogenesis. They are used especially for the  
CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
CC of skin carcinogenesis, and treatment of oesophageal and gastric  
CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESQ files  
CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
CC beta 1. The sequences given in GENESQ files AAQ78408-78487 are antisense  
CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 18 BP; 6 A; 0 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;

|  |  |  |
|--|--|--|
| Best Local Similarity 88.9%; Pred. No. 2.7e+02;<br>Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;   |  |  |
| QY   | 2375 ACCACTGACCATCTCTCTA 2392<br>  |  |
| Db   | 18 ACCTCTAACCATCTCTCTA 1   |  |
| RESULT 452   |  |  |
| AAQ78436/c   |  |  |
| ID   | AAQ78436 standard; DNA; 18 BP.   |  |
| XX   |  |  |
| AC   | AAQ78436;  |  |
| XX   |  |  |
| DT   | 25-MAR-2003 (revised)  |  |
| DT   | 27-JUN-1995 (first entry)  |  |
| XX   |  |  |
| DE   | TGF-beta gene phosphorothioate antisense oligonucleotide.  |  |
| XX   |  |  |
| KW   | Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;   |  |
| KW   | angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;   |  |
| KW   | carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  |  |
| KW   | immunosuppression; oligonucleotide; ss.  |  |
| XX   |  |  |
| OS   | Synthetic.   |  |
| XX   |  |  |
| PN   | WO9425588-A2.  |  |
| XX   |  |  |
| PD   | 10-NOV-1994.   |  |
| XX   |  |  |
| PF   | 29-APR-1994; 94WO-EP001362.  |  |
| XX   |  |  |
| PR   | 30-APR-1993; 93EP-00107089.  |  |
| PR   | 13-MAY-1993; 93EP-00107849.  |  |
| XX   |  |  |
| XX   |  |  |
| PA   | (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.   |  |
| XX   |  |  |
| PI   | Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;<br>Bogdahn U;   |  |
| XX   |  |  |
| DR   | WPI; 1994-358266/44.   |  |
| XX   |  |  |
| PT   | New transforming growth factor beta anti-sense oligo:nucleotide(s) - for<br>treating immunosuppression, tumours, etc.  |  |
| XX   |  |  |
| PS   | Claim 6; Page 57; 74pp; English.   |  |
| XX   |  |  |
| CC   | The antisense oligonucleotides are useful in the treatment of tumours in<br>which expression of TGF-beta is of relevance for pathogenicity and/or<br>inhibition of pathological angiogenesis. They are used especially for the<br>treatment of the immunosuppressive effect of TGF-beta, augmentation of<br>the proliferation of cytotoxic lymphocytes, treatment of endogenous<br>hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas<br>and malignant gliomas, including glioblastomas, treatment and prophylaxis<br>of skin carcinogenesis, and treatment of oesophageal and gastric<br>carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files<br>AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-<br>beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense<br>oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate<br>analogues. (Updated on 25-MAR-2003 to correct PN field.) |  |
| SQ   | Sequence 18 BP; 5 A; 5 C; 2 G; 6 T; 0 U; 0 Other;  |  |
| Query Match 0.3%; Score 14.8; DB 1; Length 18;<br>Best Local Similarity 88.9%; Pred. No. 2.7e+02;<br>Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |  |  |
| QY   | 1711 GGATTGAACGTATATCAGA 1728<br>  |  |
| Db   | 18 GGATTGAGCTATATCAGA 1  |  |
| RESULT 453   |  |  |
| AAQ78466/c   |  |  |
| ID   | AAQ78466 standard; DNA; 18 BP.   |  |
| XX   |  |  |
| AC   | AAQ78466;  |  |
| XX   |  |  |
| DT   | 25-MAR-2003 (revised)  |  |
| DT   | 27-JUN-1995 (first entry)  |  |
| XX   |  |  |
| DE   | TGF-beta gene phosphorothioate antisense oligonucleotide.  |  |
| XX   |  |  |
| KW   | Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;   |  |
| KW   | angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;   |  |
| KW   | carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  |  |
| KW   | immunosuppression; oligonucleotide; ss.  |  |
| XX   |  |  |
| OS   | Synthetic.   |  |
| XX   |  |  |
| PN   | WO9425588-A2.  |  |
| XX   |  |  |
| PD   | 10-NOV-1994.   |  |
| XX   |  |  |
| PF   | 29-APR-1994; 94WO-EP001362.  |  |
| XX   |  |  |
| PR   | 30-APR-1993; 93EP-00107089.  |  |
| PR   | 13-MAY-1993; 93EP-00107849.  |  |
| XX   |  |  |
| XX   |  |  |
| PA   | (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.   |  |
| XX   |  |  |
| PI   | Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;<br>Bogdahn U;   |  |
| XX   |  |  |
| DR   | WPI; 1994-358266/44.   |  |
| XX   |  |  |
| PT   | New transforming growth factor beta anti-sense oligo:nucleotide(s) - for<br>treating immunosuppression, tumours, etc.  |  |
| XX   |  |  |
| PS   | Claim 6; Page 48; 74pp; English.   |  |
| XX   |  |  |
| CC   | The antisense oligonucleotides are useful in the treatment of tumours in<br>which expression of TGF-beta is of relevance for pathogenicity and/or<br>inhibition of pathological angiogenesis. They are used especially for the<br>treatment of the immunosuppressive effect of TGF-beta, augmentation of<br>the proliferation of cytotoxic lymphocytes, treatment of endogenous<br>hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas<br>and malignant gliomas, including glioblastomas, treatment and prophylaxis<br>of skin carcinogenesis, and treatment of oesophageal and gastric<br>carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files<br>AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-<br>beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense<br>oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate<br>analogues. (Updated on 25-MAR-2003 to correct PN field.) |  |
| SQ   | Sequence 18 BP; 5 A; 5 C; 2 G; 6 T; 0 U; 0 Other;  |  |
| Query Match 0.3%; Score 14.8; DB 1; Length 18;<br>Best Local Similarity 88.9%; Pred. No. 2.7e+02;<br>Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |  |  |
| QY   | 2175 CGCCCTCTTTACATTTGAT 2192<br>  |  |
| Db   | 18 CGTCCACTTTACATTTGAT 1   |  |
| RESULT 454   |  |  |
| AAQ78423/c   |  |  |
| ID   | AAQ78423 standard; DNA; 18 BP.   |  |
| XX   |  |  |
| AC   | AAQ78423;  |  |
| XX   |  |  |
| DT   | 25-MAR-2003 (revised)  |  |
| DT   | 27-JUN-1995 (first entry)  |  |
| XX   |  |  |
| DE   | TGF-beta gene phosphorothioate antisense oligonucleotide.  |  |

XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
 KW immunosuppression; oligonucleotide; ss.  
 XX Synthetic.  
 XX W09425588-A2.  
 PN 10-NOV-1994.  
 PD 29-APR-1994; 94WO-EP001362.  
 XX 30-APR-1993; 93EP-00107089.  
 PR 13-MAY-1993; 93EP-00107849.  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
 PI Bogdahn U;  
 PI WPI; 1994-358266/44.  
 DR New transforming growth factor beta anti:sense oligo:nucleotide(s) - for  
 XX treating immunosuppression, tumours, etc.  
 PT Claim 6; Page 44; 74pp; English.  
 PS The antisense oligonucleotides are useful in the treatment of tumours in  
 XX which expression of TGF-beta is of relevance for pathogenicity and/or  
 CC inhibition of pathological angiogenesis. They are used especially for the  
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
 CC of skin carcinogenesis, and treatment of oesophageal and gastric  
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files  
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense  
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;  
 SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1527 TATATAATCGACATGCCG 1544  
 DB 18 TACAAAAATAGACATGCCG 1  
 RESULT 455  
 AAQ78483/c  
 ID AAQ78483 standard; DNA; 18 BP.  
 XX AAQ78483;  
 AC 25-MAR-2003 (revised)  
 DT 27-JUN-1995 (first entry)  
 XX TGF-beta gene phosphorothioate antisense oligonucleotide.  
 DE Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
 KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
 KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
 KW immunosuppression; oligonucleotide; ss.  
 XX Synthetic.  
 OS W09425588-A2.  
 PN

XX 10-NOV-1994.  
 PD 29-APR-1994; 94WO-EP001362.  
 XX 30-APR-1993; 93EP-00107089.  
 PR 13-MAY-1993; 93EP-00107849.  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
 PI Bogdahn U;  
 PI WPI; 1994-358266/44.  
 DR New transforming growth factor beta anti:sense oligo:nucleotide(s) - for  
 XX treating immunosuppression, tumours, etc.  
 PT Claim 6; Page 62; 74pp; English.  
 PS The antisense oligonucleotides are useful in the treatment of tumours in  
 XX which expression of TGF-beta is of relevance for pathogenicity and/or  
 CC inhibition of pathological angiogenesis. They are used especially for the  
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
 CC of skin carcinogenesis, and treatment of oesophageal and gastric  
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files  
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense  
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2439 GTCAGTCTCTTAATGC 2456  
 DB 18 GTAAAGTCTTGCAATGC 1  
 RESULT 456  
 AAQ75026/c  
 ID AAQ75026 standard; DNA; 18 BP.  
 XX AAQ75026;  
 AC 25-MAR-2003 (revised)  
 DT 03-AUG-1995 (first entry)  
 XX PCR primer.  
 DE Synthetic oligo; solid phase immunoassay; ss.  
 KW Synthetic.  
 OS Key Location/Qualifiers  
 FH misc\_difference 1  
 FT /\*tag= a  
 FT /note= "Linked to biotin"  
 XX W09426932-A1.  
 PN 24-NOV-1994.  
 PD 13-MAY-1994; 94WO-US005407.  
 PF 13-MAY-1993; 93US-00061694.  
 PR 13-MAY-1993;  
 XX

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PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Fields HA, Khudyakov YE;
XX
XX WPI; 1995-006819/01.
XX
XX Solid phase immunoassay using oligo:nucleotide as label - also new
PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for
PT diagnosing hepatitis C or E virus infection.
XX
XX Example; Page 12; 34pp; English.
XX
XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
CC They are used in a method for detecting an antigen in a subject. The
CC method involves binding the antigen to a solid support and then reacting
CC it with an immunoreactive ligand (L) bound to an oligo; removing any
CC unreacted L, and then detecting the presence of the oligo. A similar
CC method can be used to detect Ab, in which case the ligand is an oligo-
CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
CC to be detected at very low levels. An exemplary oligo is AAQ75024 which
CC can be covalently attached by the 5'- terminus to the N- or C-terminal of
CC a synthetic peptide. In the example, peptide AAR62941 was coupled to
CC oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to
CC contain HEV Abs were immobilised on plastic tubes or wells, then
CC incubated for 30-60 mins with the peptide-oligo product. The vessels were
CC washed; bound oligo was released with 0.2M glycine and amplified in a
CC separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.
CC The amplification product - AAQ75031 - was treated with uracil DNA
CC glycosylase to remove the U18 fragment, and the product captured by
CC immobilised oligo-dT. (Updated on 23-MAR-2003 to correct FN field.)
XX
XX Sequence 18 BP; 1 A; 10 C; 0 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 254 AGGAGAAGCTAGGGAGG 271
DB 18 AGGAGAAGATAGGGAGG 1
RESULT 457
AAT51660
ID AAT51660 standard; DNA; 18 BP.
XX
XX AAT51660;
AC
XX
XX 12-NOV-1997 (first entry)
DT
XX
XX Viral integrase inhibiting oligonucleotide.
DE
XX
XX Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;
KW herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;
KW respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;
KW integrase inhibition; guanosine tetrad; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 18
FT /*tag= a
FT /note= "amine moiety attached to 3' end"
XX
XX WO9703997-A1.
PN
XX
XX 06-FEB-1997.
PD
XX
XX 17-JUL-1996; 96WO-US011786.
PF
XX
XX 19-JUL-1995; 95US-0001505P.
PR 23-OCT-1995; 95US-00535168.
PR 19-MAR-1996; 96US-0013688P.
XX

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PR 25-MAR-1996; 96US-0014007P.
PR 17-APR-1996; 96US-0015714P.
PR 23-APR-1996; 96US-0016271P.
XX
XX (ARON-) ARONEX PHARM INC.
PA
XX
XX Rando RF, Pennewald S, Zengdeui JG, Ojwang JO, Hogan MB;
PI Pommier Y, Mazumder A;
XX
XX WPI; 1997-132569/12.
XX
XX Oligo:nucleotide(s) capable of forming guanosine tetrads - inhibit viral
PT enzyme responsible for integrating viral nucleic acid into the host
PT genome.
XX
XX Claim 3; Page 164; 245pp; English.
PS
XX
XX AAT51619-T51698 are oligonucleotides used to inhibit the production of
CC viruses within a host cell. The oligonucleotides may form guanosine
CC tetrads (structures formed of eight hydrogen bonds by coordination of the
CC four oxygen atoms of guanine with alkali cations believed to bind to the
CC centre of a quadruplex, and by strong stacking interactions) and are used
CC to prevent the integration of viral nucleic acid into a host genome. The
CC oligonucleotides inhibit functioning of the integrase enzyme and hence
CC prevent viral infection. Viral infections that may be treated include
CC human immunodeficiency virus (HIV), Epstein Barr virus (EBV), herpes
CC simplex virus (HSV), human papilloma virus (HPV), adenovirus, respiratory
CC syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis B virus (HBV),
CC especially HIV-1 infection
XX
XX Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 973 CCCCCCCCCACCGCCCC 990
DB 1 CCCCCCCCCCCCCCCCC 18
RESULT 458
AAV54166/C
ID AAV54166 standard; cDNA; 18 BP.
XX
XX AAV54166;
AC
XX
XX 21-DEC-1998 (first entry)
DT
XX
XX Nucleotide sequence PCR primer 3.
DE
XX
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
XX Synthetic.
OS
XX
XX WO9839437-A1.
PN
XX
XX 11-SEP-1998.
PD
XX
XX 05-MAR-1998; 98WO-JP000905.
PF
XX
XX 05-MAR-1997; 97JP-00050302.
PR
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX
XX Sakaki Y;
PI
XX
XX WPI; 1998-495844/42.
DR
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX

```

PS Example 1; Page 48; 70pp; Japanese.

XX This is the nucleotide sequence of a PCR primer used in the method of the

CC invention, involving the use of novel apoptosis-related DNAs and

CC proteins. The inventions can be used as diagnostic reagents for apoptosis

CC e.g. (monoclonal) antibodies for the protein, as a reagent in

CC immunohistological staining, as apoptosis inhibitors. It can also be used

CC for treatment of apoptosis-related diseases

XX

SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAACATC 2818

DB 18 TGAATAAAAAAAAAAAC 1

RESULT 459

AAV54169/C

ID AAV54169 standard; cDNA; 18 BP.

XX

AC AAV54169;

XX

XX 21-DEC-1998 (first entry)

XX

DE Nucleotide sequence PCR primer 6.

XX

XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;

KW immunohistological staining.

KW

XX Synthetic.

XX

XX WO9839437-A1.

XX

PD 11-SEP-1998.

XX

XX 05-MAR-1998; 98WO-JP000905.

XX

XX 05-MAR-1997; 97JP-00050302.

XX

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX

XX Sakaki Y;

XX

XX WPI; 1998-495844/42.

XX

XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or

PT treating diseases associated with apoptosis.

PT

XX Example 1; Page 49; 70pp; Japanese.

PS

XX This is the nucleotide sequence of a PCR primer used in the method of the

CC invention, involving the use of novel apoptosis-related DNAs and

CC proteins. The inventions can be used as diagnostic reagents for apoptosis

CC e.g. (monoclonal) antibodies for the protein, as a reagent in

CC immunohistological staining, as apoptosis inhibitors. It can also be used

CC for treatment of apoptosis-related diseases

XX

SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 929 AGAATAAAAAAAAAAACACC 946

DB 18 AGAATAAAAAAAAAAAC 1

RESULT 460

AAV21971

ID AAV21971 standard; DNA; 18 BP.

XX

AC AAV21971;

XX

DT 14-JUL-1998 (first entry)

XX

DE Nuclease resistant antisense oligo NBT 143 targeted against (C)18.

XX

XX Nuclease resistant; bacterial infection; antibiotic; target;

KW veterinary medicine; treatment; human; industrial process;

KW bacterial control; ss.

XX

OS Synthetic.

XX

PN WO9803533-A1.

XX

PD 29-JAN-1998.

XX

XX 23-JUL-1997; 97WO-US012961.

XX

PR 24-JUL-1996; 96US-00685575.

XX

PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.

XX

PI Arrow A, Dale RMK, Thompson TL;

XX

DR WPI; 1998-120687/11.

XX

PT Treating bacterial infections in humans or animals with

PT oligo:nucleotide(s) - resistant to nuclease and targeted to bacterial

PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)

PT with antibiotics.

XX

PS Claim 49; Page 87; 163pp; English.

XX

XX This antisense oligonucleotide is nuclease resistant and can be used in

CC the treatment of animals, including humans, having a bacterial infection.

CC The treatment comprises administration of such nuclease resistant

CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,

CC and formulated with a carrier. A compound comprising this nuclease

CC resistant oligonucleotide can be covalently linked to an antibiotic. The

CC method is used to treat infections by a wide variety of Gram-positive and

CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.

CC The methods are particularly used in immuno-compromised individuals (e.g.

CC patients with acquired immunodeficiency syndrome or those receiving

CC chemotherapy or radiation therapy), optionally in combination with, or

CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from

CC therapeutic use, the oligonucleotides can be used to control bacteria in

CC laboratory cultures, foods, beverages and industrial processes. The

CC oligonucleotides are specific for bacteria, without affecting metabolism

CC in mammalian cells. They may also activate RNase H and have a general,

CC non-specific immune-stimulating effect. The oligonucleotides can be

CC administered orally, intranasally, rectally, topically or by injection,

CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that

XX enhances cellular uptake

SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCCGCCCC 990

DB 1 CCCCCCCCCCCCCCCCC 18

RESULT 461

AAV79242

ID AAV79242 standard; DNA; 18 BP.

XX

AC AAV79242;



XX  
DT 21-OCT-2004 (revised)  
XX 31-AUG-1999 (first entry)  
DE  
DE Oligonucleotide #35 forms an intramolecular stacked tetrad structure.  
XX  
XX Column; box; stacked tetrad; inhibition; replication; pathophysiological;  
KW herpes simplex virus; HSV; human papilloma virus; Epstein Barr Virus;  
KW HPV; EBV; HIV; human immunodeficiency virus; adenovirus; RSV; HBV; HCMV;  
KW respiratory syncytial virus; hepatitis B virus; human cytomegalovirus;  
KW human T-cell leukaemia virus; HTLV; ss.  
OS  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH misc\_structure 1. .18  
FT /tag= a  
FT /notes= "forms intramolecular stacked tetrad or 3D  
FT columnar box structure"  
FT modified\_base 1. .18  
FT /tag= b  
FT /mod\_base= optionally contains phosphodiester  
FT internucleotide linkages  
XX  
XX WO9833807-A1.  
XX  
XX 06-AUG-1998.  
XX  
XX 03-FEB-1998; 98WO-US001974.  
XX  
XX 04-FEB-1997; 97US-0037374P.  
XX 09-DEC-1997; 97US-00987574.  
XX (ARON-) ARONEX PHARM INC.  
XX  
XX Rando RF, Ojwang JO, Hogan ME, Wallace TL, Cossum PA;  
XX WPI; 1998-446809/38.  
XX  
XX New guanosine-rich tetrad forming oligonucleotide(s) - used for  
PT inhibiting virus replication for treating e.g. herpes simplex, papilloma,  
PT HIV, adenovirus or hepatitis B virus infection.  
XX  
XX Disclosure; Page 146; 140pp; English.  
XX  
XX Sequences AAX79210-X79275 represent oligonucleotides (ON) which are able  
CC to form a columnar box or "stacked tetrad" structure by intramolecular  
CC internucleotide binding. The ONs are used to inhibit the replication of  
CC viruses. They are able to suppress virus production for prolonged periods  
CC after an initial short treatment regimen. They can be used for treating  
CC pathophysiological states caused by viruses such as herpes simplex virus,  
CC human papilloma virus, Epstein Barr Virus, HIV, adenovirus, respiratory  
CC syncytial virus, hepatitis B virus, human cytomegalovirus and HTLV I and  
CC II  
CC  
CC Revised record issued on 21-OCT-2004 : Correction to feature table key  
XX  
XX Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 973 CCCCCCCCCACCGCCCC 990  
DB 1 CCCCCCCCCCCCCCCCCC 18  
RESULT 462  
AAZ65449/C  
ID AAZ65449 standard; DNA; 18 BP.  
XX  
XX AAZ65449;

XX  
DT 30-MAR-2000 (first entry)  
XX  
DE Immunosuppressant inhibitor oligonucleotide TGF-beta2-9.  
XX  
XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;  
KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
KW prostaglandin E2; PGE2; immune response; tumor; aethma; Crohn's disease;  
KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
KW glomerulonephritis; acute respiratory distress syndrome; ss;  
KW atherosclerosis.  
XX  
XX Unidentified.  
OS  
XX  
XX WO9863975-A2.  
XX  
XX 16-DEC-1999.  
PD  
XX  
XX 10-JUN-1999; 99WO-EP004013.  
PF  
XX  
XX 10-JUN-1998; 98EP-00110709.  
PR  
XX 25-JUL-1998; 98EP-00113974.  
PR  
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
XX Schlingensiepen K, Schlingensiepen R, Brysch W;  
XX WPI; 2000-097470/08.  
DR  
XX  
XX Composition containing immune stimulant and inhibitor of agent that  
PT adversely affects the immune response, for treating cancers and  
PT infections.  
XX  
XX Claim 5; Fig 1; 30pp; English.  
XX  
XX This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
CC used in the invention. The invention relates to a composition which  
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
CC transforming growth factor TGF-beta, vascular endothelial growth factor  
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
CC that adversely affects the immune response. The composition also includes  
CC at least one stimulant that positively affects the immune response. This  
CC oligonucleotide is an example of an inhibitor that is used in the  
CC composition. The composition is used as an immunostimulant for the  
CC treatment of neoplasms and infections, particularly hyperproliferation;  
CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma of oesophagus, bronchi,  
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative  
CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
CC syndrome and the formation of atherosclerotic plaque  
XX  
XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1527 TATAAAATCGACATGCCG 1544  
DB 18 TACAAAATAGACATGCCG 1  
RESULT 463  
AAZ65505/C  
ID AAZ65505 standard; DNA; 18 BP.  
XX  
XX AAZ65505;  
XX  
XX 30-MAR-2000 (first entry)  
DT



KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;  
KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;  
KW monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes;  
KW glomerulonephritis; acute respiratory distress syndrome; ss;  
XX atherosclerosis.  
OS Unidentified.  
XX  
PN WO9963975-A2.  
XX  
PD 16-DEC-1999.  
XX  
PF 10-JUN-1999; 99WO-EP004013.  
XX  
PR 10-JUN-1998; 98EP-00110709.  
XX  
PR 25-JUL-1998; 98EP-00113974.  
XX  
PR (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
PA  
PI Schlingensiepen K, Schlingensiepen R, Brysch W;  
XX WPI; 2000-097470/08.  
XX  
XX Composition containing immune stimulant and inhibitor of agent that  
PT adversely affects the immune response, for treating cancers and  
PT infections.  
XX  
XX Claim 5; Fig 1; 30pp; English.  
XX  
CC This sequence is an immunosuppressant inhibitor oligonucleotide, which is  
CC used in the invention. The invention relates to a composition which  
CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.  
CC transforming growth factor TGF-beta, vascular endothelial growth factor  
CC VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors)  
CC that adversely affects the immune response. The composition also includes  
CC at least one stimulant that positively affects the immune response. This  
CC oligonucleotide is an example of an inhibitor that is used in the  
CC composition. The composition is used as an immunostimulant for the  
CC treatment of neoplasms and infections, particularly hyperproliferation;  
CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,  
CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,  
CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,  
CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,  
CC most of which are directed against TGFbeta or VEGF, are inhibitors of  
CC monocyte chemotactic protein-1 (MCP-1) and are useful as anti-  
CC inflammatory for treating e.g. asthma, Crohn's disease, ulcerative  
CC colitis, diabetes, glomerulonephritis, acute respiratory distress  
CC syndrome and the formation of atherosclerotic plaque  
XX  
XX Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1636 ATGCTTCGAATCTGGTGA 1653  
DB 18 ATGCTTCCAATTGGTGA 1  
  
RESULT 466  
AAZ90648/c  
ID AAZ90648 standard; DNA; 18 BP.  
XX  
XX AAZ90648;  
XX  
XX 13-JUN-2000 (first entry)  
XX  
XX Human adipose tissue gene amplifying primer #9.  
XX  
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.  
XX

OS Homo sapiens.  
XX  
PN JP2000037190-A.  
XX  
XX 08-FEB-2000.  
XX  
PF 23-JUL-1998; 98JP-00225228.  
XX  
PR 23-JUL-1998; 98JP-00225228.  
XX  
PA (NISR ) JAPAN TOBACCO INC.  
XX  
DR WPI; 2000-306578/27.  
XX  
XX A physiologically active protein specifically derived from mammal tissue.  
XX  
XX Example 2; Page 18; 50pp; Japanese.  
XX  
CC The invention relates to identification of genes and proteins of adipose  
CC tissue relating to obesity, particularly complications of visceral  
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,  
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the  
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention  
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51  
CC represent PCR primers amplifying the human adipose tissue genes  
XX  
XX Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2801 TGAATAAAAAAACAATC 2818  
DB 18 TGAATAAAAAAACAATC 1  
  
RESULT 467  
AAZ90645/c  
ID AAZ90645 standard; DNA; 18 BP.  
XX  
XX AAZ90645;  
XX  
XX 13-JUN-2000 (first entry)  
XX  
XX Human adipose tissue gene amplifying primer #6.  
XX  
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;  
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX JP2000037190-A.  
XX  
XX 08-FEB-2000.  
XX  
PF 23-JUL-1998; 98JP-00225228.  
XX  
PR 23-JUL-1998; 98JP-00225228.  
XX  
PA (NISR ) JAPAN TOBACCO INC.  
XX  
DR WPI; 2000-306578/27.  
XX  
XX A physiologically active protein specifically derived from mammal tissue.  
XX  
XX Example 2; Page 18; 50pp; Japanese.  
XX  
CC The invention relates to identification of genes and proteins of adipose  
CC tissue relating to obesity, particularly complications of visceral  
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,  
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the  
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention  
CC

CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51  
 CC represent PCR primers amplifying the human adipose tissue genes  
 XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;  
 SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 929 AGAAAAAACAACACC 946  
 Db 18 AGAAAAAACAAC 1

RESULT 468  
 AAA58387/c  
 ID AAA58387 standard; DNA; 18 BP.  
 XX  
 AC AAA58387;  
 XX  
 DT 01-NOV-2000 (first entry)  
 XX  
 DE Polynucleotide # 3 used in a biomolecule detection system.  
 XX  
 KW Nanocrystal; biomolecule detection; nonisotopic detection system; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200028088-A1.  
 PN  
 XX 18-MAY-2000.  
 PD  
 XX  
 XX 10-NOV-1999; 99WO-US026612.  
 PF  
 XX 10-NOV-1998; 98US-0107828P.  
 PR  
 XX 09-NOV-1999; 99US-00437076.  
 XX  
 XX (BIOC-) BIOCRYSTAL LTD.  
 PA  
 XX Barbera-Guillem E, Nelson MB, Castro S;  
 PI  
 XX WPI; 2000-376593/32.  
 DR  
 XX Functionalized nanocrystal carrying polynucleotide, used for detecting  
 PT target analyte, forms dendrimers with complementary nanocrystals to  
 PT amplify the fluorescent signal.  
 XX  
 XX Example 3; Page 69; 72pp; English.  
 PS  
 XX The present invention relates to functionalised nanocrystals for use in  
 CC nonisotopic detection systems for biomolecules e.g. nucleic acids, and  
 CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands  
 CC attached to their surfaces with one end of the polynucleotide extending  
 CC outwardly from the nanocrystal. The present sequence is one such  
 CC polynucleotide. These nanocrystals are used with a second series of  
 CC nanocrystals, which have polynucleotides complementary to the first  
 CC polynucleotides, so that the respective complementary strands hybridise  
 CC to each other and form a dendrimer. This dendrimer produces a signal  
 CC which can then be detected e.g. fluorescence. The present sequence is  
 CC composed of Guanine bases. This sequence may therefore be used with a  
 CC polynucleotide composed mainly of Cytosine bases (AAA58388)  
 XX  
 SQ Sequence 18 BP; 0 A; 0 C; 18 G; 0 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 973 CCCCCCCCCCCCCCCCCC 990  
 Db 18 CCCCCCCCCCCCCCCCCC 1

RESULT 469  
 ABL57543/c  
 ID ABL57543 standard; DNA; 18 BP.  
 XX  
 AC ABL57543;  
 XX  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Nucleic acid probe h.  
 XX  
 KW Concentration; quantification; mutation detection; polymorphic;  
 KW polymerase chain reaction; PCR; probe; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN EP1046717-A2.  
 XX  
 PD 25-OCT-2000.  
 XX  
 PF 20-APR-2000; 2000EP-00108643.  
 XX  
 PR 20-APR-1999; 99JP-00111601.  
 XX  
 XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.  
 PA (KANK-) KANKYO ENG CO LTD.  
 XX  
 PI Kurane R, Kanagawa T, Kanagata Y, Kurata S, Yamada K, Yokomaku T;  
 PI Koyama O, Furusho K;  
 XX  
 XX WPI; 2000-657765/64.  
 DR  
 XX Determining the concentration of a target nucleic acid, useful e.g. for  
 PT detecting genetic mutations, comprises using a fluorescently labeled  
 PT probe in which emission is reduced by binding to the target nucleic acid.  
 XX  
 XX Example 5; Page 21; 55pp; English.  
 PS  
 XX The invention relates to the determination of the concentration of a  
 CC nucleic acid target, using a fluorescently labeled probe which produces  
 CC reduced fluorescence emission when hybridised to the target nucleic acid.  
 CC The method comprises measuring the reduction in emission caused by  
 CC hybridisation. The new method is particularly used to quantify target  
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
 CC quantifying microbial cells in co-cultures or symbiotic systems, for  
 CC detecting gene mutations or polymorphisms, and for analysing melting  
 CC curves of target nucleic acids to determine a Tm value. Methods of the  
 CC invention allow target nucleic acids to be quantified quickly, easily and  
 CC accurately. Particularly there is no need to remove unbound probe, and no  
 CC materials are introduced that inhibit amplification by Taq polymerase (so  
 CC conventional PCR conditions can be used). The specificity of PCR is kept  
 CC high (amplification of primer dimers is delayed), and the limit of  
 CC quantitation is reduced. Complex probes are not needed, and amplification  
 CC can be monitored in real time. The working graph for data analysis  
 CC (automatically generated by a computer) has a higher correlation  
 CC coefficient than conventional graphs so more accurate quantitation is  
 CC possible. The current sequence represents a nucleic acid probe of the  
 CC invention that was used for investigating the base selectivity of a  
 CC target nucleic acid  
 XX  
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1162 ATATATATTTTCTTCTAC 1179  
 Db 18 ATATATATTTTCTTCTAC 1

RESULT 470  
 AAS13708



XX EP1133988-A1.  
XX  
XX 19-SEP-2001.  
XX  
XX 11-MAR-2000; 2000EP-00105190.  
XX  
XX 11-MAR-2000; 2000EP-00105190.  
XX  
XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
XX  
XX Schlingensiepen K, Schlingensiepen R;  
XX WPI; 2001-604124/69.  
XX  
XX Mixture useful in preparation of medicament for treating tumors and  
PT immune disorders, comprises an inhibitor or suppressor of expression of a  
PT gene, and a molecule binding to expression product of the gene.  
XX  
XX Claim 16; Page 2; 16pp; English.  
XX  
XX The invention relates to a mixture comprising an inhibitor or suppressor  
CC of a gene and a molecule binding to an expression product of that gene.  
CC The gene is selected from the group consisting of TGF-beta, erbB-2, MIA,  
CC c-jun, junB, c-fos, VCAM, NF-kappaB p65, NF-kappaB p50, ICAM, VEGF and NF  
CC -kappa B 2. Molecules including drugs are used to modulate biological  
CC functions through gene products and their derivatives - like e.g.  
CC glycosylated, phosphorylated or otherwise modified gene products, have  
CC either stimulated or inhibited gene products and/or their derivatives.  
CC The mixture is useful in the preparation of a medicament for treating  
CC tumours, immune disorders or for improving organ or cell transplantation  
CC or cell expansion, where inhibition of tumour growth, improvement of  
CC organ or cell transplantation or cell expansion and enhancement or  
CC inhibition of immune response is enhanced in a supra-additive manner. The  
CC mixture is useful in drug target validation, i.e., to identify genes that  
CC are relevant for certain pathological state by testing the effect of the  
CC mixture on a cell system or organism. The present sequence is a human  
CC oligonucleotide useful in drug target validation  
XX  
XX Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1527 TATAAATCGACATGCG 1544  
DB 18 TACAAAATAGACATGCG 1  
RESULT 473  
ID AAF23524 standard; DNA; 18 BP.  
XX  
XX AAF23524;  
AC  
XX 22-MAR-2001 (first entry)  
DT  
XX Primer #2.  
DE  
XX Primer; mRNA; amplification; ss.  
XX  
XX Unidentified.  
OS  
XX WO200075356-A1.  
PN  
XX 14-DEC-2000.  
PD  
XX 04-JUN-1999; 99WO-US012461.  
XX  
XX 04-JUN-1999; 99WO-US012461.  
PR  
XX (LINS/) LIN S.  
PA

PA (YING/) YING S.  
PA (CHUO/) CHUONG C.  
XX (WIDE/) WIDELITZ R B.  
XX  
XX Lin S, Ying S, Chuong C, Widelitz RB;  
PI WPI; 2001-061734/07.  
XX  
XX Generating amplified messenger RNA sequences from single cells, involves  
PT cycling steps of reverse transcription, denaturation, double-stranded DNA  
PT sequences and in vitro transcription.  
XX  
XX Disclosure; Page 17; 31pp; English.  
XX  
XX The present invention relates to generating amplified messenger RNAs with  
CC polymerase reaction activity, comprising cycling steps of reverse  
CC transcription, denaturation, double-stranded cDNA synthesis and in vitro  
CC transcription. The invention is used for generating amplified mRNAs from  
CC limited mRNAs from single cells  
XX  
XX Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 973 CCCCCCCCCACCCGCCCC 990  
DB 1 CCCCCCCCCCCCCCCCCC 18  
RESULT 474  
ID ABL30793/c  
XX ABL30793 standard; DNA; 18 BP.  
XX  
XX ABL30793;  
AC  
XX 21-MAR-2002 (first entry)  
DT  
XX Human HLA genotyping oligonucleotide SEQ ID NO 282.  
DE  
XX Human; human leukocyte antigen; HLA; genotype; polymorphism;  
KW immunogenetic; transplantation; genetic disease; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200192572-A1.  
PN  
XX 06-DEC-2001.  
PD  
XX  
XX 01-JUN-2001; 2001WO-JP004662.  
PF  
XX  
XX 01-JUN-2000; 2000JP-00164798.  
PR  
XX  
XX (NISN) NITSSHINBO IND INC.  
PA (SYST-) SYSTEM RES INC.  
PA  
XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;  
PI WPI; 2002-122074/16.  
XX  
XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
PT individuals e.g. by determining immunogenetic differences when  
PT transplanting between them.  
XX  
XX Claim 10; Page 146; 345pp; Japanese.  
PS  
XX The invention relates to a typing kit for judging human leukocyte antigen  
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base  
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of  
CC genes e.g. belonging to HLA class I antigens on human genome and  
CC containing gene polymorphisms as alloantigens have been immobilised as  
CC primers for amplification of cleaved nucleic acids relating to gene

CC polymorphisms. The method is useful for judging HLA genotypes of  
 CC individuals by determining immunogenetic differences before transplanting  
 CC between them, providing genetic information to decide compatibility of  
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,  
 CC pancreas, Langerhans islet in pancreas and cornea, susceptibility  
 CC diagnosis of genetic diseases and identifying individuals  
 XX  
 SQ Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2914 CTGCAGTGGTGCCTCC 2931  
 Db 18 CTGCAGTAGTGCCACC 1  
 RESULT 475  
 ACA62280  
 ID ACA62280 standard; DNA; 18 BP.  
 XX  
 AC ACA62280;  
 DT 12-AUG-2003 (first entry)  
 DE  
 DE Oligo (dC) primer.  
 XX  
 XX ss; PCR; primer; antisense therapy; mRNA expression profile;  
 KW promoter containing primer.  
 XX  
 OS Synthetic.  
 PN US2003022318-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 07-SEP-2001; 2001US-00949305.  
 XX  
 PR 25-JAN-2000; 2000US-00494212.  
 XX  
 XX (EPIC-) EPICLONE INC.  
 PA  
 PI Lin S, Ying S;  
 XX  
 XX WPI; 2003-479488/45.  
 DR  
 XX Improved polymerase thermocycling reaction for nucleic acid  
 PT amplification, by thermal cycling of promoter-linked nucleic acid  
 PT template synthesis and in vitro transcriptional amplification of nucleic  
 PT acid sequences.  
 XX  
 PS Example 3; Page 14; 28pp; English.  
 XX  
 CC The invention relates to an improved polymerase thermocycling reaction  
 CC (M1) for linear amplification of nucleic acid sequences, involves  
 CC denaturing a number of nucleic acid templates (I), combining the  
 CC denatured (I) with a promoter-containing primer (P1), a primer (P2), a  
 CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,  
 CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA  
 CC polymerase, contacting P1 with (I) to generate a number of promoter-  
 CC containing templates, denaturing the promoter-containing templates,  
 CC contacting P2 with the denatured promoter-containing templates to  
 CC generate a number of promoter-containing double-stranded DNA templates,  
 CC where the double-stranded nucleic acid templates are flanked by P1 in one  
 CC end and P2 in the other end of the other orientation, transcribing the  
 CC promoter-containing double-stranded DNA templates to form a number of  
 CC amplified RNA sequences, including the primer region of the promoter-  
 CC containing double-stranded DNA templates, contacting the amplified RNA  
 CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA  
 CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method  
 CC is useful for improved polymerase thermocycling reaction for linear  
 CC amplification of nucleic acid sequences, and thus for producing mRNA

CC expression profile of a cell by M1 to generate multiple copies of the  
 CC mRNA. M1 is also useful for determining aberrant protein production of  
 CC cells in a diseased state, by generating an expression profile by the  
 CC above method, of cells in both normal and diseased states, comparing the  
 CC expression profile of the cells in the normal and diseased states, the  
 CC determining the differences in mRNA composition of the cell(s) in the  
 CC diseased state, isolating the mRNA sequences of cell(s) in the diseased  
 CC state that differ from mRNA in cell(s) in non-diseased state, amplifying  
 CC the isolated mRNA by M1, and determining aberrant protein function of the  
 CC protein coded for by the isolated mRNA. M1 is also useful for treating a  
 CC cell in a diseased state caused by aberrant protein production, by  
 CC determining protein expression of a cell in a diseased state, determining  
 CC the mRNA sequence for the aberrant proteins, synthesising an antisense  
 CC sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and  
 CC delivering a pharmaceutically effective dosage of a composition  
 CC comprising the anti-sense mRNA and a compatible lipid based biological  
 CC carrier. M1 is also useful for predicting the efficacy of a proposed drug  
 CC targeted against an aberrant protein, by determining aberrant protein  
 CC production of cell in a diseased state by the above method, amplifying  
 CC the aberrant protein by M1 and using recombinant techniques to determine  
 CC the effect of proposed drug on the aberrant protein. M1 is also useful  
 CC for differential screening of tissue-specific gene expression at a  
 CC cellular level, for preparing labeled RNA/DNA probes for a gene chip  
 CC technology, and for determining the efficacy of a drug regimen against a  
 CC gene or its cDNAs. The present sequence is an Oligo (dC) primer used to  
 CC produce second strand cDNA in the method of the invention  
 XX  
 SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 973 CCCCCCACCACGCCCC 990  
 Db 1 CCCCCCCCCCCCCCCCCC 18  
 RESULT 476  
 ADB54824/c  
 ID ADB54824 standard; DNA; 18 BP.  
 XX  
 AC ADB54824;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Hybridisation oligonucleotide 362 used to analyse genomic DNA region.  
 XX  
 XX colon cell proliferative disorder; non methylated CpG dinucleotide;  
 KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;  
 KW probe.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003072821-A2.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 27-FEB-2003; 2003WO-EP002035.  
 XX  
 PR 27-FEB-2002; 2002EP-00004551.  
 XX  
 XX (EPIC-) EPICENOMICS AG.  
 PA  
 PI Adorjan P, Burger M, Maier S, Nimrich I, Becker E, Lesche R;  
 PI Rujan T, Schmitt A;  
 XX  
 XX WPI; 2003-731620/69.  
 XX  
 PT Detecting and differentiating between colon cell proliferative disorders  
 PT associated with a gene or its regulatory regions comprises contacting a  
 PT target nucleic acid in a biological sample obtained from the subject with  
 PT a reagent.

XX PS Claim 36; Page 46; 74pp; English.

CC The invention relates to a novel method for detecting and differentiating  
CC between colon cell proliferative disorders associated with at least one  
CC gene or its regulatory regions. The method comprises contacting a target  
CC nucleic acid in a biological sample obtained from the subject with at  
CC least one reagent or a series of reagents, where the reagent or series of  
CC reagents, distinguishes between methylated and non methylated CpG  
CC dinucleotides within the target nucleic acid. The molecules of the  
CC invention demonstrate cytostatic activity whilst the method may be useful  
CC for detecting and differentiating between colon cell proliferative  
CC disorders, including cancers such as colon adenoma and colon carcinoma.  
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for  
CC determining cytosine methylation state or single nucleotide  
CC polymorphisms. The current sequence is that of the hybridisation  
CC oligonucleotide of the invention which was used to analyse the genomic  
CC DNA region.

XX SQ Sequence 18 BP; 0 A; 0 C; 5 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2808 AAAAAAAAAATCAAAACAA 2825  
Db 18 AAAAAACCAACCAAAACAA 1

RESULT 477

ADCS4808/c

ID ADC64808 standard; DNA; 18 BP.

XX AC ADC64808;

XX DT 18-DEC-2003 (first entry)

XX DE 4B4 clone cDNA library linker primer SEQ ID NO:29.

XX KW humanised; polypeptide antigen; protein antigen; decreased antigenicity;  
KW CD8; T lymphoblast; CD8 T cell; cancer; linker; primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN KR2002066383-A.

XX PD 16-AUG-2002.

XX PF 07-FEB-2002; 2002KR-00006974.

XX PR 08-FEB-2001; 2001KR-00006212.

XX PR (IMMUNO-) IMMUNOMICS CO LTD.

XX PA Kwon BS;

XX PI WPI; 2003-145050/14.

XX DR New humanized polypeptide antigen with decreased antigenicity and it's  
XX encoding gene, for the treatment of tumors and AIDS.

XX PT Disclosure; Page 3; 18pp; Korean.

XX CC The present invention describes a humanised polypeptide antigen with  
CC decreased antigenicity, which binds to 4-1BB of CD8 T lymphoblasts to  
CC activate CD8 T cells, and it's encoding gene. The humanised polypeptide  
CC antigen can be used in the treatment of cancer. The present sequence  
CC represents a linker primer which is used in the exemplification of the  
CC present invention.

XX SQ Sequence 18 BP; 1 A; 2 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2577 AAAAAAAAAAATGGAG 2594  
Db 18 AAAAAAAAAAACTCGAG 1

RESULT 478

ADL06307/c

ID ADL06307 standard; DNA; 18 BP.

XX AC ADL06307;

XX DT 06-MAY-2004 (first entry)

XX DE Kid lingual tissue cDNA library associated linker #1.

XX KW kid pregastric esterase; kPGE; rennet; enzyme-modified cheese; kosher;  
KW vegetarian; polyHis-enterokinase; esterase expression; lipase expression;  
KW goat; linker; cDNA library; lingual tissue; ss.

XX OS Synthetic.

XX PN US6582948-B1.

XX PD 24-JUN-2003.

XX PF 14-JAN-2002; 2002US-00043665.

XX PR 05-NOV-1998; 98US-00186489.

XX PA (INFL ) INT FLAVORS & FRAGRANCES INC.

XX PI Bolen PL, Cihak PL, Scharpf LG;

XX DR WPI; 2003-656428/52.

XX PT Recombinant kid pregastric esterase useful for producing of enzyme  
PT modified cheeses acceptable to kosher and vegetarian consumers.

XX PS Disclosure; Fig 6; 35pp; English.

XX CC The invention describes an isolated kid pregastric esterase (kPGE)  
CC polynucleotide (I) encoding a fully defined sequence of 378 amino acids  
CC as given in the specification. Also described are: a transforming nucleic  
CC acid molecule comprising a plasmid or vector comprising (i); a non-kid  
CC cell capable of recombinantly expressing the kid pregastric esterase,  
CC which has been transformed with the transforming nucleic acid; and  
CC recombinantly producing kid pregastric esterase. The polynucleotides and  
CC methods are useful for producing kPGE in very pure form free of the other  
CC substances found in the present commercial rennet formulations. The  
CC uncontaminated kPGE is also useful for producing enzyme-modified cheeses  
CC (EMC's) acceptable to kosher and vegetarian consumers. The fusion  
CC polynucleotide of kid pregastric esterase and polyHis-enterokinase  
CC increases expression of esterases and lipases when fused to the N  
CC terminal of the enzyme. This sequence represents a linker or primer  
CC oligonucleotide used in the creation of a kid lingual tissue cDNA library  
CC used in the isolation of a kid pregastric esterase.

XX SQ Sequence 18 BP; 1 A; 2 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2577 AAAAAAAAAAATGGAG 2594  
Db 18 AAAAAAAAAAACTCGAG 1



RESULT 479  
ADL06309  
ID ADL06309 standard; DNA; 18 BP.  
XX  
AC ADL06309;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Kid lingual tissue cDNA library associated linker #3.  
XX  
DE kid pregastric esterase; kPGE; rennet; enzyme-modified cheese; kosher;  
KW  
KW vegetarian; polyHis-encokinase; esterase expression; lipase expression;  
KW  
KW goat; linker; cDNA library; lingual tissue; ss.  
XX  
OS Synthetic.  
XX  
XX US6582948-B1.  
PN  
XX  
PD 24-JUN-2003.  
XX  
PF 14-JAN-2002; 2002US-00043665.  
XX  
PR 05-NOV-1998; 98US-00186489.  
XX  
PA (INFL ) INT FLAVORS & FRAGRANCES INC.  
XX  
PI Bolen PL, Cihak PL, Scharpf LG;  
XX  
XX WPI; 2003-656428/62.  
DR  
XX  
XX Recombinant kid pregastric esterase useful for producing of enzyme  
PT modified cheeses acceptable to kosher and vegetarian consumers.  
PT  
PS Disclosure; Fig 6; 35pp; English.  
XX  
XX The invention describes an isolated kid pregastric esterase (kPGE)  
CC polynucleotide (I) encoding a fully defined sequence of 378 amino acids  
CC as given in the specification. Also described are: a transforming nucleic  
CC acid molecule comprising a plasmid or vector comprising (I); a non-kid  
CC cell capable of recombinantly expressing the kid pregastric esterase,  
CC which has been transformed with the transforming nucleic acid; and  
CC recombinantly producing kid pregastric esterase. The polynucleotides and  
CC methods are useful for producing kPGE in very pure form free of the other  
CC substances found in the present commercial rennet formulations. The  
CC uncontaminated kPGE is also useful for producing enzyme-modified cheeses  
CC (EMC's) acceptable to kosher and vegetarian consumers. The fusion  
CC polynucleotide of kid pregastric esterase and polyHis-enterokinase  
CC increases expression of esterases and lipases when fused to the N  
CC terminal of the enzyme. This sequence represents a linker or primer  
CC oligonucleotide used in the creation of a kid lingual tissue cDNA library  
CC used in the isolation of a kid pregastric esterase.  
XX  
SQ Sequence 18 BP; 13 A; 2 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2577 AAAAAAAAAAATTCGAG 2594  
|||||  
DB 1 AAAAAAAAAAATTCGAG 18  
  
RESULT 480  
ADF31330/C  
ID ADF31330 standard; DNA; 18 BP.  
XX  
AC ADF31330;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human MEGSIN gene related primer seq id 13.  
XX

KW nephrotropic; antidiabetic; antiinflammatory; dermatological;  
KW immunosuppressive; gene therapy; MEGSIN gene expression supressor;  
KW positive transcription regulatory activity; human; MEGSIN;  
KW transcriptional regulatory agent; transcription promoter;  
KW transcription inhibitor; renal disease;  
KW kidney mesangial cell proliferation; Iga glomerulonephritis;  
KW systemic lupus erythematosus; SLE; nephropathy; diabetic nephropathy;  
KW cryoglobulin; nephropathy; renal disease; PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
XX JP2003310268-A.  
PN  
XX  
PD 05-NOV-2003.  
XX  
XX 23-APR-2002; 2002JP-00121315.  
PF  
XX  
XX 23-APR-2002; 2002JP-00121315.  
PR  
XX  
XX (KURO/) KUROKAWA K.  
PA (MIYA/) MIYATA T.  
XX  
XX WPI; 2004-015356/02.  
DR  
XX  
XX Novel transcriptional regulatory DNA sequence of MEGSIN gene, useful for  
PT regulating mesangial cell specific transcription, and for identifying  
PT compounds which control expression of MEGSIN gene.  
XX  
XX Disclosure; SEQ ID NO 13; 20pp; Japanese.  
XX  
XX The invention describes DNA (I) which has positive transcription  
CC regulatory activity having at least 15 continuous bases containing a  
CC specific 9 base pair sequence of a fully defined human MEGSIN gene  
CC sequence of 4230 nucleotides as given in specification, or a sequence of  
CC at least 15 continuous bases of (SI) in which one or more bases are  
CC substituted, deleted and/or added other than the specific 9 base pair  
CC sequence. (I) is useful for screening of compound which couples with (I),  
CC which controls coupling of (I) and AP-1, and which controls  
CC transcriptional activity, respectively. A transcriptional regulatory  
CC agent (II) containing (I) is useful for regulating transcription of  
CC MEGSIN gene. (II) is useful either as a transcription promoter or  
CC transcription inhibitor of the MEGSIN gene, and transcription inhibitor  
CC is useful for treating renal diseases associated with proliferation of  
CC kidney mesangial cells such as Iga glomerulonephritis, systemic lupus  
CC erythematosus (SLE), nephropathy, diabetic nephropathy, cryoglobulin and  
CC nephropathy. (I) allows identification of compounds that regulate  
CC transcription of human MEGSIN gene, and thus for treating MEGSIN gene  
CC associated renal diseases. This sequence represents a primer associated  
CC with the human MEGSIN gene.  
XX  
SQ Sequence 18 BP; 9 A; 3 C; 2 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3611 GATCATTTCAGATTGTATA 3628  
|||||  
DB 18 GTTCATTTCAGTTGTATA 1  
  
RESULT 481  
ADO28562  
ID ADO28562 standard; DNA; 18 BP.  
XX  
AC ADO28562;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Displacement oligo for immuno-PCR assay for PSA protein.  
XX  
XX ss; analyte; detection; prostate specific antigen; peptide nucleic acid;  
KW prostate specific antigen.

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XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT misc_difference 1..18
XX FT /*tag= a
XX FT /note= "optionally the sugar-phosphate internucleotide
XX FT backbone is replaced by an amide backbone to form a
XX FT peptide nucleic acid compound"
XX PN WO2004042030-A2.
XX PD 21-MAY-2004.
XX PF 03-NOV-2003; 2003WO-US035153.
XX PR 01-NOV-2002; 2002US-0423173P.
XX PA (LEUC-) LEUCADIA TECHNOLOGIES INC.
XX PI Jablonski E, Driver D, Adams T;
XX DR WPI; 2004-419704/39.
XX PT Detecting a non-nucleic acid analyte present in a sample comprises
XX PT specifically detecting the presence of a nucleic acid marker in the
XX PT eluted analyte-dependent reporter/second receptor complex.
XX PS Example 8; SEQ ID NO 6; 75pp; English.
XX CC The invention relates to a method of detecting a non-nucleic acid analyte
XX CC present in a sample comprises specifically detecting the presence of a
XX CC nucleic acid marker in the eluted analyte-dependent reporter/second
XX CC receptor complex, where the detection of nucleic acid marker indicates
XX CC the presence of analyte in the sample. The methods and kits are useful
XX CC for detecting a non-nucleic acid analyte present in a sample. They are
XX CC also useful for labelling antibodies and other proteins with a nucleic
XX CC acid, especially DNA, and for purifying antibodies and analytes. The
XX CC invention provides a method that detects analytes present at vanishingly
XX CC low levels or concentrations with high sensitivity and low background.
XX CC This sequence corresponds to a displacement oligonucleotide for a
XX CC displacement immuno-PCR assay for prostate specific antigen. The sugar-
XX CC phosphate backbone of the oligonucleotide can be replaced by an amide
XX CC backbone to produce a peptide nucleic acid molecule.
XX SQ Sequence 18 BP; 0 A; 5 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2344 CTTCCCTTCCTGCTGTGT 2361
Db 1 CTTCCCTTCCTGCTGTGT 18

RESULT 482
ADO26670/c
ID ADO26670 standard; DNA; 18 BP.
XX AC ADO26670;
XX DT 12-AUG-2004 (first entry)
XX DE Synthetic leader sequence encoding DNA SEQ ID NO:63.
XX KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX OS Synthetic.
XX PN WO2004042059-A1.
XX PD 21-MAY-2004.

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XX PF 10-NOV-2003; 2003WO-AU001487.
XX PR 08-NOV-2002; 2002US-0425163P.
XX PA (UYQU ) UNIV QUEENSLAND.
XX PI Frazer IH;
XX DR WPI; 2004-411519/38.
XX DR P-PSDB; ADO26671.
XX PT Constructing synthetic polynucleotide for modulating the quality of a
XX PT selected phenotype displayed by an organism comprises replacing a first
XX PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX PS Example 1; SEQ ID NO 63; 86pp; English.
XX CC The present invention describes a method for constructing a synthetic
XX CC polynucleotide from which a polypeptide is producible to confer a
XX CC selected phenotype to an organism of interest or part in a different
XX CC quality than that conferred by a parent polynucleotide that encodes the
XX CC same polypeptide. The method comprises: (a) selecting a first codon of
XX CC the parent polynucleotide for replacement with a synonymous codon, where
XX CC the synonymous codon is selected on the basis that it exhibits a
XX CC different phenotypic preference than the first codon in a comparison of
XX CC phenotypic preferences in test organisms or parts, where the test
XX CC organism are selected from organisms of the same species as the organism
XX CC of interest and organisms that are related to the organisms of interest;
XX CC and (b) replacing the first codon with the synonymous codon to construct
XX CC the synthetic polynucleotide. Also described: (1) a method for
XX CC determining the phenotypic preference of a first codon in an organism of
XX CC interest or its parts; (2) a synthetic polynucleotide constructed from
XX CC the method above; (3) an organism of interest or part containing a
XX CC synthetic polynucleotide constructed from the method above; (4) an
XX CC organism of interest or part containing a synthetic construct that
XX CC comprises a regulatory polynucleotide operably linked to a tandem repeat
XX CC of a first codon fused in frame with a reporter polynucleotide that
XX CC encodes a reporter protein, which produces, or is predicted to produce a
XX CC selected phenotype or a phenotype of the same class as the selected
XX CC phenotype in the organism or part; (5) a method of modulating the quality
XX CC of a selected phenotype that is displayed by an organism of interest or
XX CC part and that results from the expression of a parent polynucleotide that
XX CC encodes the polypeptide; (6) a method of enhancing the quality of a
XX CC selected phenotype that is displayed by an organism of interest or part
XX CC and that results from the expression of a parent polynucleotide that
XX CC encodes the polypeptide; and (7) a method of reducing the quality of a
XX CC selected phenotype that is displayed by an organism of interest or part
XX CC and that results from the expression of a parent polynucleotide that
XX CC encodes the polypeptide. The method is useful for constructing a
XX CC synthetic polynucleotide from which a polypeptide is producible to confer
XX CC a selected phenotype to an organism of interest or part in a different
XX CC quality than that conferred by a parent polynucleotide that encodes the
XX CC same polypeptide. It is useful for modulating the quality of a selected
XX CC phenotype displayed by an organism or part. The present sequence encodes
XX CC a synthetic leader sequence, which is used in an example from the present
XX CC invention.
XX SQ Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2667 CAGCAACACCAACCAACAA 2684
Db 18 CAACAACAAACAAACAA 1

RESULT 483
ADO26652/c
ID ADO26652 standard; DNA; 18 BP.
XX XX

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AC ADO26652;  
XX 12-AUG-2004 (first entry)  
DE Synthetic leader sequence encoding DNA SEQ ID NO:45.  
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.  
KW Synthetic.  
OS  
XX WO2004042059-A1.  
PN 21-MAY-2004.  
XX 10-NOV-2003; 2003WO-AU001487.  
XX 08-NOV-2002; 2002US-0425163P.  
PR (UYQU ) UNIV QUEENSLAND.  
PA Frazer IH;  
XX WPI; 2004-411519/38.  
PI P-PSDB; ADO26653.  
XX Constructing synthetic polynucleotide for modulating the quality of a  
PT selected phenotype displayed by an organism comprises replacing a first  
PT codon with a synonymous codon to construct the synthetic polynucleotide.  
XX Example 1; SEQ ID NO 45; 86pp; English.  
XX The present invention describes a method for constructing a synthetic  
CC polynucleotide from which a polypeptide is producible to confer a  
CC selected phenotype to an organism of interest or part in a different  
CC quality than that conferred by a parent polynucleotide that encodes the  
CC same polypeptide. The method comprises: (a) selecting a first codon of  
CC the parent polynucleotide for replacement with a synonymous codon, where  
CC the synonymous codon is selected on the basis that it exhibits a  
CC different phenotypic preference than the first codon in a comparison of  
CC phenotypic preferences in test organisms or parts, where the test  
CC organism are selected from organisms of the same species as the organism  
CC of interest and organisms that are related to the organisms of interest;  
CC and (b) replacing the first codon with the synonymous codon to construct  
CC the synthetic polynucleotide. Also described: (1) a method for  
CC determining the phenotypic preference of a first codon in an organism of  
CC interest or its parts; (2) a synthetic polynucleotide constructed from  
CC the method above; (3) an organism or interest or part containing a  
CC synthetic polynucleotide constructed from the method above; (4) an  
CC organism or interest or part containing a synthetic construct that  
CC comprises a regulatory polynucleotide operably linked to a tandem repeat  
CC of a first codon fused in frame with a reporter polynucleotide that  
CC encodes a reporter protein, which produces, or is predicted to produce a  
CC selected phenotype or a phenotype of the same class as the selected  
CC phenotype in the organism or part; (5) a method of modulating the quality  
CC of a selected phenotype that is displayed by an organism of interest or  
CC part and that results from the expression of a parent polynucleotide that  
CC encodes the polypeptide; (6) a method of enhancing the quality of a  
CC selected phenotype that is displayed by an organism of interest or part  
CC and that results from the expression of a parent polynucleotide that  
CC encodes the polypeptide; (7) a method of reducing the quality of a  
CC selected phenotype that is displayed by an organism of interest or part  
CC and that results from the expression of a parent polynucleotide that  
CC encodes the polypeptide. The method is useful for constructing a  
CC synthetic polynucleotide from which a polypeptide is producible to confer  
CC a selected phenotype to an organism of interest or part in a different  
CC quality than that conferred by a parent polynucleotide that encodes the  
CC same polypeptide. It is useful for modulating the quality of a selected  
CC phenotype displayed by an organism or part. The present sequence encodes  
CC a synthetic leader sequence, which is used in an example from the present  
CC invention.  
XX Sequence 18 BP; 0 A; 0 C; 18 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 973 CCCCCCCCCACCGCGCCC 990  
DB 18 CCCCCCCCCCCCCCCCCC 1  
RESULT 484  
ADO26640/c  
ID ADO26640 standard; DNA; 18 BP.  
XX  
AC ADO26640;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Synthetic leader sequence encoding DNA SEQ ID NO:33.  
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.  
OS Synthetic.  
XX WO2004042059-A1.  
PN 21-MAY-2004.  
XX 10-NOV-2003; 2003WO-AU001487.  
PF 08-NOV-2002; 2002US-0425163P.  
PR (UYQU ) UNIV QUEENSLAND.  
XX Frazer IH;  
XX WPI; 2004-411519/38.  
DR P-PSDB; ADO26641.  
XX Constructing synthetic polynucleotide for modulating the quality of a  
PT selected phenotype displayed by an organism comprises replacing a first  
PT codon with a synonymous codon to construct the synthetic polynucleotide.  
XX Example 1; SEQ ID NO 33; 86pp; English.  
XX The present invention describes a method for constructing a synthetic  
CC polynucleotide from which a polypeptide is producible to confer a  
CC selected phenotype to an organism of interest or part in a different  
CC quality than that conferred by a parent polynucleotide that encodes the  
CC same polypeptide. The method comprises: (a) selecting a first codon of  
CC the parent polynucleotide for replacement with a synonymous codon, where  
CC the synonymous codon is selected on the basis that it exhibits a  
CC different phenotypic preference than the first codon in a comparison of  
CC phenotypic preferences in test organisms or parts, where the test  
CC organism are selected from organisms of the same species as the organism  
CC of interest and organisms that are related to the organisms of interest;  
CC and (b) replacing the first codon with the synonymous codon to construct  
CC the synthetic polynucleotide. Also described: (1) a method for  
CC determining the phenotypic preference of a first codon in an organism of  
CC interest or its parts; (2) a synthetic polynucleotide constructed from  
CC the method above; (3) an organism or interest or part containing a  
CC synthetic polynucleotide constructed from the method above; (4) an  
CC organism or interest or part containing a synthetic construct that  
CC comprises a regulatory polynucleotide operably linked to a tandem repeat  
CC of a first codon fused in frame with a reporter polynucleotide that  
CC encodes a reporter protein, which produces, or is predicted to produce a  
CC selected phenotype or a phenotype of the same class as the selected  
CC phenotype in the organism or part; (5) a method of modulating the quality  
CC of a selected phenotype that is displayed by an organism of interest or  
CC part and that results from the expression of a parent polynucleotide that  
CC encodes the polypeptide; (6) a method of enhancing the quality of a  
CC selected phenotype that is displayed by an organism of interest or part  
CC and that results from the expression of a parent polynucleotide that  
CC encodes the polypeptide; (7) a method of reducing the quality of a  
CC selected phenotype that is displayed by an organism of interest or part  
CC and that results from the expression of a parent polynucleotide that  
CC encodes the polypeptide. The method is useful for constructing a  
CC synthetic polynucleotide from which a polypeptide is producible to confer  
CC a selected phenotype to an organism of interest or part in a different  
CC quality than that conferred by a parent polynucleotide that encodes the  
CC same polypeptide. It is useful for modulating the quality of a selected  
CC phenotype displayed by an organism or part. The present sequence encodes  
CC a synthetic leader sequence, which is used in an example from the present  
CC invention.  
XX Sequence 18 BP; 0 A; 0 C; 18 G; 0 T; 0 U; 0 Other;

CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide. The method is useful for constructing a  
 CC synthetic polynucleotide from which a polypeptide is producible to confer  
 CC a selected phenotype to an organism of interest or part in a different  
 CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. It is useful for modulating the quality of a selected  
 CC phenotype displayed by an organism or part. The present sequence encodes  
 CC a synthetic leader sequence, which is used in an example from the present  
 CC invention.

XX SQ Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2666 ACAGCAACACCAACCA 2683

Db 18 ACAACACCAACCAACA 1

RESULT 485

ADO26688

ID ADO26688 standard; DNA; 18 BP.

AC ADO26688;

DT 12-AUG-2004 (first entry)

XX Synthetic leader sequence encoding DNA SEQ ID NO:81.

DE phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

XX WO2004042059-A1.

XX 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

XX 08-NOV-2002; 2002US-0425163P.

XX (UYQU ) UNIV QUEENSLAND.

XX Frazer IH;

XX WPI; 2004-411519/38.

DR P-PSDB; ADO26689.

XX Constructing synthetic polynucleotide for modulating the quality of a  
 PT selected phenotype displayed by an organism comprises replacing a first  
 PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 81; 86pp; English.

XX The present invention describes a method for constructing a synthetic  
 CC polynucleotide from which a polypeptide is producible to confer a  
 CC selected phenotype to an organism of interest or part in a different  
 CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. The method comprises: (a) selecting a first codon of  
 CC the parent polynucleotide for replacement with a synonymous codon, where  
 CC the synonymous codon is selected on the basis that it exhibits a  
 CC different phenotypic preference than the first codon in a comparison of  
 CC phenotypic preferences in test organisms or parts, where the test  
 CC organism are selected from organisms of the same species as the organism  
 CC of interest and organisms that are related to the organisms of interest;  
 CC and (b) replacing the first codon with the synonymous codon to construct  
 CC the synthetic polynucleotide. Also described: (1) a method for  
 CC determining the phenotypic preference of a first codon in an organism of  
 CC interest or its parts; (2) a synthetic polynucleotide constructed from  
 CC the method above; (3) an organism of interest or part containing a

CC synthetic polynucleotide constructed from the method above; (4) an  
 CC organism of interest or part containing a synthetic construct that  
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat  
 CC of a first codon fused in frame with a reporter polynucleotide that  
 CC encodes a reporter protein, which produces, or is predicted to produce a  
 CC selected phenotype or a phenotype of the same class as the selected  
 CC phenotype in the organism or part; (5) a method of modulating the quality  
 CC of a selected phenotype that is displayed by an organism of interest or  
 CC part and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide; (6) a method of enhancing the quality of a  
 CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide; and (7) a method of reducing the quality of a  
 CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide. The method is useful for constructing a  
 CC synthetic polynucleotide from which a polypeptide is producible to confer  
 CC a selected phenotype to an organism of interest or part in a different  
 CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. It is useful for modulating the quality of a selected  
 CC phenotype displayed by an organism or part. The present sequence encodes  
 CC a synthetic leader sequence, which is used in an example from the present  
 CC invention.

XX SQ Sequence 18 BP; 0 A; 18 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 973 CCCCCCCCCACCCGCC 990

Db 1 CCCCCCCCCCCCCCCC 18

RESULT 486

ADO26708

ID ADO26708 standard; DNA; 18 BP.

AC ADO26708;

DT 12-AUG-2004 (first entry)

XX Synthetic leader sequence encoding DNA SEQ ID NO:101.

DE phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

XX WO2004042059-A1.

XX 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

XX 08-NOV-2002; 2002US-0425163P.

XX (UYQU ) UNIV QUEENSLAND.

XX Frazer IH;

XX WPI; 2004-411519/38.

DR P-PSDB; ADO26709.

XX Constructing synthetic polynucleotide for modulating the quality of a  
 PT selected phenotype displayed by an organism comprises replacing a first  
 PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 101; 86pp; English.

XX The present invention describes a method for constructing a synthetic  
 CC polynucleotide from which a polypeptide is producible to confer a  
 CC selected phenotype to an organism of interest or part in a different

CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. The method comprises: (a) selecting a first codon of  
 CC the parent polynucleotide for replacement with a synonymous codon, where  
 CC the synonymous codon is selected on the basis that it exhibits a  
 CC different phenotypic preference than the first codon in a comparison of  
 CC phenotypic preferences in test organisms or parts, where the test  
 CC organism are selected from organisms of the same species as the organism  
 CC of interest and organisms that are related to the organisms of interest;  
 CC and (b) replacing the first codon with the synonymous codon to construct  
 CC the synthetic polynucleotide. Also described: (1) a method for  
 CC determining the phenotypic preference of a first codon in an organism of  
 CC interest or its parts; (2) a synthetic polynucleotide constructed from  
 CC the method above; (3) an organism or interest or part containing a  
 CC synthetic polynucleotide constructed from the method above; (4) an  
 CC organism or interest or part containing a synthetic construct that  
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat  
 CC of a first codon fused in frame with a reporter polynucleotide that  
 CC encodes a reporter protein, which produces, or is predicted to produce a  
 CC selected phenotype or a phenotype of the same class as the selected  
 CC phenotype in the organism or part; (5) a method of modulating the quality  
 CC of a selected phenotype that is displayed by an organism of interest or  
 CC part and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide; (6) a method of enhancing the quality of a  
 CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide; and (7) a method of reducing the quality of a  
 CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide. The method is useful for constructing a  
 CC synthetic polynucleotide from which a polypeptide is producible to confer  
 CC a selected phenotype to an organism of interest or part in a different  
 CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. It is useful for modulating the quality of a selected  
 CC phenotype displayed by an organism or part. The present sequence encodes  
 CC a synthetic leader sequence, which is used in an example from the present  
 CC invention.

XX Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2666 ACAGCAACACCAACCA 2683

DB 1 ACAACACACCAACACACA 18

RESULT 487

ADO26642

XX ADO26642 standard; DNA; 18 BP.

AC ADO26642;

DT 12-AUG-2004 (first entry)

DE Synthetic leader sequence encoding DNA SEQ ID NO:35.

DE phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

PN WO2004042059-A1.

PD 21-MAY-2004.

PF 10-NOV-2003; 2003WO-AU001487.

PR 08-NOV-2002; 2002US-0425163P.

PA (UYQU ) UNIV QUEENSLAND.

PI Frazer IH;

XX WPI; 2004-411519/38.  
 DR P-PSDB; ADO26643.  
 XX  
 PT Constructing synthetic polynucleotide for modulating the quality of a  
 PT selected phenotype displayed by an organism comprises replacing a first  
 PT codon with a synonymous codon to construct the synthetic polynucleotide.  
 PS Example 1; SEQ ID NO 35; 86pp; English.

CC The present invention describes a method for constructing a synthetic  
 CC polynucleotide from which a polypeptide is producible to confer a  
 CC selected phenotype to an organism of interest or part in a different  
 CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. The method comprises: (a) selecting a first codon of  
 CC the parent polynucleotide for replacement with a synonymous codon, where  
 CC the synonymous codon is selected on the basis that it exhibits a  
 CC different phenotypic preference than the first codon in a comparison of  
 CC phenotypic preferences in test organisms or parts, where the test  
 CC organism are selected from organisms of the same species as the organism  
 CC of interest and organisms that are related to the organisms of interest;  
 CC and (b) replacing the first codon with the synonymous codon to construct  
 CC the synthetic polynucleotide. Also described: (1) a method for  
 CC determining the phenotypic preference of a first codon in an organism of  
 CC interest or its parts; (2) a synthetic polynucleotide constructed from  
 CC the method above; (3) an organism or interest or part containing a  
 CC synthetic polynucleotide constructed from the method above; (4) an  
 CC organism or interest or part containing a synthetic construct that  
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat  
 CC of a first codon fused in frame with a reporter polynucleotide that  
 CC encodes a reporter protein, which produces, or is predicted to produce a  
 CC selected phenotype or a phenotype of the same class as the selected  
 CC phenotype in the organism or part; (5) a method of modulating the quality  
 CC of a selected phenotype that is displayed by an organism of interest or  
 CC part and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide; (6) a method of enhancing the quality of a  
 CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide; and (7) a method of reducing the quality of a  
 CC selected phenotype that is displayed by an organism of interest or part  
 CC and that results from the expression of a parent polynucleotide that  
 CC encodes the polypeptide. The method is useful for constructing a  
 CC synthetic polynucleotide from which a polypeptide is producible to confer  
 CC a selected phenotype to an organism of interest or part in a different  
 CC quality than that conferred by a parent polynucleotide that encodes the  
 CC same polypeptide. It is useful for modulating the quality of a selected  
 CC phenotype displayed by an organism or part. The present sequence encodes  
 CC a synthetic leader sequence, which is used in an example from the present  
 CC invention.

XX Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

SQ Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2667 CAGCAACACCAACCA 2684

DB 1 CAACACACCAACACACA 18

RESULT 488

ADS90816

ID ADS90816 standard; DNA; 18 BP.

XX ADS90816;

XX 18-NOV-2004 (first entry)

DE Oligonucleotide of the invention SEQ ID NO:1832.

XX ss; cell proliferative disorder; breast; methylation; cytostatic;  
 KW gene therapy; single nucleotide polymorphism; SNP.

XX OS Unidentified.  
 XX PN WO2004035803-A2.  
 XX PD 29-APR-2004.  
 XX PF 01-OCT-2003; 2003WO-EP010881.  
 XX PR 01-OCT-2002; 2002DE-01045779.  
 XX PR 07-JAN-2003; 2003DE-01000096.  
 XX PR 17-APR-2003; 2003DE-01017955.  
 XX PA (EPIG-) EPIGENOMICS AG.  
 XX PI Roekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;  
 XX PI Nimrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;  
 XX DR WPI; 2004-348468/32.  
 XX XX Predicting responsiveness of a subject with breast cell proliferative  
 XX PT disorder, useful for treating or differentiating breast cell  
 XX PT proliferative disorders comprises analyzing methylation pattern of a  
 XX FT genomic DNA from the subject.  
 XX XX Disclosure; SEQ ID NO 1832; 104pp; English.  
 XX CC The invention relates to a novel method for predicting the responsiveness  
 XX CC of a subject with a cell proliferative disorder of the breast tissues to  
 XX CC a therapy comprising analysing the methylation pattern of a target  
 XX CC nucleic acid by contacting at least one of the target nucleic acids in a  
 XX CC biological sample obtained from the subject prior to or during treatment.  
 XX CC The method of the invention has cytostatic activity, and may have a use  
 XX CC in gene therapy. The set of oligonucleotides comprising at least two of  
 XX CC the oligomers are useful for detecting the cytosine methylation state  
 XX CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The  
 XX CC methods, nucleic acid, oligonucleotide, and kit are useful for the  
 XX CC treatment, characterisation, classification and/or differentiation, of  
 XX CC breast cell proliferative disorders. The method is also useful for  
 XX CC predicting the responsiveness of a subject with a cell proliferative  
 XX CC disorder of the breast tissues to a therapy. The present sequence is used  
 XX CC in the exemplification of the invention.  
 XX SQ Sequence 18 BP; 3 A; 0 C; 5 G; 10 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.8; DB 1; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 2.7e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3275 TTTTAATTGTAATGGTT 3292  
 ||||| ||||| |||||  
 Db 1 TTTTGATTGTAGATGGTT 18  
 RESULT 489  
 ABN87920/C  
 ID ABN87920 standard; DNA; 15 BP.  
 XX AC ABN87920;  
 XX AC  
 XX DT 12-AUG-2002 (first entry)  
 XX DE Human GSR allele specific oligonucleotide primer SEQ ID NO:39.  
 XX KW Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP;  
 XX KW gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;  
 XX KW primer; ss.  
 XX OS Homo sapiens.  
 XX XX Key Location/Qualifiers  
 XX FT misc\_feature 14 /\*tag= a  
 XX FT

FT XX /note= "polymorphic base"  
 XX PN WO200242320-A2.  
 XX PD 30-MAY-2002.  
 XX PF 13-NOV-2001; 2001WO-US046473.  
 XX PR 10-NOV-2000; 2000US-0247202P.  
 XX PA (GENA-) GENAISANCE PHARM INC.  
 XX PI Bieglecki KM, Sanchis A, Sausker EA, Sun X;  
 XX PI WPI; 2002-471719/50.  
 XX DR New genetic variants of Glutathione reductase isogenes, useful for  
 XX PT improving efficiency and reliability in drug development for treating  
 XX PT hemolytic anemia.  
 XX PS Claim 14; Page 14; 137pp; English.  
 XX CC The present invention describes genetic variants of the human glutathione  
 XX CC reductase (GSR) gene (I). (I) has antianaemic activity and can be used in  
 XX CC gene therapy. (I) can be used in screening for drugs targeting (I) that  
 XX CC are useful for treating haemolytic anaemia. Methods from the present  
 XX CC invention can be used: for improving the efficiency and reliability of  
 XX CC several steps in the discovery and development of drugs for treating  
 XX CC diseases associated with GSR activity; for haplotyping, which is also  
 XX CC used by the pharmaceutical research scientist to validate GSR as a  
 XX CC candidate target for treating a specific condition or disease predicted  
 XX CC to be associated with GSR activity, e.g. haemolytic anaemia, and in the  
 XX CC design of clinical trials for treating a specific condition of disease  
 XX CC associated with GSR activity; and for screening compounds targeting GSR.  
 XX CC (I) is useful in studying the expression and function of GSR, and in  
 XX CC expressing GSR protein for use in screening for candidate drugs to treat  
 XX CC diseases related to GSR activity. (I) is also useful in studying the  
 XX CC effect of the variation on the biological activity of GSR as well as on  
 XX CC the binding affinity of candidate drugs targeting GSR for the treatment  
 XX CC of haemolytic anaemia. The present sequence represents an allele specific  
 XX CC oligonucleotide (ASO) primer for the human GSR gene, which is given in  
 XX CC the exemplification of the present invention. N.B. The polymorphic base  
 XX CC (showing a single nucleotide polymorphism) in the ASO primer is shown  
 XX CC using an IUPAC ambiguity code (as given in the present invention)  
 XX SQ Sequence 15 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 1 Other;  
 Query Match 0.3%; Score 14.6; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2574 TTAAAAAATAAAAAA 2588  
 |:|||||  
 Db 15 TWAATAAAAAA 1  
 RESULT 490  
 AAQ78445/C  
 ID AAQ78445 standard; DNA; 16 BP.  
 XX AC AAQ78445;  
 XX AC  
 XX DT 25-MAR-2003 (revised)  
 XX DT 27-JUN-1995 (first entry)  
 XX DE TGF-beta gene phosphorothioate antisense oligonucleotide.  
 XX KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;  
 XX KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;  
 XX KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;  
 XX KW immunosuppression; oligonucleotide; ss.  
 XX OS Synthetic.

XX WO9425588-A2.  
 PN 10-NOV-1994.  
 XX  
 PD  
 XX  
 XX 29-APR-1994; 94WO-EP001362.  
 PF  
 XX 30-APR-1993; 93EP-00107089.  
 PR 13-MAY-1993; 93EP-00107849.  
 XX  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA  
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;  
 PI Bogdahn U;  
 XX WPI; 1994-358266/44.  
 DR  
 XX New transforming growth factor beta antisense oligo:nucleotide(s) - for  
 PT treating immunosuppression, tumours, etc.  
 PT  
 XX Claim 6; Page 51; 74pp; English.  
 PS  
 XX The antisense oligonucleotides are useful in the treatment of tumours in  
 CC which expression of TGF-beta is of relevance for pathogenicity and/or  
 CC inhibition of pathological angiogenesis. They are used especially for the  
 CC treatment of the immunosuppressive effect of TGF-beta, augmentation of  
 CC the proliferation of cytotoxic lymphocytes, treatment of endogenous  
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas  
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis  
 CC of skin carcinogenesis, and treatment of oesophageal and gastric  
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files  
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-  
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense  
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate  
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 16 BP; 1 A; 3 C; 4 G; 8 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1851 CACCACAAAGACAGGA 1866  
 Db 16 CACCATAAAGACAGGA 1  
 RESULT 491  
 AAV48961/c  
 ID AAV48961 standard; DNA; 16 BP.  
 XX  
 AC AAV48961;  
 XX  
 DT 15-OCT-1998 (first entry)  
 DE  
 XX TGF-beta2 antisense oligonucleotide TGF-beta2-32.  
 DE  
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 KW  
 XX Synthetic.  
 OS Homo sapiens.  
 OS  
 XX EP856579-A1.  
 PN  
 XX 05-AUG-1998.  
 PD  
 XX 31-JAN-1997; 97EP-00101531.  
 PF  
 XX 31-JAN-1997; 97EP-00101531.  
 XX  
 PR 31-JAN-1997; 97EP-00101531.  
 XX  
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA  
 XX Schlingensiepen K, Brysch W;  
 PI WPI; 1998-400910/35.  
 XX

PI Schlingensiepen K, Brysch W;  
 XX WPI; 1998-400910/35.  
 XX  
 PT Preparation of antisense oligo:nucleotide(s) which lack long runs of  
 PT consecutive guanine or inosine - and have specific ratio of residues  
 PT able to form two or three hydrogen bonds, have greater activity and  
 PT reduced toxicity, used therapeutically or to modulate growth of cells in  
 PT culture.  
 XX  
 PS Claim 10; Fig 8a; 286pp; English.  
 PS  
 XX AAV48930-49007 represent antisense oligonucleotides directed against  
 CC transforming growth factor-beta2 (TGF-beta2). Of these, only  
 CC oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
 CC beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
 CC little effect. The oligonucleotides exemplify the invention. The  
 CC specification describes oligonucleotides that contain 8-30 nucleotides,  
 CC which contain at most 8 nucleotides that can each form three hydrogen  
 CC bonds to cytosine; do not contain four consecutive nucleotides able to  
 CC form three H-bonds each to four consecutive cytosines; do not contain two  
 CC sequences of three consecutive nucleotides each able to form three H-  
 CC bonds to three consecutive cytosines, and the ratio between residues able  
 CC to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
 CC = 0.33-0.72. The oligonucleotides are used to modulate expression of  
 CC genes, particularly the genes for p53, Erb-2, junB, junD, TGF-beta 1 or  
 CC beta 2 to control proliferation of primary cell cultures (e.g. bone  
 CC marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
 CC keratinocytes). The oligonucleotides can also be used to analyse function  
 CC of proteins (by altering their expression or activity) and  
 CC therapeutically, e.g. in cases of cancer or (targeting TGF) for  
 CC stimulating the immune system  
 XX  
 SQ Sequence 16 BP; 5 A; 4 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2245 CTAACCTTCGTGCTGG 2260  
 Db 16 CCAACTTCGTGCTGG 1  
 RESULT 492  
 AAV48954/c  
 ID AAV48954 standard; DNA; 16 BP.  
 XX  
 AC AAV48954;  
 XX  
 DT 15-OCT-1998 (first entry)  
 DE  
 XX TGF-beta2 antisense oligonucleotide TGF-beta2-25.  
 DE  
 XX Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide;  
 KW modulate; gene expression; ss.  
 KW  
 XX Synthetic.  
 OS Homo sapiens.  
 OS  
 XX EP856579-A1.  
 PN  
 XX 05-AUG-1998.  
 PD  
 XX 31-JAN-1997; 97EP-00101531.  
 PF  
 XX 31-JAN-1997; 97EP-00101531.  
 XX  
 PR (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.  
 PA  
 XX Schlingensiepen K, Brysch W;  
 PI WPI; 1998-400910/35.  
 XX



XX Preparation of antisense oligo:nucleotide(s) which lack long runs of  
PT consecutive guanosine or inosine - and have specific ratio of residues  
PT able to form two or three hydrogen bonds, have greater activity and  
PT reduced toxicity, used therapeutically or to modulate growth of cells in  
PT culture.  
XX  
XX Claim 10; Fig 8a; 286pp; English.  
XX  
XX AAV48930-49007 represent antisense oligonucleotides directed against  
XX transcribing growth factor-beta2 (TGF-beta2). Of these, only  
XX oligonucleotides AAV48930-67 resulted in significant reduction in TGF-  
XX beta 2 protein expression, while oligonucleotides AAV48968-49007 had  
XX little effect. The oligonucleotides exemplify the invention. The  
XX specification describes oligonucleotides that contain 8-30 nucleotides,  
XX which contain at most 8 nucleotides that can each form three hydrogen  
XX bonds to cytosine; do not contain four consecutive nucleotides able to  
XX form three H-bonds each to four consecutive cytosines; do not contain two  
XX sequences of three consecutive nucleotides each able to form three H-  
XX bonds to three consecutive cytosines, and the ratio between residues able  
XX to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R  
XX = 0.33-0.72. The oligonucleotides are used to modulate expression of  
XX genes, particularly the genes for p53, ErbB-2, junB, junD, TGF-beta 1 or  
XX beta 2 to control proliferation of primary cell cultures (e.g. bone  
XX marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or  
XX keratinocytes). The oligonucleotides can also be used to analyse function  
XX of proteins (by altering their expression or activity) and  
XX therapeutically, e.g. in cases of cancer or (targeting TGF) for  
XX stimulating the immune system  
XX  
XX Sequence 16 BP; 4 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2078 CTCTACAGACTGAG 2093  
Db 16 CTCTACAGACTTGAG 1

RESULT 493  
AAAX18362/c  
ID AAAX18362 standard; DNA; 16 BP.  
XX  
XX AAAX18362;  
XX  
XX 11-MAY-1999 (first entry)  
XX  
XX RT-PCR primer of the invention SEQ ID 3.  
XX  
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
XX  
XX Synthetic.  
XX  
XX JP11032765-A.  
XX  
XX 09-FEB-1999.  
XX  
XX 18-JUL-1997; 97JP-00208312.  
XX  
XX 18-JUL-1997; 97JP-00208312.  
XX  
XX (TAKI ) TAKARA SHUZO CO LTD.  
XX  
XX WPI; 1999-183822/16.  
XX  
XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
XX  
XX Disclosure; Page 10; 19pp; Japanese.

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
CC natural number indicating the repetition of alpha; beta = thymine; n =  
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
CC repetition of gamma, in which thymine expressed by gamma is composed of  
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
CC useful as primers for RT-PCR and determination of base sequences. The new  
CC sequences allow for reproductive and highly efficient analysis of gene  
CC sequences  
XX  
XX Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAAACA 2816  
Db 16 TGAATAAAAAAAAAAAAA 1

RESULT 494  
AAAX18363/c  
ID AAAX18363 standard; DNA; 16 BP.  
XX  
XX AAAX18363;  
XX  
XX 11-MAY-1999 (first entry)

XX  
XX RT-PCR primer of the invention SEQ ID 4.  
XX  
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
XX  
XX Synthetic.  
XX  
XX JP11032765-A.  
XX  
XX 09-FEB-1999.  
XX  
XX 18-JUL-1997; 97JP-00208312.  
XX  
XX 18-JUL-1997; 97JP-00208312.  
XX  
XX (TAKI ) TAKARA SHUZO CO LTD.  
XX  
XX WPI; 1999-183822/16.  
XX  
XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
XX  
XX Disclosure; Page 10; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates  
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta  
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or  
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =  
CC natural number indicating the repetition of alpha; beta = thymine; n =  
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or  
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the  
CC repetition of gamma, in which thymine expressed by gamma is composed of  
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are  
CC useful as primers for RT-PCR and determination of base sequences. The new  
CC sequences allow for reproductive and highly efficient analysis of gene  
CC sequences  
XX  
XX Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



|                       |   |                                    |     |
|-----------------------|---|------------------------------------|-----|
| QY                    | 929   | AGAAAAAACAACAAA                    | 944 |
| Db                    | 16  | AGAAAAAACAACAAA                    | 1   |
| RESULT 495            |   |                                    |     |
| ADL46313/C            |   |                                    |     |
| ID                    | ABL46313  | standard; DNA; 16 BP.              |     |
| XX                    |   |                                    |     |
| AC                    | ABL46313;   |                                    |     |
| XX                    |   |                                    |     |
| DT                    | 26-APR-2002   | (first entry)                      |     |
| XX                    |   |                                    |     |
| DE                    | Mouse scavenger receptor class B type 1 oligonucleotide                   | SEQ ID NO:280.                     |     |
| XX                    |   |                                    |     |
| KW                    | Nucleic acid accessible hybridisation site; detection; hybridisation;     |                                    |     |
| KW                    | characterisation; identification; nucleic acid structure; diagnosis;      |                                    |     |
| KW                    | PCR primer; probe; ss.  |                                    |     |
| XX                    |   |                                    |     |
| OS                    | Mus sp.   |                                    |     |
| OS                    | Synthetic.  |                                    |     |
| PN                    | WO200198537-A2.   |                                    |     |
| XX                    |   |                                    |     |
| PD                    | 27-DEC-2001.  |                                    |     |
| XX                    |   |                                    |     |
| PF                    | 15-JUN-2001; 2001WO-US019401.   |                                    |     |
| XX                    |   |                                    |     |
| PR                    | 17-JUN-2000; 2000US-0212308P.   |                                    |     |
| PR                    | 15-JUN-2001; 2001US-00212308.   |                                    |     |
| XX                    |   |                                    |     |
| PA                    | (THIR-) THIRD WAVE TECHNOLOGIES INC.                                      |                                    |     |
| XX                    |   |                                    |     |
| PI                    | Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;                         |                                    |     |
| XX                    |   |                                    |     |
| DR                    | WPI; 2002-049698/06.  |                                    |     |
| XX                    |   |                                    |     |
| PT                    | Identifying oligonucleotides hybridizing to nucleic acids containing      |                                    |     |
| PT                    | secondary structure, useful in clinical diagnosis, comprises identifying  |                                    |     |
| PT                    | primers that interact with the target to form an extension product under  |                                    |     |
| PT                    | amplification conditions.   |                                    |     |
| XX                    |   |                                    |     |
| PS                    | Claim 48; Fig 79A; 409pp; English.  |                                    |     |
| XX                    |   |                                    |     |
| CC                    | The present invention describes a method for identifying oligonucleotides |                                    |     |
| CC                    | with desired hybridisation properties to nucleic acid targets containing  |                                    |     |
| CC                    | secondary structure. The method comprises amplifying a target nucleic     |                                    |     |
| CC                    | acid having at least one accessible and one inaccessible site. Primers    |                                    |     |
| CC                    | that form an extension product are identified as the oligonucleotides     |                                    |     |
| CC                    | which can interact with the folded target nucleic acid. Oligonucleotides  |                                    |     |
| CC                    | from the present invention can be used in novel detection methods for     |                                    |     |
| CC                    | clinical diagnostic purposes, including the detection and identification  |                                    |     |
| CC                    | of pathogenic organisms (e.g. HIV). The method allows the ability to      |                                    |     |
| CC                    | rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent   |                                    |     |
| CC                    | sequences used in the exemplification of the present invention            |                                    |     |
| XX                    |   |                                    |     |
| SQ                    | Sequence 16 BP; 1 A; 7 C; 1 G; 7 T; 0 U; 0 Other;                         |                                    |     |
| Query Match           | 0.3%;   | Score 14.4; DB 1; Length 16;       |     |
| Best Local Similarity | 93.8%;  | Pred. No. 2.3e+02;                 |     |
| Matches               | 15; Conservative  | 0; Mismatches 1; Indels 0; Gaps 0; |     |
| QY                    | 65  | TGGGAGAGAAAGAGAG                   | 80  |
| Db                    | 16  | TGGGAGAGAAACAGAG                   | 1   |
| RESULT 496            |   |                                    |     |
| ADL49413              |   |                                    |     |
| ID                    | ADL49413  | standard; RNA; 17 BP.              |     |
| XX                    |   |                                    |     |
| AC                    | ADL49413;   |                                    |     |
| XX                    |   |                                    |     |

|                       |  |                                     |      |
|-----------------------|--|-------------------------------------|------|
| DT                    | 20-MAY-2004  | (first entry)                       |      |
| XX                    |  |                                     |      |
| DE                    | Human PKR substrate sequence #527.   |                                     |      |
| XX                    |  |                                     |      |
| KW                    | antisense oligonucleotide; neurite growth inhibitor; NOGO;                   |                                     |      |
| KW                    | prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;                       |                                     |      |
| KW                    | protein kinase PKR; cerebrovascular accident;                                |                                     |      |
| KW                    | central nervous system injury; CNS injury; spinal cord injury; cancer;       |                                     |      |
| KW                    | melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;      |                                     |      |
| KW                    | restenosis; asthma; Crohn's disease; diabetes; obesity;                      |                                     |      |
| KW                    | autoimmune disease; lupus; multiple sclerosis; transplant rejection;         |                                     |      |
| KW                    | graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;         |                                     |      |
| KW                    | allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;            |                                     |      |
| XX                    | substrate; ds.   |                                     |      |
| OS                    | Unidentified.  |                                     |      |
| XX                    |  |                                     |      |
| PN                    | WO200281628-A2.  |                                     |      |
| XX                    |  |                                     |      |
| PD                    | 17-OCT-2002.   |                                     |      |
| XX                    |  |                                     |      |
| PF                    | 03-APR-2002; 2002WO-US010512.  |                                     |      |
| XX                    |  |                                     |      |
| PR                    | 05-APR-2001; 2001US-00827395.  |                                     |      |
| PR                    | 29-MAY-2001; 2001US-0294412P.  |                                     |      |
| PR                    | 28-AUG-2001; 2001US-0315315P.  |                                     |      |
| XX                    |  |                                     |      |
| PA                    | (RIBO-) RIBOZYME PHARM INC.  |                                     |      |
| XX                    |  |                                     |      |
| PI                    | Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;                   |                                     |      |
| XX                    |  |                                     |      |
| DR                    | WPI; 2003-058513/05.   |                                     |      |
| XX                    |  |                                     |      |
| PT                    | Novel enzymatic nucleic acid that down-regulates expression of neurite       |                                     |      |
| PT                    | growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or      |                                     |      |
| PT                    | protein kinase PKR genes, for treating cancer and inflammatory disease.      |                                     |      |
| XX                    |  |                                     |      |
| PS                    | Claim 59; SEQ ID NO 2946; 317pp; English.                                    |                                     |      |
| XX                    |  |                                     |      |
| CC                    | The invention comprises nucleic acids (e.g. antisense oligonucleotides)      |                                     |      |
| CC                    | that down regulate the expression or inhibit the function of a receptor      |                                     |      |
| CC                    | for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),     |                                     |      |
| CC                    | IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the        |                                     |      |
| CC                    | invention are useful for treating: cerebrovascular accident, central         |                                     |      |
| CC                    | nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,      |                                     |      |
| CC                    | lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,        |                                     |      |
| CC                    | restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune        |                                     |      |
| CC                    | disease, lupus, multiple sclerosis, transplant/graft rejection, and allergic |                                     |      |
| CC                    | ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic       |                                     |      |
| CC                    | conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The        |                                     |      |
| CC                    | nucleic acids of the invention are also useful for down-regulating the       |                                     |      |
| CC                    | expression of a target gene and as a diagnostic tool to examine genetic      |                                     |      |
| CC                    | drifts and mutations within diseased cells or to detect the presence of a    |                                     |      |
| CC                    | target RNA in a cell. The present RNA sequence represents a human PKR        |                                     |      |
| CC                    | substrate sequence.  |                                     |      |
| XX                    |  |                                     |      |
| SQ                    | Sequence 17 BP; 4 A; 1 C; 1 G; 0 T; 11 U; 0 Other;                           |                                     |      |
| Query Match           | 0.3%;  | Score 14.4; DB 1; Length 17;        |      |
| Best Local Similarity | 25.0%;   | Pred. No. 2.6e+02;                  |      |
| Matches               | 4; Conservative  | 11; Mismatches 1; Indels 0; Gaps 0; |      |
| QY                    | 2745   | TTTTTTTTTTTAAAGGA                   | 2760 |
| Db                    | 1  | UUUUUUUUUUUAGA                      | 16   |
| RESULT 497            |  |                                     |      |
| ADL49412              |  |                                     |      |
| ID                    | ADL49412   | standard; RNA; 17 BP.               |      |
| XX                    |  |                                     |      |
| AC                    | ADL49412;  |                                     |      |
| XX                    |  |                                     |      |



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OS Homo sapiens.
XX WO9323057-A1.
XX 25-NOV-1993..
XX 13-MAY-1993; 93WO-US004573.
XX 14-MAY-1992; 92US-00882822.
XX 14-MAY-1992; 92US-00882885.
XX 26-AUG-1992; 92US-00936110.
XX 26-AUG-1992; 92US-00936421.
XX 26-AUG-1992; 92US-00936422.
XX 26-AUG-1992; 92US-00936531.
XX 26-AUG-1992; 92US-00936532.
XX 07-DEC-1992; 92US-00987131.
XX 19-JAN-1993; 93US-00006122.
XX 19-JAN-1993; 93US-00008910.
XX (RIBO-) RIBOZYME PHARM INC.
PA Thompson JD, Draper KG;
XX WPI; 1993-386203/48.
XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
PT with tumours or mRNA expressed from gene encoding multiple drug
PT resistance.
XX Claim 3; Fig 10; 69pp; English.
XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC associated with development or maintenance of chronic myelogenous
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
CC lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
CC leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
CC The full length mRNAs containing these target sequences, encode aberrant
CC cellular proteins which are able to control cellular proliferation and
CC are directly linked to a leukemic phenotype. These target sequences are
CC identified by the ribozyme of the invention. The ribozymes is formed in a
CC hammerhead motif, but may also be formed in the motif of a hairpin,
CC hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
CC may be used to inhibit the development or expression of a transformed
CC phenotype in man and other animals by modulating expression of the
CC corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
CC and transformed cells elicits inhibition of the transformed state.
CC Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the
CC mechanism of drug resistance used by transformed cells and thus enhances
CC drug therapies for tumours. The ribozymes may also be used to study
CC genetic drift and mutations within cells. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX Sequence 17 BP; 9 A; 2 C; 5 G; 0 T; 1 U; 0 Other;
SQ Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 869 TCATTCTCTCTCTT 884
DB 16 TCGATTCTCTCTCTT 1
RESULT 500
AAQ51975/C
ID AAQ51975 standard; RNA; 17 BP.
XX AAQ51975;
AC AAQ51975;
XX 25-MAR-2003 (revised)
DT 26-MAY-1994 (first entry)
XX
DE B-cell mRNA ribozyme cleavable nucleotide 297.
XX Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
XX actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
XX adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
XX human; chronic myelogenous leukemia; CML; follicular lymphoma;
XX B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
XX neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
XX hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX Homo sapiens.
OS WO9323057-A1.
XX 25-NOV-1993.
XX 13-MAY-1993; 93WO-US004573.
XX 14-MAY-1992; 92US-00882822.
XX 14-MAY-1992; 92US-00882885.
XX 26-AUG-1992; 92US-00936110.
XX 26-AUG-1992; 92US-00936421.
XX 26-AUG-1992; 92US-00936422.
XX 26-AUG-1992; 92US-00936531.
XX 26-AUG-1992; 92US-00936532.
XX 07-DEC-1992; 92US-00987131.
XX 19-JAN-1993; 93US-00006122.
XX 19-JAN-1993; 93US-00008910.
XX (RIBO-) RIBOZYME PHARM INC.
PA Thompson JD, Draper KG;
XX WPI; 1993-386203/48.
XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
PT with tumours or mRNA expressed from gene encoding multiple drug
PT resistance.
XX Claim 3; Fig 7; 69pp; English.
XX The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC associated with development or maintenance of chronic myelogenous
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
CC lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
CC leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
CC The full length mRNAs containing these target sequences, encode aberrant
CC cellular proteins which are able to control cellular proliferation and
CC are directly linked to a leukemic phenotype. These target sequences are
CC identified by the ribozyme of the invention. The ribozymes is formed in a
CC hammerhead motif, but may also be formed in the motif of a hairpin,
CC hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
CC may be used to inhibit the development or expression of a transformed
CC phenotype in man and other animals by modulating expression of the
CC corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
CC and transformed cells elicits inhibition of the transformed state.
CC Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the
CC mechanism of drug resistance used by transformed cells and thus enhances
CC drug therapies for tumours. The ribozymes may also be used to study
CC genetic drift and mutations within cells. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX Sequence 17 BP; 4 A; 7 C; 4 G; 0 T; 2 U; 0 Other;
SQ Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2915 TCGATGGGTGCCCTC 2930
DB 17 TGAAGTGGGTGCCCTC 2

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CC is lower than that required of antisense molecules, and is highly  
 CC specific. The present sequence is used in the exemplification of the  
 CC present invention

SQ Sequence 17 BP; 6 A; 2 C; 2 G; 0 T; 7 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
 Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1034 TCTCTTTTAAAGGAA 1049  
 Db 1 UUCAUUUUUAAAGGAA 16

RESULT 503  
 AAX71256  
 ID AAX71256 standard; RNA; 17 BP.  
 XX AC AAX71256;  
 XX XX  
 XX 28-JUL-1999 (first entry)  
 XX Human KDR VEGF receptor hammerhead ribozyme substrate #268.  
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX OS Homo sapiens.  
 XX PN WO9715662-A2.  
 XX PD 01-MAY-1997.  
 XX PF 25-OCT-1996; 96WO-US017480.  
 XX PR 26-OCT-1995; 95US-0005974P.  
 XX PR 11-JAN-1996; 96US-00584040.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PA (CHIR ) CHIRON CORP.  
 XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX WPI; 1997-259017/23.  
 XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 105; 218pp; English.  
 XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 3 A; 7 C; 2 G; 0 T; 5 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 2.6e+02;  
 Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TCTCCTTCGACGTGAC 1828

Db 2 UCUCUCCUCCACGUGAC 17

RESULT 504  
 AAX75078/C  
 ID AAX75078 standard; RNA; 17 BP.  
 XX AC AAX75078;  
 XX XX  
 XX 28-JUL-1999 (first entry)  
 XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #606.  
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX OS Mus sp.  
 XX PN WO9715662-A2.  
 XX PD 01-MAY-1997.  
 XX PF 25-OCT-1996; 96WO-US017480.  
 XX PR 26-OCT-1995; 95US-0005974P.  
 XX PR 11-JAN-1996; 96US-00584040.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PA (CHIR ) CHIRON CORP.  
 XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX WPI; 1997-259017/23.  
 XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 173; 218pp; English.  
 XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 0 A; 1 C; 5 G; 0 T; 11 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 ACAGCAACCAACCA 2681  
 Db 17 ACAGCAACCAACCA 2

RESULT 505  
 AAV93711  
 ID AAV93711 standard; RNA; 17 BP.  
 XX AC AAV93711;  
 XX XX  
 XX 18-FEB-1999 (first entry)

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XX DE Human B-raf substrate nucleotide position 2458.
XX AC
XX AC AAV93709;
XX AC AAV93709;
XX DT 18-FEB-1999 (first entry)
XX DE Human B-raf substrate nucleotide position 2456.
XX DE
XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
XX KW screening; identification; synthesis; deprotection; purification; cancer;
XX KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
XX KW restenosis; rheumatoid arthritis; ss.
XX OS Homo sapiens.
XX PN WO9850530-A2.
XX PD 12-NOV-1998.
XX PF 05-MAY-1998; 98WO-US009249.
XX PR 09-MAY-1997; 97US-0046059P.
XX PR 09-JUN-1997; 97US-0049002P.
XX PR 03-JUL-1997; 97US-0051718P.
XX PR 22-AUG-1997; 97US-0056808P.
XX PR 02-OCT-1997; 97US-0061321P.
XX PR 02-OCT-1997; 97US-0061324P.
XX PR 05-NOV-1997; 97US-0064866P.
XX PR 19-DEC-1997; 97US-0068212P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
XX PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
XX PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX WPI; 1999-009494/01.
XX DT
XX DT Identifying new catalytic nucleic acid that modulates selected processes
XX PT - especially ribozymes that cleave Raf RNA for treating cancer,
XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
XX PT used as antiviral agents and synthons.
XX PS Claim 177; Page 172; 259pp; English.
XX CC A method has been developed for the identification of a nucleic acid
XX CC capable of modulating a process in a biological system. The method
XX CC comprises: (a) introducing into the system a random library of nucleic
XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX CC in systems where modulation has occurred and/or determining the sequence
XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with
XX CC endonuclease activity and catalytic activity, from the present invention,
XX CC are used to modulate gene expression in plant and mammalian cells and to
XX CC cleave target nucleic acid, particularly for treating systemic diseases
XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX CC ascites and infection. They may also be used to detect genetic drift and
XX CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are
XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX CC generally any condition associated with the level of c-raf. Introduction
XX CC of sugar/phosphate modifications increases stability against nuclease and
XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
XX CC method, specifically for modulating the expression of a Raf gene
XX SQ Sequence 17 BP; 2 A; 2 C; 2 G; 0 T; 11 U; 0 Other;
XX Query Match 0.3%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 31.2%; Pred. No. 2.6e+02;
XX Matches 5; Conservative 10; Mismatches 1; Indels 0; Gaps 0;
QY 2744 CTTTCTTTTAAAGG 2759
Db 1 CUCUUUUUUUAAGG 16
RESULT 506

```

```
QY      2743 TCTTTTCTTTTCTTTTAAAG 2758
      :||: :::::|||||
Db      2 UCUCUUUUUUUUUUAAG 17

RESULT 507
AAAX14708
ID      AAX14708 standard; DNA; 17 BP.
XX
AC      AAX14708;
XX
DT      24-MAR-1999 (first entry)
XX
DE      Triple helix forming nucleotides 1205-1218 of superoxide dismutase gene.
XX
KW      Triple-helix forming region; Triplex formation; DNA detection;
KW      identification; bacteria; oncogene; virus; ds.
XX
OS      Homo sapiens.
XX
PN      US5861244-A.
XX
PD      19-JAN-1999.
XX
PF      22-DEC-1993; 93US-00173489.
XX
PR      29-OCT-1992; 92US-00968436.
XX
PS      (PROP-) PROFILE DIAGNOSTIC SCI INC.
XX
PI      Hepburn AG, Wang C;
XX
DR      WPI; 1999-130384/11.
XX
PT      Assay of genetic sequences based on triplex formation from double
PT      stranded analyte - and hybrid of anchor and reporter sequences, with
PT      reporter released if triplex formation occurs, used e.g. to identify
PT      bacteria.
XX
PS      Disclosure; Col 17-18; 168pp; English.
XX
CC      The present sequence represents a potential triple-helix forming region.
CC      It can be used to demonstrate the assay of the invention. The assay
CC      comprises adding a sample containing double-stranded DNA test sequences,
CC      e.g. containing the present sequence, to an aqueous medium containing at
CC      least one complex of anchor DNA, attached to a solid support, and
CC      reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC      designed to form a triple-strand structure with part of the test
CC      sequence. Triplex formation results in displacement of the reporter DNA
CC      which is detected as an indication of the presence of the DNA test
CC      sequence. The method is used to detect DNA sequences, particularly for
CC      identification of bacteria (by detecting genes for ribosomal RNA) in
CC      clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ      Sequence 17 BP; 1 A; 14 C; 0 G; 2 T; 0 U; 0 Other;

      Query Match      0.3%; Score 14.4; DB 1; Length 17;
      Best Local Similarity 93.8%; Pred. No. 2.6e+02;
      Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      975 CCCCCCACCCTCCCTCC 990
      |||||
Db      2 CCCCCCACCCTCCCTCC 17

RESULT 508
AAAX14705
ID      AAX14705 standard; DNA; 17 BP.
XX
AC      AAX14705;
XX
DT      24-MAR-1999 (first entry)
XX
```

```
DE      Triple helix third strand of SOD1 gene nucleotides 1084-1110.
XX
KW      Triplex formation; DNA detection; triple helix; identification; bacteria;
KW      oncogene; virus; ss.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
PN      US5861244-A.
XX
PD      19-JAN-1999.
XX
PF      22-DEC-1993; 93US-00173489.
XX
PR      29-OCT-1992; 92US-00968436.
XX
PA      (PROP-) PROFILE DIAGNOSTIC SCI INC.
XX
PI      Hepburn AG, Wang C;
XX
DR      WPI; 1999-130384/11.
XX
PT      Assay of genetic sequences based on triplex formation from double
PT      stranded analyte - and hybrid of anchor and reporter sequences, with
PT      reporter released if triplex formation occurs, used e.g. to identify
PT      bacteria.
XX
PS      Disclosure; Col 17-18; 168pp; English.
XX
CC      The present sequence represents a polynucleotide that is able to form a
CC      triple helix with a double stranded sequence. Cytosine bases in the
CC      present can be replaced with 5-methylcytosine for increased triplex
CC      stability. The present sequence is used in the assay of the invention,
CC      where it can be part of the anchor DNA or reporter DNA sequence. The
CC      assay comprises adding a sample containing double-stranded DNA test
CC      sequences to an aqueous medium containing at least one complex of anchor
CC      DNA, attached to a solid support, and reporter DNA, where either a part
CC      of the anchor DNA or reporter DNA is designed to form a triple-strand
CC      structure with part of the test sequence. Triplex formation results in
CC      displacement of the reporter DNA which is detected as an indication of
CC      the presence of the DNA test sequence. The method is used to detect DNA
CC      sequences, particularly for identification of bacteria (by detecting
CC      genes for ribosomal RNA) in clinical samples, but also detection of
CC      oncogenes and Hepatitis B virus
XX
SQ      Sequence 17 BP; 0 A; 13 C; 1 G; 3 T; 0 U; 0 Other;

      Query Match      0.3%; Score 14.4; DB 1; Length 17;
      Best Local Similarity 93.8%; Pred. No. 2.6e+02;
      Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2930 CCCCCTCCCTCCCTCC 2945
      |||||
Db      1 CCCCCTCCCTCCCTCC 16

RESULT 509
AAZ57107
ID      AAZ57107 standard; DNA; 17 BP.
XX
AC      AAZ57107;
XX
DT      24-MAR-2000 (first entry)
XX
DE      Human FCMD-causing protein related oligonucleotide.
XX
KW      Fukuyama-type congenital muscular dystrophy-causing protein; FCMD;
KW      detection; muscular dystrophy; diagnosis; ss.
XX
OS      Homo sapiens.
XX
PN      JF11313682-A.
XX
```

PD 16-NOV-1999.  
 XX 30-APR-1998; 98JP-00137703.  
 XX 30-APR-1998; 98JP-00137703.  
 PR (SAKA ) OTSUKA PHARM CO LTD.  
 XX WPI; 2000-090363/08.  
 XX A Fukuyama-type congenital muscular dystrophy-causing protein - for  
 PT preparing its specific antibody.  
 XX  
 XX Example 2; Page 13; 32pp; Japanese.  
 XX The present invention describes a Fukuyama-type congenital muscular  
 CC dystrophy (FCMD)-causing protein isolated from human. Also described in  
 CC the present invention is a method for the detection of gene abnormality  
 CC for FCMD diagnosis by detecting the presence of a mutated FCMD-causing  
 CC DNA having a mutation causing functional insufficiency of the FCMD-  
 CC causing protein coded in the base sequence of 7389 nucleotides in the  
 CC gene of a person to be tested. The FCMD-causing protein is useful in the  
 CC preparation of its specific antibody. The present sequence represents an  
 CC oligonucleotide used in the exemplification of the present invention  
 XX  
 XX Sequence 17 BP; 12 A; 0 C; 2 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2576 AAAAAAAAAAAATTG 2591  
 DB 1 AAAAAAAAAAAATTG 16  
 RESULT 510  
 AAF05267  
 ID AAF05267 standard; DNA; 17 BP.  
 XX AAF05267;  
 XX  
 XX 16-FEB-2001 (first entry)  
 XX Hammerhead ribozyme substrate #2486.  
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
 KW interferon alpha; ss.  
 XX Homo sapiens.  
 XX WO200061729-A2.  
 XX 19-OCT-2000.  
 XX 11-APR-2000; 2000WO-US009721.  
 XX 12-APR-1999; 99US-0129390P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;  
 WPI; 2000-647423/62.  
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
 PT useful for producing e.g. granulocyte colony stimulating factor protein,  
 PT interferon alpha and erythropoietin.  
 XX Claim 18; Page 113; 164pp; English.  
 XX The present invention relates to enzymatic and antisense nucleic acid  
 CC molecules that act as inhibitors of the expression of repressor genes

CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
 CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).  
 CC Inhibition of the repressors removes prevents inhibition (and  
 CC consequently increases expression of) genes involved in the production of  
 CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha  
 XX  
 XX Sequence 17 BP; 3 A; 4 C; 9 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 424 AGCAGCAGCGGGC 439  
 DB 2 AGCAGTAGCGGGC 17  
 RESULT 511  
 AAF06339/C  
 ID AAF06339 standard; DNA; 17 BP.  
 XX AAF06339;  
 XX 16-FEB-2001 (first entry)  
 XX Hammerhead ribozyme substrate #3136.  
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
 KW interferon alpha; ss.  
 XX Homo sapiens.  
 XX WO200061729-A2.  
 XX 19-OCT-2000.  
 XX 11-APR-2000; 2000WO-US009721.  
 XX 12-APR-1999; 99US-0129390P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;  
 WPI; 2000-647423/62.  
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
 PT useful for producing e.g. granulocyte colony stimulating factor protein,  
 PT interferon alpha and erythropoietin.  
 XX Claim 42; Page 127; 164pp; English.  
 XX The present invention relates to enzymatic and antisense nucleic acid  
 CC molecules that act as inhibitors of the expression of repressor genes  
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
 CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).  
 CC Inhibition of the repressors removes prevents inhibition (and  
 CC consequently increases expression of) genes involved in the production of  
 CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha  
 XX  
 XX Sequence 17 BP; 2 A; 1 C; 1 G; 0 T; 13 U; 0 Other;  
 SQ  
 Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3805 AAAAGATAAAACCAA 3820  
 DB 17 AAAAGATAAAACCAA 2



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RESULT 512
AAF03387/c
ID AAF03387 standard; DNA; 17 BP.
XX
AC AAF03387;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1682.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 94; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 94; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 2 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1620 TCAACAATGGAGAAA 1635
DB 17 TCACAAATGAAGAAA 2

RESULT 513
AAF06340/c
ID AAF06340 standard; DNA; 17 BP.
XX
AC AAF06340;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #3137.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1620 TCAACAATGGAGAAA 1635
DB 17 TCACAAATGAAGAAA 2

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XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 42; Page 127; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 1 A; 2 C; 1 G; 0 T; 13 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3805 AAAAGATAAAACCAA 3820
DB 16 AAAAGATAAAACCAA 1

RESULT 514
AAF03071/c
ID AAF03071 standard; DNA; 17 BP.
XX
AC AAF03071;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1366.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 37; Page 87; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid

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CC molecules that act as inhibitors of the expression of repressor genes  
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
 CC factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).  
 CC Inhibition of the repressors removes prevents inhibition (and  
 CC consequently increases expression of) genes involved in the production of  
 CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha  
 CC  
 SQ Sequence 17 BP; 4 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 826 GAGTTCAGATCAGCCA 841  
 |||||  
 Db 16 GACTTCAGATCAGCCA 1

RESULT 515  
 AAH95613  
 ID AAH95613 standard; RNA; 17 BP.

XX AAH95613;  
 AC  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human Chk1 ribozyme substrate SEQ ID NO: 1038.

XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;  
 KW RNA cleavage; cancer; ss.

OS Homo sapiens.  
 XX  
 FN WO200157206-A2.

XX 09-AUG-2001.  
 XX 02-FEB-2001; 2001WO-US003504.  
 XX 03-FEB-2000; 2000US-0179983P.

XX (RIBO-) RIBOZYME PHARM INC.  
 PA (FATT/) FATTAEY A R.

XX Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;  
 XX WPI; 2001-496922/54.

XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid  
 PT molecules, which downregulates expression of a checkpoint kinase-1 gene,  
 PT useful for treating colorectal, lung, breast or prostate cancers.

XX Claim 4; Page 79; 115pp; English.

XX The present invention provides nucleic acid molecules capable of  
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)  
 CC gene. These may be antisense or ribozyme sequences, and are useful in the  
 CC treatment of diseases associated with conditions affected by Chk1 levels,  
 CC including cancer. The present sequence is an oligonucleotide described in  
 CC the exemplification of the invention

XX Sequence 17 BP; 11 A; 4 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 2.6e+02;  
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 932 AAAAAAAAAAACCT 947  
 |||||  
 Db 1 AAAAAAAAAACUACCU 16

RESULT 516  
 ABK00233  
 ID ABK00233 standard; RNA; 17 BP.  
 XX  
 AC ABK00233;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human NOGO Hammerhead Ribozyme #233.  
 XX  
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNzyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200159103-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US004273.  
 XX  
 PR 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 PI Blatt L, Mcswiggen J, Chowrira BM;  
 XX WPI; 2001-607195/69.  
 DR  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 PS  
 XX Claim 88; Page 69; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA motif) or  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with an NYN motif) or  
 CC an amberyzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a hammerhead ribozyme of the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1587 AGACCTACTTCAGAA 1602  
 Db 2 AGAUCUACUUCAGAA 17  
 RESULT 517  
 ABQ99687  
 ID ABQ99687 standard; DNA; 17 BP.  
 XX  
 AC ABQ99687;  
 XX  
 DT 08-NOV-2002 (first entry)  
 XX  
 DE Murine Ikbkap exon 27 acceptor site.  
 XX  
 DE Murine; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; ds;  
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening.  
 KW Mus sp.  
 XX  
 OS WO200259381-A2.  
 XX  
 PN 01-AUG-2002.  
 PD  
 XX  
 PF 07-JAN-2002; 2002WO-US000473.  
 XX  
 PR 06-JAN-2001; 2001US-0260080P.  
 XX  
 PA (GEO ) GEN HOSPITAL CORP.  
 XX  
 PI Slaugenhaupt S, Gusella JF;  
 XX  
 DR WPI; 2002-674806/72.  
 XX  
 PT New IKBKAP genes with mutations, useful for identifying a subject with  
 PT familial dysautonomia (FD), or for rapid carrier screening in the  
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or  
 PT prenatal diagnosis.  
 XX  
 PS Disclosure; Fig 11; 109pp; English.  
 XX  
 CC The present invention relates to methods and compositions useful for  
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day  
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM  
 CC 223900). It was found that mutations in the IKBKAP gene (see ABQ80565)  
 CC are associated with FD. The mutation associated with the major haplotype  
 CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine  
 CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced  
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD  
 CC patients, although they continue to express varying levels of wild-type  
 CC message in a tissue-specific manner. The mutation associated with the  
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine  
 CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.  
 CC This bp mutation causes an arginine to proline missense mutation (R896P)  
 CC in the IKBKAP protein, which is predicted to disrupt a potential  
 CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for

CC identifying a subject with FD and for rapid carrier screening. The IKBKAP  
 CC gene maps to chromosome 9q31. A mouse model of FD was created in an  
 CC example from the invention. Expression of murine Ikbkap was examined  
 CC using both mouse embryo and adult mouse multiple tissue Northern blots.  
 CC The blots were probed with a 1045bp PCR fragment that contains exons 2  
 CC through 11, which was generated using PCR primers ABQ80563-ABQ80564.  
 CC ABQ99662-ABQ99733 are the murine Ikbkap exon and intron boundaries  
 XX  
 SQ Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2745 TTTTITTTTTTAAAGGA 2760  
 Db 2 TTTTITTTTTTCAGGA 17  
 RESULT 518  
 ABT39218  
 ID ABT39218 standard; DNA; 17 BP.  
 XX  
 AC ABT39218;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Tumour suppression related human fukutin oligo SEQ ID No 4855.  
 XX  
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; protein chip; gene therapy; tumour suppression;  
 KW human fukutin; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025175-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004208.  
 XX  
 PR 17-SEP-2001; 2001PR-00011978.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313353/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 601; 720pp; French.  
 XX  
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterised by development of tumours or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these

CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 9 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1727 GATCCTTAATCCAA 1742  
DB 1 GATCATTAAATCCAA 16

RESULT 519  
ABZ59895  
ID ABZ59895 standard; RNA; 17 BP.  
AC ABZ59895;  
XX  
XX 21-MAR-2003 (first entry)  
DE Human K-Ras DNzyme substrate #7.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;  
KW anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200297114-A2.  
PN  
XX  
PD 05-DEC-2002.  
XX  
XX 29-MAY-2002; 2002WO-US016940.  
PF  
XX  
XX 29-MAY-2001; 2001US-0294140P.  
PR  
XX 06-JUN-2001; 2001US-0296249P.  
PR  
XX 10-SEP-2001; 2001US-0318471P.  
PR  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX  
XX Mcswiggen J;  
PI  
XX  
XX WPI; 2003-140484/13.  
DR  
XX  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX  
PS Claim 58; Page 85; 185pp; English.  
XX  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosolic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention  
XX  
XX Sequence 17 BP; 3 A; 5 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 422 GCAGGCAGCGCGC 437  
DB 2 GGAGGCAGCGCGC 17

## RESULT 520

ACC66553  
ID ACC66553 standard; DNA; 17 BP.  
XX  
XX ACC66553;  
XX  
XX 01-JUL-2003 (first entry)  
DE Murine oligonucleotide associated with tumour supression, SEQ ID 3800.  
XX  
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; ss.  
XX  
XX Mus musculus.  
OS  
XX  
XX WO2003025176-A2.  
PN  
XX  
XX 27-MAR-2003.  
PD  
XX  
XX 17-SEP-2002; 2002WO-IB004210.  
PF  
XX  
XX 17-SEP-2001; 2001FR-00011979.  
PR  
XX  
XX (MOLE-) MOLECULAR ENGINES LAB.  
PA  
XX  
XX Telerman A, Amson R, Tuijnder M;  
PI  
XX  
XX WPI; 2003-333167/31.  
DR  
XX  
XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
XX Disclosure; Page 475; 738pp; French.  
PS  
XX  
XX The present invention relates to murine oligonucleotides (ACC62754-  
CC ACC6806), which are associated with tumour suppression, tumour  
CC reversion, apoptosis and virus resistance. The oligonucleotides are  
CC useful as (1) as probes and primers for detecting, identifying,  
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
CC recombinant polypeptides. The oligonucleotides are useful for preparation  
CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia  
XX  
SQ Sequence 17 BP; 8 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2566 ATCAGTGTTTAAAAA 2581  
DB 2 ATCAGTCTTTAAAAA 17

RESULT 521  
ACC64890  
ID ACC64890 standard; DNA; 17 BP.  
XX  
XX ACC64890;  
XX  
XX 01-JUL-2003 (first entry)  
DT  
XX







CC experimental models. The nucleotides (also vectors containing them and  
 CC cells containing the vectors), the encoded polypeptides and antibodies  
 CC (Ab) against the polypeptide are useful for prevention and/or treatment  
 CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis  
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.

XX Sequence 17 BP; 4 A; 8 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 833 GATCAGCCACTCCGCA 848  
 Db 1 GATCAGCCACCCGCA 16  
 |||||

RESULT 528

ID ADB40890 standard; DNA; 17 BP.

XX AC ADB40890;

XX 18-DEC-2003 (revised)  
 DT 04-DEC-2003 (first entry)

DE Tumour suppression/reversion associated nucleotide #1213.

XX cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;  
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.

XX Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

XX 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-441574/41.

XX New nucleic acid encoding human prostate membrane-specific antigen,  
 PT useful e.g. for treatment of tumors and viral infection, also related  
 PT polypeptide and antibodies.

XX Disclosure; Page 173; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,  
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
 CC sequence having at least 80% identity, after optimal alignment, with the  
 CC nucleotides, a sequence that hybridizes under stringent conditions with  
 CC the nucleotides, or the complement, or corresponding RNA, of the  
 CC nucleotides. The nucleotides are used as probes or primers for detecting,  
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
 CC sense and antisense sequences, of nucleotides involved in tumour  
 CC suppression or reversion, apoptosis and or viral resistance, to produce  
 CC recombinant polypeptides, and to prepare transgenic animals, as  
 CC experimental models. The nucleotides (also vectors containing them and  
 CC cells containing the vectors), the encoded polypeptides and antibodies  
 CC (Ab) against the polypeptide are useful for prevention and/or treatment

CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis  
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.

XX Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAAACATC 2818

Db 16 AAAAAAAAAAAGATC 1  
 |||||

RESULT 529

ID ADE31052/c

XX ADE31052 standard; DNA; 17 BP.

XX AC ADE31052;

XX 29-JAN-2004 (first entry)

XX Cholesterol homeostasis/adipogenesis related DNA seq id 439.

XX expression vector; anorectic; antiarteriosclerotic; cardiant;  
 KW obesity; elevated cholesterol; elevated lipid; adipogenesis;  
 KW atherosclerosis; diabetes mellitus;  
 KW coronary artery heart disease; cholesterol homeostasis; ss;  
 KW differential expression.

XX Homo sapiens.

XX US2003180764-A1.

XX 25-SEP-2003.

XX 08-JAN-2003; 2003US-00339793.

XX 09-JAN-2002; 2002US-0347286P.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Shang J, Bowen B;

XX WPI; 2003-830986/77.

XX Polynucleotides differentially regulated in response to cholesterol and  
 PT adipogenesis are useful to detect and treat associated conditions such as  
 PT obesity, atherosclerosis, diabetes mellitus and coronary artery heart  
 PT disease.

XX Claim 8; SEQ ID NO 439; 59pp; English.

XX The invention describes a composition comprising at least one expression  
 CC vector comprising a polynucleotide of the invention. The composition has  
 CC anorectic, antiarteriosclerotic, cardiant and antidiabetic properties.  
 CC The invention is used to detect and treat conditions associated with  
 CC elevated cholesterol and lipid or during adipogenesis, particularly  
 CC obesity, atherosclerosis, diabetes mellitus or coronary artery heart  
 CC disease. This sequence represents a polynucleotide differentially  
 CC expressed during cholesterol homeostasis and adipogenesis.

XX Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



|                       |   |
|-----------------------|---|
| Qy                    | 2138 CTACTGCTTTAGAAAT 2153<br>  |
| Ds                    | 17 CTACTGCTTTAGAGAT 2   |
| <br>                  |   |
| RESULT 530            |   |
| ID                    | ADF62143 standard; DNA; 17 BP.  |
| XX                    | AC ADF62143;  |
| XX                    | DT 12-FEB-2004 (first entry)  |
| XX                    | DE Human PCCP1 DNA fragment SEQ ID 4-directed probe - SEQ ID 47.          |
| XX                    | chromatin organisation modifier; CHROMO domain; cytostatic; PCCP1;        |
| KW                    | prostate cancer candidate protein 1; tumour; gene therapy; vaccine;       |
| KW                    | human; ss; probe.   |
| OS                    | Homo sapiens.   |
| XX                    | WO2003050284-A1.  |
| XX                    | PD 19-JUN-2003.   |
| XX                    | Pf 22-NOV-2002; 2002WO-US037506.  |
| XX                    | PR 10-DEC-2001; 2001US-0339764P.  |
| PA                    | (AMSH ) AMERSHAM BIOSCIENCES SV CORP.                                     |
| PI                    | Guo J;  |
| XX                    | WPI; 2003-532916/50.  |
| XX                    | New prostate cancer candidate protein 1 (PCCP1), useful for preparing a   |
| PT                    | composition for treating or preventing a disorder associated with         |
| PT                    | decreased or increased expression or activity of PCCP1 e.g., tumor.       |
| XX                    | Example 2; SEQ ID NO 47; 164pp; English.                                  |
| XX                    | The invention relates to a novel isolated nucleic acid that encodes a     |
| CC                    | protein with a chromatin organisation modifier (CHROMO) domain. The       |
| CC                    | polynucleotide of the invention demonstrates cytostatic activity and may  |
| CC                    | be useful for preparing a composition for treating or preventing a        |
| CC                    | disorder associated with decreased or increased expression or activity of |
| CC                    | PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as |
| CC                    | during gene therapy and vaccine production procedures. The current        |
| CC                    | sequence is that of the human PCCP1-related DNA fragment SEQ ID 4-        |
| CC                    | directed probe of the invention. Note: The current sequence is not shown  |
| CC                    | within the specification per se but was retrieved from the WipoWeb        |
| CC                    | database.   |
| XX                    | Sequence 17 BP; 3 A; 9 C; 5 G; 0 T; 0 U; 0 Other;                         |
| XX                    | Query Match 0.3%; Score 14.4; DB 1; Length 17;                            |
| Best Local Similarity | 93.8%; Pred. No. 2.6e+02;   |
| Matches               | 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                       |
| Qy                    | 616 CGCGCGCAGCACG 631   |
| Ds                    | 2 CGCGCGCAGCACG 17  |
| <br>                  |   |
| RESULT 531            |   |
| ID                    | ADF62144 standard; DNA; 17 BP.  |
| XX                    | AC ADF62144;  |
| XX                    | DT 12-FEB-2004 (first entry)  |
| XX                    | Human PCCP1 DNA fragment SEQ ID 4-directed probe - SEQ ID 48.             |
| XX                    | chromatin organisation modifier; CHROMO domain; cytostatic; PCCP1;        |
| KW                    | prostate cancer candidate protein 1; tumour; gene therapy; vaccine;       |
| KW                    | human; ss; probe.   |
| OS                    | Homo sapiens.   |
| XX                    | WO2003050284-A1.  |
| XX                    | PD 19-JUN-2003.   |
| XX                    | Pf 22-NOV-2002; 2002WO-US037506.  |
| XX                    | PR 10-DEC-2001; 2001US-0339764P.  |
| PA                    | (AMSH ) AMERSHAM BIOSCIENCES SV CORP.                                     |
| PI                    | Guo J;  |
| XX                    | WPI; 2003-532916/50.  |
| XX                    | New prostate cancer candidate protein 1 (PCCP1), useful for preparing a   |
| PT                    | composition for treating or preventing a disorder associated with         |
| PT                    | decreased or increased expression or activity of PCCP1 e.g., tumor.       |
| XX                    | Example 2; SEQ ID NO 47; 164pp; English.                                  |
| XX                    | The invention relates to a novel isolated nucleic acid that encodes a     |
| CC                    | protein with a chromatin organisation modifier (CHROMO) domain. The       |
| CC                    | polynucleotide of the invention demonstrates cytostatic activity and may  |
| CC                    | be useful for preparing a composition for treating or preventing a        |
| CC                    | disorder associated with decreased or increased expression or activity of |
| CC                    | PCCP1 (prostate cancer candidate protein 1), such as a tumour, as well as |
| CC                    | during gene therapy and vaccine production procedures. The current        |
| CC                    | sequence is that of the human PCCP1-related DNA fragment SEQ ID 4-        |
| CC                    | directed probe of the invention. Note: The current sequence is not shown  |
| CC                    | within the specification per se but was retrieved from the WipoWeb        |
| CC                    | database.   |
| XX                    | Sequence 17 BP; 3 A; 9 C; 5 G; 0 T; 0 U; 0 Other;                         |
| XX                    | Query Match 0.3%; Score 14.4; DB 1; Length 17;                            |
| Best Local Similarity | 93.8%; Pred. No. 2.6e+02;   |
| Matches               | 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                       |
| Qy                    | 616 CGCGCGCAGCACG 631   |
| Ds                    | 2 CGCGCGCAGCACG 17  |
| <br>                  |   |
| RESULT 532            |   |
| ID                    | AD148299/C  |
| XX                    | AC AD148299;  |
| XX                    | DT 15-APR-2004 (first entry)  |
| XX                    | Human tumour suppression/reversion-related DNA sequence SeqID802.         |
| XX                    | tumour suppression; tumour reversion; apoptosis; virus resistance;        |
| KW                    | cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;     |
| KW                    | primer; PCR; gene chip; antisense; viral disease; tumour;                 |
| KW                    | cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human. |
| OS                    | Homo sapiens.   |
| XX                    | WO2003025177-A2.  |
| XX                    | PD 27-MAR-2003.   |
| XX                    | Pf 17-SEP-2002; 2002WO-IB004523.  |
| XX                    |   |

PR 17-SEP-2001; 2001FR-00011980.  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Telerman A, Amson R, Tuijnder M;  
XX  
DR WPI; 2003-313354/30.  
XX  
XX  
XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
XX  
PS Disclosure; SEQ ID NO 802; 30pp; French.  
XX  
XX This invention relates to novel isolated nucleic acid sequences involved  
CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
CC and/or resistance to viruses. The invention may be useful for the  
CC development of compounds with a cytostatic, virucide, neuroprotective,  
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
CC probes and primers for detecting, identifying, quantifying and/or  
CC amplifying nucleic acid, for example as one component of a gene chip, in  
CC vitro as antisense reagents and for production of recombinant  
CC polypeptides. The invention may therefore be useful for preparation of  
CC pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
CC present sequence is that of a nucleic acid sequence of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/publishedpct\_sequences  
XX  
SQ Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2138 CTACTGCTTTAGAAAT 2153  
Db 17 CTACTGCTTTAGAGAT 2  
RESULT 533  
ADI49153/c  
ID ADI49153 standard; DNA; 17 BP.  
AC ADI49153;  
XX  
DT 15-APR-2004 (first entry)  
XX  
XX Human tumour suppression/reversion-related DNA sequence SeqID1656.  
DE  
DE tumour suppression; tumour reversion; apoptosis; virus resistance;  
XX cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;  
XX primer; PCR; gene chip; antisense; viral disease; tumour;  
XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2003025177-A2.  
XX  
XX 27-MAR-2003.  
XX  
XX 17-SEP-2002; 2002WO-IB004523.  
XX  
XX 17-SEP-2001; 2001FR-00011980.  
XX  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX  
XX Telerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-313354/30.  
XX  
XX This invention relates to novel isolated nucleic acid sequences involved  
CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
CC and/or resistance to viruses. The invention may be useful for the  
CC development of compounds with a cytostatic, virucide, neuroprotective,  
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
CC probes and primers for detecting, identifying, quantifying and/or  
CC amplifying nucleic acid, for example as one component of a gene chip, in  
CC vitro as antisense reagents and for production of recombinant  
CC polypeptides. The invention may therefore be useful for preparation of  
CC pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
CC present sequence is that of a nucleic acid sequence of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/publishedpct\_sequences  
XX  
SQ Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

PT New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
XX Disclosure; SEQ ID NO 1656; 30pp; French.  
XX  
XX This invention relates to novel isolated nucleic acid sequences involved  
CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
CC and/or resistance to viruses. The invention may be useful for the  
CC development of compounds with a cytostatic, virucide, neuroprotective,  
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
CC probes and primers for detecting, identifying, quantifying and/or  
CC amplifying nucleic acid, for example as one component of a gene chip, in  
CC vitro as antisense reagents and for production of recombinant  
CC polypeptides. The invention may therefore be useful for preparation of  
CC pharmaceuticals for prevention and/or treatment of viral diseases that  
CC are characterised by development of tumours or cell degeneration,  
CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
CC present sequence is that of a nucleic acid sequence of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/publishedpct\_sequences  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 512 CCGGCCTCTGTGGATC 527  
Db 16 CCGGCCTCTGTGGATC 1  
RESULT 534  
ADI50684/c  
ID ADI50684 standard; DNA; 17 BP.  
XX  
XX AC ADI50684;  
XX  
XX DT 15-APR-2004 (first entry)  
XX  
XX Human tumour suppression/reversion-related DNA sequence SeqID3187.  
DE  
DE tumour suppression; tumour reversion; apoptosis; virus resistance;  
XX cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;  
XX primer; PCR; gene chip; antisense; viral disease; tumour;  
XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2003025177-A2.  
XX  
XX 27-MAR-2003.  
XX  
XX 17-SEP-2002; 2002WO-IB004523.  
XX  
XX 17-SEP-2001; 2001FR-00011980.  
XX  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX  
XX Telerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-313354/30.  
XX  
XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
XX Disclosure; SEQ ID NO 3187; 30pp; French.  
XX  
XX This invention relates to novel isolated nucleic acid sequences involved  
CC in the phenomena of tumour suppression, tumour reversion, apoptosis

CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, indentifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences

XX Sequence 17 BP; 3 A; 8 C; 1 G; 5 T; 0 U; 0 Other;  
 SQ

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 167 TCGGAGAGAGGATC 182  
 ||| ||||| ||||| |||||  
 Db 16 TCGGAGAGAGGATC 1

RESULT 535  
 ADI49419  
 ID ADI49419 standard; DNA; 17 BP.  
 AC ADI49419;  
 XX  
 DT 15-APR-2004 (first entry)  
 DE Human tumour suppression/reversion-related DNA sequence SeqID1922.  
 XX  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025177-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004523.  
 XX  
 PR 17-SEP-2001; 2001FR-00011980.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313354/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; SEQ ID NO 1922; 30pp; French.  
 XX  
 CC This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, indentifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences

CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences

XX Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;  
 SQ

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 821 GATCGAGTTGATC 836  
 ||| ||||| ||||| |||||  
 Db 1 GATCTGAGTTGATC 16

RESULT 536  
 ADI52640  
 ID ADI52640 standard; DNA; 17 BP.  
 XX  
 AC ADI52640;  
 XX  
 DT 15-APR-2004 (first entry)  
 DE Human tumour suppression/reversion-related DNA sequence SeqID5143.  
 XX  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025177-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004523.  
 XX  
 PR 17-SEP-2001; 2001FR-00011980.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313354/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; SEQ ID NO 5143; 30pp; French.  
 XX  
 CC This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, indentifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences

XX Sequence 17 BP; 4 A; 3 C; 4 G; 6 T; 0 U; 0 Other;  
 SQ

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 821 GATCGAGTTCAGATC 836  
 |||||  
 DB 1 GATCTGAGTTCAGATC 16

RESULT 537  
 ADI51580/c  
 ID ADI51580 standard; DNA; 17 BP.  
 XX  
 AC ADI51580;  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Human tumour suppression/reversion-related DNA sequence SeqID4083.  
 XX  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytosolic; virucide; neuroprotective; neurotropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025177-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004523.  
 XX  
 PR 17-SEP-2001; 2001FR-00011980.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313354/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; SEQ ID NO 4083; 30pp; French.  
 XX  
 CC This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration.  
 CC Specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2803 AAAAAAAAAACATC 2818  
 |||||  
 DB 16 AAAAAAAAAAGATC 1

RESULT 538  
 ADI52683/c  
 ID ADI52683 standard; DNA; 17 BP.  
 XX  
 AC ADI52683;  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Human tumour suppression/reversion-related DNA sequence SeqID5186.  
 XX  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytosolic; virucide; neuroprotective; neurotropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025177-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004523.  
 XX  
 PR 17-SEP-2001; 2001FR-00011980.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313354/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; SEQ ID NO 5186; 30pp; French.  
 XX  
 CC This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration.  
 CC Specifically cancer but also Alzheimer's disease and schizophrenia. The  
 CC present sequence is that of a nucleic acid sequence of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/publishedpct\_sequences  
 XX  
 SQ Sequence 17 BP; 2 A; 7 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 2.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 167 TCGCGAGAGAGATC 182  
 |||||  
 DB 16 TCGAGGAGAGAGATC 1

RESULT 539  
 ACC51571  
 ID ACC51571 standard; DNA; 17 BP.  
 XX  
 AC ACC51571;  
 XX





```

Db      2 CUCCCCGCCGCGCC 17

RESULT 544
AAZ222554
ID   AAZ222554 standard; DNA; 18 BP.
XX
AC   AAZ222554;
DT
DT      26-NOV-1999 (first entry)
XX
DE   Antisense oligonucleotide for inhibitor-kappa B kinase-alpha mRNA.
XX
KW   Human; inhibitor-kappa B kinase-alpha; antisense oligonucleotide;
KW   inflammation; asthma; diabetes; multiple sclerosis; dermatitis; leukemia;
KW   inflammatory bowel disease; rhinitis; allograft rejection; primer; ss.
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5962673-A.
XX
PD   05-OCT-1999.
XX
PF   20-NOV-1998; 98US-00197360.
XX
PR   20-NOV-1998; 98US-00197360.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP, Cowseert LM;
XX
DR   WPI; 1999-571297/48.
XX
PT   Antisense inhibition of the gene encoding Inhibitor-kappa B Kinase-alpha,
PT   useful for treating diseases associated with an inflammatory response
PT   e.g. asthma, diabetes.
XX
PS   Example 13; Col 36; 32pp; English.
XX
CC   Antisense oligonucleotides AAZ22543-82, are 8-30 nucleotides in length,
CC   and are targeted to inhibitor-kappa B kinase-alpha mRNA. The antisense
CC   oligonucleotides may be used for treating diseases with an inflammatory
CC   component such as asthma, diabetes, multiple sclerosis, dermatitis,
CC   leukemia, inflammatory bowel disease, rhinitis and allograft rejection.
CC   They may also have diagnostic and research applications
XX
SQ   Sequence 18 BP; 4 A; 1 C; 1 G; 12 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   3727 TATTTTATGTTATGTC 3742
      |||||
Db    1 TATTTTATGTTATTC 16

RESULT 545
AAI8953/c
ID   AAI8953 standard; DNA; 18 BP.
XX
AC   AAI8953;
XX
DT      14-MAY-1999 (first entry)
XX
DE   Fructose:glucose ratio determining gene PCR MS6 primer.
XX
KW   Fructose:glucose ratio determining gene; mature tomato fruit; flavour;
KW   MS6 primer; MS8 primer; PCR primer; molecular marker; ss.
XX
OS   Synthetic.
XX

PN   WO9904621-A1.
XX
PD   04-FEB-1999.
XX
PF   16-JUL-1998; 98WO-11000336.
XX
PR   23-JUL-1997; 97IL-00121373.
XX
PA   (ISRA ) ISRAEL MIN AGRIC.
XX
PI   Levin I, Shaffer AA;
XX
DR   WPI; 1999-142457/12.
XX
New molecular marker for a gene determining fructose:glucose ratio in
mature tomatoes - useful for finding this gene and producing tomato
seeds, plants and/or fruit with an increased fructose to glucose ratio.
Claim 2; Page 11; 17pp; English.
XX
The present invention describes a molecular marker for a gene determining
fructose:glucose ratio in mature tomatoes. Also described are: (1)
breeding tomato plants that produce tomatoes having superior taste
characteristics. At least one Lycopersicon esculentum plant is crossed
with a Lycopersicon spp. to produce hybrid (F1) seeds, which grow into F1
plants that produce seeds. These seeds produce plants, which produce ripe
fruit, in which the fructose:glucose content is determined using the
marker gene; and (2) tomato plants produced by the method, and their
fruit and seeds. The marker is useful for finding (and cloning) genes
that produce tomatoes having superior taste characteristics. The marker
gene is also useful in a method of breeding tomato plants for selecting
plants producing fruit having desired characteristics, including a higher
fructose:glucose ratio than that of standard L. esculentum. The molecular
marker enables the selection of tomato plants at the young seedling
stage, and eliminates undesirable environmental effects on the plant
phenotype, which can limit the effectiveness of selection for a phenotype
characteristic. The present sequence represents a primer used in
producing an amplification product for use as the marker
XX
SQ   Sequence 18 BP; 0 A; 10 C; 0 G; 8 T; 0 U; 0 Other;

Query Match      0.3%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   66 GGGAGAGAAAGAGAGA 81
      |||||
Db    18 GGGAGAGAGAGAGAGA 3

RESULT 546
AAA58386/c
ID   AAA58386 standard; DNA; 18 BP.
XX
AC   AAA58386;
XX
DT      01-NOV-2000 (first entry)
XX
DE   Polynucleotide # 2 used in a biomolecule detection system.
XX
KW   Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS   Synthetic.
XX
PN   WO200028088-A1.
XX
PD   18-MAY-2000.
XX
PF   10-NOV-1999; 99WO-US026612.
XX
PR   10-NOV-1998; 98US-0107828P.
XX
PR   09-NOV-1999; 99US-00437076.
XX

```

PA (BIOC-) BIOCRYSTAL LTD.  
XX Barbra-Guillem E, Nelson MB, Castro S;  
XX WPI; 2000-376593/32.  
XX Functionalized nanocrystal carrying polynucleotide, used for detecting  
PT target analyte, forms dendrimers with complementary nanocrystals to  
PT amplify the fluorescent signal.  
XX Example 3; Page 69; 72pp; English.  
XX The present invention relates to functionalised nanocrystals for use in  
CC nonisotopic detection systems for biomolecules e.g. nucleic acids,  
CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands  
CC attached to their surfaces with one end of the polynucleotide extending  
CC outwardly from the nanocrystal. The present sequence is one such of  
CC polynucleotide. These nanocrystals are used with a second series of  
CC nanocrystals, which have polynucleotides complementary to the first  
CC polynucleotides, so that the respective complementary strands hybridise  
CC to each other and form a dendrimer. This dendrimer produces a signal  
CC which can then be detected e.g. fluorescence. The present sequence is  
CC composed mainly of Thymine bases. This sequence may therefore be used  
CC with a polynucleotide composed mainly of Adenine bases (AAA58385)  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 931 AAAAAAAAAACCAACC 946  
Db 17 AAAAAAAAAACCAACC 2  
RESULT 547  
ABL56900/c  
ID ABL56900 standard; DNA; 18 BP.  
XX  
AC ABL56900;  
XX  
DT 26-JUL-2002 (first entry)  
XX  
DE Nucleic acid probe c.  
XX  
KW Concentration; quantification; mutation detection; polymorphic;  
KW polymerase chain reaction; PCR; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1046717-A2.  
XX  
PD 25-OCT-2000.  
XX  
PF 20-APR-2000; 2000EP-00108643.  
XX  
PR 20-APR-1999; 99JP-00111601.  
XX  
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;  
XX  
DR WPI; 2000-657765/64.  
XX  
XX Determining the concentration of a target nucleic acid, useful e.g. for  
PT detecting genetic mutations, comprises using a fluorescently labeled  
PT probe in which emission is reduced by binding to the target nucleic acid.  
XX Example 5; Page 21; 55pp; English.  
PS

XX The invention relates to the determination of the concentration of a  
CC nucleic acid target, using a fluorescently labeled probe which produces  
CC reduced fluorescence emission when hybridised to the target nucleic acid.  
CC The method comprises measuring the reduction in emission caused by  
CC hybridisation. The new method is particularly used to quantify target  
CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
CC quantifying microbial cells in co-cultures or symbiotic systems, for  
CC detecting gene mutations or polymorphisms, and for analysing melting  
CC curves of target nucleic acids to determine a Tm value. Methods of the  
CC invention allow target nucleic acids to be quantified quickly, easily and  
CC accurately. Particularly there is no need to remove unbound probe, and no  
CC materials are introduced that inhibit amplification by Taq polymerase (so  
CC conventional PCR conditions can be used). The specificity of PCR is kept  
CC high (amplification of primer dimers is delayed), and the limit of  
CC quantitation is reduced. Complex probes are not needed, and amplification  
CC can be monitored in real time. The working graph for data analysis  
CC (automatically generated by a computer) has a higher correlation  
CC coefficient than conventional graphs so more accurate quantitation is  
CC possible. The current sequence represents a nucleic acid probe of the  
CC invention that was used for investigating the base selectivity of a  
CC target nucleic acid  
XX  
SQ Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1162 ATATATATTTTCTT 1177  
Db 18 ATATATATTTTCTT 3  
RESULT 548  
ABL57542/c  
ID ABL57542 standard; DNA; 18 BP.  
XX  
AC ABL57542;  
XX  
DT 26-JUL-2002 (first entry)  
XX  
DE Nucleic acid probe g.  
XX  
KW Concentration; quantification; mutation detection; polymorphic;  
KW polymerase chain reaction; PCR; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1046717-A2.  
XX  
PD 25-OCT-2000.  
XX  
PF 20-APR-2000; 2000EP-00108643.  
XX  
PR 20-APR-1999; 99JP-00111601.  
XX  
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;  
XX  
DR WPI; 2000-657765/64.  
XX  
XX Determining the concentration of a target nucleic acid, useful e.g. for  
PT detecting genetic mutations, comprises using a fluorescently labeled  
PT probe in which emission is reduced by binding to the target nucleic acid.  
XX Example 5; Page 21; 55pp; English.  
XX  
XX The invention relates to the determination of the concentration of a



CC nucleic acid target, using a fluorescently labeled probe which produces  
 CC reduced fluorescence emission when hybridised to the target nucleic acid.  
 CC The method comprises measuring the reduction in emission caused by  
 CC hybridisation. The new method is particularly used to quantify target  
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
 CC quantifying microbial cells in co-cultures or symbiotic systems, for  
 CC detecting gene mutations or polymorphisms, and for analysing melting  
 CC curves of target nucleic acids to determine a Tm value. Methods of the  
 CC invention allow target nucleic acids to be quantified quickly, easily and  
 CC accurately. Particularly there is no need to remove unbound probe, and no  
 CC materials are introduced that inhibit amplification by Taq polymerase (so  
 CC conventional PCR conditions can be used). The specificity of PCR is kept  
 CC high (amplification of primer dimers is delayed), and the limit of  
 CC quantitation is reduced. Complex probes are not needed, and amplification  
 CC can be monitored in real time. The working graph for data analysis  
 CC (automatically generated by a computer) has a higher correlation  
 CC coefficient than conventional graphs so more accurate quantitation is  
 CC possible. The current sequence represents a nucleic acid probe of the  
 CC invention that was used for investigating the base selectivity of a  
 CC target nucleic acid  
 XX  
 SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
 |||||  
 Db 18 ATATATATTTTCTT 3

RESULT 549  
 ABL56899/c  
 ID ABL56899 standard; DNA; 18 BP.  
 XX  
 AC ABL56899;  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Nucleic acid probe b.  
 XX Concentration; quantification; mutation detection; polymorphic;  
 KW polymerase chain reaction; PCR; probe; ss.  
 XX Unidentified.  
 XX EP1046717-A2.  
 PN 25-OCT-2000.  
 PD 20-APR-2000; 2000EP-00108643.  
 XX 20-APR-1999; 99JP-00111601.  
 PR (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
 XX (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
 PA (KANK-) KANKYO ENG CO LTD.  
 XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
 PI Koyama O, Furusho K;  
 XX WPI; 2000-657765/64.  
 DR  
 XX  
 PT Determining the concentration of a target nucleic acid, useful e.g. for  
 PT detecting genetic mutations, comprises using a fluorescently labeled  
 PT probe in which emission is reduced by binding to the target nucleic acid.  
 XX  
 PS Example 5; Page 21; 55pp; English.  
 XX  
 CC The invention relates to the determination of the concentration of a  
 CC nucleic acid target, using a fluorescently labeled probe which produces  
 CC reduced fluorescence emission when hybridised to the target nucleic acid.

CC The method comprises measuring the reduction in emission caused by  
 CC hybridisation. The new method is particularly used to quantify target  
 CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
 CC quantifying microbial cells in co-cultures or symbiotic systems, for  
 CC detecting gene mutations or polymorphisms, and for analysing melting  
 CC curves of target nucleic acids to determine a Tm value. Methods of the  
 CC invention allow target nucleic acids to be quantified quickly, easily and  
 CC accurately. Particularly there is no need to remove unbound probe, and no  
 CC materials are introduced that inhibit amplification by Taq polymerase (so  
 CC conventional PCR conditions can be used). The specificity of PCR is kept  
 CC high (amplification of primer dimers is delayed), and the limit of  
 CC quantitation is reduced. Complex probes are not needed, and amplification  
 CC can be monitored in real time. The working graph for data analysis  
 CC (automatically generated by a computer) has a higher correlation  
 CC coefficient than conventional graphs so more accurate quantitation is  
 CC possible. The current sequence represents a nucleic acid probe of the  
 CC invention that was used for investigating the base selectivity of a  
 CC target nucleic acid  
 XX  
 SQ Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
 |||||  
 Db 18 ATATATATTTTCTT 3

RESULT 550  
 ABL57540/c  
 ID ABL57540 standard; DNA; 18 BP.  
 XX  
 AC ABL57540;  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Nucleic acid probe d.  
 XX Concentration; quantification; mutation detection; polymorphic;  
 KW polymerase chain reaction; PCR; probe; ss.  
 XX Unidentified.  
 XX EP1046717-A2.  
 PN 25-OCT-2000.  
 PD 20-APR-2000; 2000EP-00108643.  
 XX 20-APR-1999; 99JP-00111601.  
 PR (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
 PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
 PA (KANK-) KANKYO ENG CO LTD.  
 XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
 PI Koyama O, Furusho K;  
 XX WPI; 2000-657765/64.  
 DR  
 XX  
 PT Determining the concentration of a target nucleic acid, useful e.g. for  
 PT detecting genetic mutations, comprises using a fluorescently labeled  
 PT probe in which emission is reduced by binding to the target nucleic acid.  
 XX  
 PS Example 5; Page 21; 55pp; English.  
 XX  
 CC The invention relates to the determination of the concentration of a  
 CC nucleic acid target, using a fluorescently labeled probe which produces  
 CC reduced fluorescence emission when hybridised to the target nucleic acid.  
 CC The method comprises measuring the reduction in emission caused by  
 CC hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
 CC quantifying microbial cells in co-cultures or symbiotic systems, for  
 CC detecting gene mutations or polymorphisms, and for analysing melting  
 CC curves of target nucleic acids to determine a Tm value. Methods of the  
 CC invention allow target nucleic acids to be quantified quickly, easily and  
 CC accurately. Particularly there is no need to remove unbound probe, and no  
 CC materials are introduced that inhibit amplification by Taq polymerase (so  
 CC conventional PCR conditions can be used). The specificity of PCR is kept  
 CC high (amplification of primer dimers is delayed), and the limit of  
 CC quantitation is reduced. Complex probes are not needed, and amplification  
 CC can be monitored in real time. The working graph for data analysis  
 CC (automatically generated by a computer) has a higher correlation  
 CC coefficient than conventional graphs so more accurate quantitation is  
 CC possible. The current sequence represents a nucleic acid probe of the  
 CC invention that was used for investigating the base selectivity of a  
 CC target nucleic acid

SQ Sequence 18 BP; 14 A; 0 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 ATATATATTTTCTT 1177  
 Db 18 ATATATATTTTCTT 3

RESULT 551  
 AAF75598/c  
 ID AAF75598 standard; DNA; 18 BP.  
 XX AAF75598;  
 DT 10-MAY-2001 (first entry)  
 DE Binary encoded sequence tag method anchored primer #3.  
 XX Binary encoded sequence tag; BEST; nucleic acid analysis;  
 KW gene expression; adaptor; PCR primer; ss.  
 XX Synthetic.  
 OS  
 XX WO200112855-A2.  
 PN 22-FEB-2001.  
 XX 11-AUG-2000; 2000WO-US022164.  
 XX 13-AUG-1999; 99US-0148870P.  
 PR 06-APR-2000; 2000US-00544713.  
 XX (UYUA ) UNIV YALE.  
 PA Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;  
 PI WPI; 2001-202878/20.  
 DR Producing binary sequence tags, useful for analyzing nucleic acid  
 XX sequence tags, gene expression or gene-expression patterns, involves  
 PT generating nucleic acid fragments, which are mixed with offset adaptors  
 PT and adaptor-indexers.  
 XX Disclosure; Page 101; 101pp; English.  
 PS  
 XX The present invention describes a method of producing binary sequence  
 CC tags from nucleic acid fragments in a sample, involving incubating the  
 CC sample with cleaving reagents, mixing offset adaptors with the sample,  
 CC incubating with more cleaving reagents and mixing the sample with adaptor  
 CC -indexers where the adaptors are coupled to binary sequence tags. The  
 CC method is useful in sequence analysis, including analysis and comparison  
 CC of gene expression, nucleic acid samples and genomes

SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2816  
 Db 18 TGAATAAAAAAAAAA 3

RESULT 552  
 ABA97627/c  
 ID ABA97627 standard; DNA; 18 BP.  
 XX ABA97627;  
 AC ABA97627;  
 XX 11-APR-2002 (first entry)  
 DE Probe g.  
 XX ss; fluorochrome; nucleic acid probe; fluorescence.  
 KW Unidentified.  
 OS  
 XX JP2001286300-A.  
 PN 16-OCT-2001.  
 PD 20-APR-2000; 2000JP-00120097.  
 XX 20-APR-1999; 99JP-00111601.  
 PR 24-AUG-1993; 99JP-00236666.  
 PR 30-AUG-1993; 99JP-00242693.  
 PR 01-FEB-2000; 2000JP-00028896.  
 XX (BIOI-) BIOINDUSTRY KYOKAI SH.  
 PA (KANK-) KANKYO ENG KK.  
 PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.  
 XX WPI; 2002-134193/18.  
 DR Measurement of nucleic acids, using a nucleic acid probe and analysis of  
 PT the obtained data.  
 XX Example 5; Page 17; 34pp; Japanese.  
 PS This invention relates to a method for measuring nucleic acids using a  
 XX nucleic acid probe labelled with a fluorochrome. The nucleic acid probe  
 CC decreases the fluorescence of the fluorochrome when hybridised with a  
 CC target nucleic acid, the decrease in the fluorescence is measured. The  
 CC method can be used for measuring a target nucleic acid

SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1153 TTTTATATATATA 1168  
 Db 16 TTTTATATATATA 1

RESULT 553  
 ABA97623/c  
 ID ABA97623 standard; DNA; 18 BP.  
 XX ABA97623;  
 AC ABA97623;  
 XX 11-APR-2002 (first entry)  
 DT Probe b.

XX ss; fluorochrome; nucleic acid probe; fluorescence.  
XX Unidentified.  
XX JP2001286300-A.  
XX 16-OCT-2001.  
XX 20-APR-2000; 2000JP-00120097.  
XX 20-APR-1999; 99JP-00111601.  
PR 24-AUG-1999; 99JP-00236666.  
PR 30-AUG-1999; 99JP-00242693.  
PR 01-FEB-2000; 2000JP-00028896.  
XX (BIOI-) BIOINDUSTRY KYOKAI SH.  
PA (KANK-) KANKYO ENG KK.  
PA (KEI2-) KEIZAI SANGYOSHOU SANGYO GIJUTSU SOGO KEN.  
XX WPI; 2002-134193/18.  
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of  
PT the obtained data.  
XX Example 5; Page 17; 34pp; Japanese.  
CC This invention relates to a method for measuring nucleic acids using a  
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe  
CC decreases the fluorescence of the fluorochrome when hybridised with a  
CC target nucleic acid, the decrease in the fluorescence is measured. The  
CC method can be used for measuring a target nucleic acid  
XX  
XX Sequence 18 BP; 13 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1153 TTCTTTTATATATA 1168  
DB 16 TTTTATATATATA 1  
XX  
RESULT 554  
ABL95900/c  
ID ABL95900 standard; DNA; 18 BP.  
XX  
AC ABL95900;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe g for assaying nucleic acids.  
XX  
XX Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
XX Unidentified.  
XX  
XX WO200208414-A1.  
XX  
XX 31-JAN-2002.  
XX  
XX 27-JUN-2001; 2001WO-IB001147.  
XX  
XX 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
XX 31-JAN-2002.  
XX  
XX 27-JUN-2001; 2001WO-IB001147.  
XX  
XX 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI

PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX  
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
XX Example 12; Page 60; 152pp; Japanese.  
XX  
XX The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX  
SQ Sequence 18 BP; 13 A; 0 C; 1 G; 4 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1153 TTCTTTTATATATA 1168  
DB 16 TTTTATATATATA 1  
XX  
RESULT 555  
ABL95896/c  
ID ABL95896 standard; DNA; 18 BP.  
XX  
AC ABL95896;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe b for assaying nucleic acids.  
XX  
XX Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
XX Unidentified.  
XX  
XX WO200208414-A1.  
XX  
XX 31-JAN-2002.  
XX  
XX 27-JUN-2001; 2001WO-IB001147.  
XX  
XX 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
XX WPI; 2002-195876/25.  
XX  
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
XX Example 12; Page 60; 152pp; Japanese.  
XX



Best Local Similarity 93.8%; Pred. No. 3e+02; Mismatches 0; Gaps 0;  
Matches 15; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950  
DB 16 AAAAAACAACCTTTC 1

RESULT 558  
ABZ10512/C  
ID ABZ10512 standard; DNA; 18 BP.  
XX AC ABZ10512;  
DT 16-JAN-2003 (first entry)  
XX DE Haematopoietic cell proliferation disorder related oligonucleotide #652.  
XX KW Human; haematopoietic cell proliferation disorder; cytostatic;  
XX KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
XX KW cytosine methylation state; probe; primer; ss.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO20027272-A2.  
XX PD 03-OCT-2002.  
XX PF 26-MAR-2002; 2002WO-EP003401.  
XX PR 26-MAR-2001; 2001US-0278333P.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Berlin K, Braun A, Disler J, Guetig D, Howe A, Mueller J;  
XX PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
XX PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
XX PI Schwöpe I, Ziebarth H;  
XX WPI; 2003-018942/01.  
XX  
XX Detecting and differentiating between hematopoietic cell proliferative  
XX disorders, comprises contacting a target nucleic acid with a reagent that  
XX distinguishes between methylated and non-methylated CpG dinucleotides.  
XX  
XX Claim 15; Page 47; 117pp; English.

XX The present invention describes a method for detecting and  
XX differentiating between haematopoietic cell proliferative disorders  
XX associated with at least 1 gene and/or their regulatory regions in a  
XX subject. The method comprises contacting a target nucleic acid in a  
XX biological sample obtained from the subject with at least 1 reagent,  
XX which distinguishes between methylated and non-methylated CpG  
XX dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
XX represent specifically claimed nucleotide sequences from the present  
XX invention. Oligonucleotides from the present invention can be used: for  
XX differentiating between healthy haematopoietic cells and proliferative  
XX disorder haematopoietic cells; for differentiating between acute  
XX lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
XX determining the cytosine methylation state and/or single nucleotide  
XX polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
XX related sequences and their complements; and as primers for the  
XX amplification of haematopoietic cell proliferation disorder related DNA  
XX sequences. The nucleotide sequences from the present invention can also  
XX be used for detecting a predisposition to, differentiation between  
XX subclasses, diagnosis, prognosis, treatment and/or monitoring of  
XX haematopoietic cell proliferative disorders. The present method enables a  
XX highly specific classification of haematopoietic cell proliferative  
XX disorders allowing for improved and informed treatment of patients  
XX  
XX Sequence 18 BP; 4 A; 0 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02; Mismatches 0; Gaps 0;  
Matches 15; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950  
DB 16 AAAAAACAACCTTTC 1

RESULT 559  
ADB54528/C  
ID ADB54528 standard; DNA; 18 BP.  
XX AC ADB54528;  
DT 04-DEC-2003 (first entry)  
XX DE Hybridisation oligonucleotide 66 used to analyse genomic DNA region.  
XX KW colon cell proliferative disorder; non methylated CpG dinucleotide;  
XX KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;  
XX KW probe.  
XX OS Unidentified.  
XX PN WO2003072821-A2.  
XX PD 04-SEP-2003.  
XX PF 27-FEB-2003; 2003WO-EP002035.  
XX PR 27-FEB-2002; 2002EP-00004551.  
XX PA (EPIG-) EPIGENOMICS AG.  
XX PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;  
XX PI Rujan T, Schmitt A;  
XX WPI; 2003-731620/69.  
XX  
XX Detecting and differentiating between colon cell proliferative disorders  
XX associated with a gene or its regulatory regions comprises contacting a  
XX target nucleic acid in a biological sample obtained from the subject with  
XX a reagent.  
XX  
XX Claim 36; Page 30; 74pp; English.

XX The invention relates to a novel method for detecting and differentiating  
XX between colon cell proliferative disorders associated with at least one  
XX gene or its regulatory regions. The method comprises contacting a target  
XX nucleic acid in a biological sample obtained from the subject with at  
XX least one reagent or a series of reagents, where the reagent or series of  
XX reagents, distinguishes between methylated and non methylated CpG  
XX dinucleotides within the target nucleic acid. The molecules of the  
XX invention demonstrate cytostatic activity whilst the method may useful  
XX for detecting and differentiating between colon cell proliferative  
XX disorders, including cancers such as colon adenoma and colon carcinoma.  
XX The FNA (peptide nucleic acid)-oligomers are useful as probes for  
XX determining cytosine methylation state or single nucleotide  
XX polymorphisms. The current sequence is that of the hybridisation  
XX oligonucleotide of the invention which was used to analyse the genomic  
XX DNA region.  
XX  
XX Sequence 18 BP; 4 A; 0 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02; Mismatches 0; Gaps 0;  
Matches 15; Conservative 0; Indels 1; Indels 0; Gaps 0;

QY 935 AAAAAACAACCTTTC 950  
DB 16 AAAAAACAACCTTTC 1

RESULT 560  
 ADB54950  
 ID ADB54950 standard; DNA; 18 BP.  
 XX AC ADB54950;  
 XX DT 04-DEC-2003 (first entry)  
 XX DE Hybridisation oligonucleotide 486 used to analyse genomic DNA region.  
 XX KW colon cell proliferative disorder; non methylated CpG dinucleotide;  
 KW cytosinatic; cancer; adenoma; carcinoma; cytosine methylation state; ss;  
 KW Probe.  
 XX OS Unidentified.  
 XX PN WO2003072821-A2.  
 XX PD 04-SEP-2003.  
 XX PF 27-FEB-2003; 2003WO-EP002035.  
 XX PR 27-FEB-2002; 2002BP-00004551.  
 XX PA (EPIC-) EPIGENOMICS AG.  
 XX PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;  
 PI Rujan T, Schmitt A;  
 XX WPI; 2003-731620/69.  
 XX DR Detecting and differentiating between colon cell proliferative disorders  
 PT associated with a gene or its regulatory regions comprises contacting a  
 PT target nucleic acid in a biological sample obtained from the subject with  
 PT a reagent.  
 XX PS Claim 36; Page 28; 74pp; English.  
 XX CC The invention relates to a novel method for detecting and differentiating  
 CC between colon cell proliferative disorders associated with at least one  
 CC gene or its regulatory regions. The method comprises contacting a target  
 CC nucleic acid in a biological sample obtained from the subject with at  
 CC least one reagent or a series of reagents, where the reagent or series of  
 CC reagents, distinguishes between methylated and non methylated CpG  
 CC dinucleotides within the target nucleic acid. The molecules of the  
 CC invention demonstrate cytosinatic activity whilst the method may useful  
 CC for detecting and differentiating between colon cell proliferative  
 CC disorders, including cancers such as colon adenoma and colon carcinoma.  
 CC The PNA (peptide nucleic acid)-oligomers are useful as probes for  
 CC determining cytosine methylation state or single nucleotide  
 CC polymorphisms. The current sequence is that of the hybridisation  
 CC oligonucleotide of the invention which was used to analyse the genomic  
 CC DNA region.  
 XX SQ Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4130 AGTTTGGTTGAGTTT 4145  
 Db 3 AGTTTGGTTGAGTTT 18  
 RESULT 561  
 ADC70020/c  
 ID ADC70020 standard; DNA; 18 BP.  
 XX AC ADC70020;  
 XX DT 18-DEC-2003 (first entry)

XX DE Primer oligo used for analysing CpG islands in genomic DNA (SeqID 509).  
 XX KW PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;  
 KW adenocarcinoma; squamous cell carcinoma; cytosinatic; probe; PNA-oligomer;  
 KW cytosine methylation state.  
 XX OS Unidentified.  
 XX PN WO2003052135-A2.  
 XX PD 26-JUN-2003.  
 XX PF 10-DEC-2002; 2002WO-EP014026.  
 XX PR 14-DEC-2001; 2001DE-01061625.  
 XX PA (EPIC-) EPIGENOMICS AG.  
 XX PI Burger M, Field JK, Genc B, Liloglou T, Lipscher E, Maier S;  
 PI Nimmrich I;  
 XX WPI; 2003-533029/50.  
 XX DR Detecting and differentiating cytosine methylation state of genomic DNA,  
 PT useful for diagnosing, treating prognosticating and/or monitoring lung  
 PT cell proliferative disorders e.g. adenocarcinoma and squamous cell  
 PT carcinoma.  
 XX PS Claim 15; SEQ ID NO 509; 58pp; English.  
 XX CC This invention relates to a novel method for detecting and  
 CC differentiating between lung cell proliferative disorders associated with  
 CC at least one gene and/or their regulatory regions. Specifically, it  
 CC refers to a method comprising contacting a target nucleic acid in a  
 CC biological sample with at least one reagent, wherein the reagent is able  
 CC to distinguish between methylated and non-methylated CpG dinucleotides  
 CC present in the target DNA. As such, it is possible to further  
 CC differentiate and diagnose medical conditions including adenocarcinoma  
 CC and squamous cell carcinoma and their respective adjacent lung tissue.  
 CC The present invention describes cytosinatic oligomers and PNA-oligomers  
 CC that are useful as probes for determining the cytosine methylation state  
 CC or single nucleotide polymorphisms (SNPs) of the target sequence. This  
 CC oligonucleotide sequence is a primer oligomer used for the analysis of  
 CC CpG positions within genomic DNA, used in an exemplification of the  
 CC invention.  
 XX SQ Sequence 18 BP; 4 A; 0 C; 5 G; 9 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 935 AAAAAACAACCTTTC 950  
 Db 16 AAAAAACAACCTTTC 1  
 RESULT 562  
 AAD61014  
 ID AAD61014 standard; DNA; 18 BP.  
 XX AC AAD61014;  
 XX DT 15-JAN-2004 (first entry)  
 XX DE Human inhibitor-kappa B kinase-alpha antisense oligo, ISIS 23503.  
 XX KW Human; inhibitor-kappa B kinase-alpha; hyperproliferative condition;  
 KW cancer; inflammation; juvenile diabetes mellitus; myasthenia gravis;  
 KW Grave's disease; rheumatoid arthritis; allograft rejection; asthma;  
 KW systemic lupus erythematosus; bowel disease; multiple sclerosis;  
 KW psoriasis; dermatitis; thinitis; antithyroid; neuroprotective; allergy;

XX KW immunosuppressive; therapy; phosphorothioate backbone; antisense; ss.  
XX OS Homo sapiens.  
OS Synthetic.  
XX FH Key Location/Qualifiers  
FT modified\_base 1..18  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
FT modified\_base 1..4  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'methoxyethyl nucleotides; All cytidines are  
FT methylcytidines"  
FT modified\_base 15..18  
FT /\*tag= C  
FT /mod\_base= OTHER  
FT /note= "2'methoxyethyl nucleotides; All cytidines are  
FT methylcytidines"  
XX US2003092654-A1.  
XX PD 15-MAY-2003.  
XX PD 13-MAY-2002; 2002US-00145857.  
XX PF 20-NOV-1998; 98US-00197360.  
XX PR 22-JUL-1999; 99WO-US016603.  
XX PR 27-JUL-2001; 2001US-00856074.  
XX XX (MONI/) MONIA B P.  
XX PA (COWS/) COWSERT L M.  
XX XX  
XX PI Monia BP, Cowser LM;  
XX WPI; 2003-765489/72.  
XX DR Antisense compound targeted to a nucleic acid molecule encoding human  
XX PT inhibitor-kappa B kinase-alpha, useful for treating human having a  
XX PT disease or condition such as cancer, asthma, juvenile diabetes mellitus.  
XX XX  
XX PS Example 15; Page 21; Opp; English.  
XX CC The invention relates to an antisense compound targeted to a nucleic  
XX CC acid molecule encoding human inhibitor-kappa B kinase-alpha where the  
XX CC antisense compound inhibits the expression of human inhibitor-kappa B  
XX CC kinase-alpha. The invention is useful for inhibiting expression of  
XX CC inhibitor of kappa B kinase-alpha in human cells or tissues. The  
XX CC invention is also useful for treating hyperproliferative condition such  
XX CC as cancer, inflammatory conditions such as asthma, juvenile diabetes  
XX CC mellitus, myasthenia gravis, Grave's disease, rheumatoid arthritis,  
XX CC allograft rejection, inflammatory bowel disease, multiple sclerosis,  
XX CC psoriasis, lupus erythematosus, systemic lupus erythematosus, contact  
XX CC dermatitis, rhinitis and various allergies. The present sequence is an  
XX CC antisense oligonucleotide targeted to human inhibitor-kappa B kinase-  
XX CC alpha DNA  
XX SQ Sequence 18 BP; 4 A; 1 C; 1 G; 12 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3727 TATTTATGATTGTC 3742  
DB 1 TATTTATGATTATC 16  
RESULT 563  
ADE84380/c  
ID ADE84380 standard; DNA; 18 BP.  
XX

AC ADE84380;  
XX 29-JAN-2004 (first entry)  
XX DE Human lymphoid cell proliferative disorder gene CpG analysis oligo #86.  
XX XX  
XX KW Lymphoid cell proliferative disorder; methylation;  
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;  
KW diffuse large B-cell lymphoma; mantle cell lymphoma;  
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;  
KW follicular lymphoma; diagnosis; prognosis; primer; ss.  
XX XX  
XX OS Homo sapiens.  
XX PN WO2003044226-A2.  
XX PD 30-MAY-2003.  
XX XX  
XX PF 25-NOV-2002; 2002WO-EP013265.  
XX PR 23-NOV-2001; 2001DE-01057491.  
XX PR 28-DEC-2001; 2001DE-01064501.  
XX XX  
XX PA (EPIG-) EPIGENOMICS AG.  
XX XX  
XX PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;  
XX WPI; 2003-457621/43.  
XX DR  
XX XX  
XX PT Detecting and differentiating between lymphoid cell proliferative  
XX PT disorders comprises contacting a target nucleic acid with at least one  
XX PT reagent that distinguishes between methylated and non-methylated CpG  
XX PT dinucleotides.  
XX XX  
XX PS Claim 30; SEQ ID NO 376; 448pp; English.  
XX CC  
XX CC The invention relates to a method of detecting and differentiating  
XX CC between lymphoid cell proliferative disorders associated with at least  
XX CC one gene and/or their regulatory regions in a subject by contacting a  
XX CC target nucleic acid in a biological sample obtained from the subject with  
XX CC at least one reagent or series of reagents that distinguish between  
XX CC methylated and non-methylated CpG dinucleotides within the target nucleic  
XX CC acid. The genes and/or their regulatory regions are preferably selected  
XX CC from MDR1, CSNK2B, BGR4, AR, CDK4, RB2, CDC25A, GPII beta, MYO1, CDH3,  
XX CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB12, TGFBR2, TP73, CDKN1C,  
XX CC GSK3beta, ESRI, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic  
XX CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences  
XX CC of the genes are useful for detecting the methylation state of all the  
XX CC CpG dinucleotides within one or more the sequences, or their complements,  
XX CC for determining the cytosine methylation state and or single nucleotide  
XX CC polymorphisms (SNPs), and for differentiating at least two of the medical  
XX CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,  
XX CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular  
XX CC lymphoma. They are also useful for detecting of a predisposition to,  
XX CC differentiation between subclasses, diagnosis, prognosis, treating and/or  
XX CC monitoring of lymphoid cell proliferative disorder. This sequence  
XX CC represents an oligonucleotide used to analyse of CpG positions within the  
XX CC above mentioned genes.  
XX SQ Sequence 18 BP; 4 A; 0 C; 5 G; 9 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 935 AAAAAACAAACCTTTC 950  
DB 16 AAAAAACAAACCTTTC 1  
RESULT 564  
ADN74905/c



ADN74905 standard; DNA; 18 BP.  
ADN74905;  
29-JUL-2004 (first entry)  
Human CLCN2 gene 74-117 deletion identification PCR primer SEQ ID:18.  
voltage-gated chloride channel; CIC-2; CLCN2; human; chromosome 3;  
neurological disease, neuroprotective; anticonvulsant;  
idiopathic generalised epilepsy; childhood absence epilepsy;  
juvenile absence epilepsy; juvenile myoclonic epilepsy; epilepsy;  
grand mal seizure; PCR; primer; ss.  
Homo sapiens.  
Synthetic.  
WO2004039979-A1.  
13-MAY-2004.  
30-OCT-2003; 2003WO-EP012086.  
30-OCT-2002; 2002US-0422102P.  
(RHEI-) RHEINISCHE FRIEDRICH-WILHELMS-UNIV BONN.  
Heils A, Haug K;  
WPI; 2004-390325/36.  
New voltage-gated chloride channel CIC-2 polynucleotides and  
polypeptides, useful in diagnosing and treating a neurological disease or  
disorder such as idiopathic generalized epilepsy.  
Claim 19; SEQ ID NO 18; 124pp; English.  
The present invention describes a nucleic acid molecule (I) comprising a  
sequence encoding a polypeptide which has an amino acid sequence of a  
voltage-gated chloride channel CIC-2, where the glycine (Gly) residue  
corresponding to position 715 of the wild-type voltage-gated chloride  
channel CIC-2 comprising a 898 amino acid sequence of SEQ ID NO:2, is  
replaced by another amino acid residue. The voltage-gated chloride  
channel CIC-2 is encoded by the CLCN2 gene. The human CLCN2 gene is  
located on chromosome 3, more specifically to 3q26. Also described: (1) a  
vector comprising (1); (2) a host transformed with the vector of (1) or  
transformed with (1); (3) a method of producing the polypeptide encoded  
by (1); (4) a polypeptide encoded by (1) produced by the method of (3);  
(5) an antibody specifically directed to the polypeptide of (4), where  
the antibody specifically reacts with an epitope generated and/or formed  
apart from specifically binding to (1) or to the polypeptide of (4); (7) a  
primer or pair of primers capable of specifically amplifying (1); (8) a  
composition comprising (1), the vector of (1), the polypeptide of (4),  
the antibody of (5), the aptamer of (6) and the primer or pair of primers  
of (7); (9) a method of diagnosing a neurological disease or a  
susceptibility to a neurological disease; (10) a pharmaceutical  
composition comprising (1); (11) a method of treating a neurological  
disease; (12) a kit comprising (1) the vector of (1), the host of (2),  
the polypeptide of (4), the antibody of (5), the aptamer of (6) and the  
primer or pair of primers of (7); (13) a method of identifying or  
screening for molecules capable of specifically interacting with the  
polypeptide of (4); (14) a method of characterising molecules capable of  
altering the characteristic of the polypeptide of (4); and (15) a method  
of producing a pharmaceutical composition. (1) has neuroprotective and  
anticonvulsant activities. The nucleic acid molecule, vector,  
polypeptide, antibody, aptamer and the primer or pair of primers from the  
present invention can be used in preparing a diagnostic or pharmaceutical  
composition for the detection and treatment of a neurological disease or  
disorder, i.e. idiopathic generalised epilepsy (IGE), e.g. childhood  
absence epilepsy (CAE), juvenile absence epilepsy (JAE), juvenile  
myoclonic epilepsy (JME) or epilepsy with grand mal seizures on awakening  
(EGMA). The present sequence represents a PCR primer for the human CLCN-2

CC gene, which is given in the exemplification of the present invention.  
XX  
SQ Sequence 18 BP; 2 A; 8 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 96 GAGCTCTGGGGCAGGC 111  
Db 18 GAGCTCTGGGGCAGGC 3  
RESULT 565  
ADO79612/C  
ID ADO79612 standard; DNA; 18 BP.  
XX  
AC ADO79612;  
DT 26-AUG-2004 (first entry)  
XX  
DE KIAA0783 extend primer #4.  
XX  
KW Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPf3;  
CENPC1; SNP; single nucleotide polymorphism; PHF14;  
KW PHD finger protein 14; chromosome 7p21.3; zinc finger protein;  
KW transcription factor; extend; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2004047514-A2.  
XX  
PD 10-JUN-2004.  
XX  
PF 25-NOV-2003; 2003WO-US037943.  
PR 25-NOV-2002; 2002US-0429136P.  
PR 24-JUL-2003; 2003US-0490234P.  
XX  
XX (SEQU-) SEQUENOM INC.  
XX  
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;  
WPI; 2004-441037/41.  
XX  
PT Identifying a subject at risk of breast cancer by detecting the presence  
of polymorphic variations in the DLG1, KIAA0783, DPf3 or CENPC1 regions  
which are associated with breast cancer in a nucleic acid sample from a  
subject.  
XX  
XX Example 4; Page 78; 227pp; English.  
XX  
CC The present invention relates to a method for identifying a subject at  
risk of breast cancer. The method comprising detecting the presence or  
absence of one or more polymorphic variations associated with breast  
cancer in a nucleic acid sample from a subject. The nucleic acid sample  
comprises the DLG1 region (ADO79402), KIAA0783 region (ADO79403), DPf3  
region (ADO79404) or CENPC1 region (ADO79405). The gene DLG1 (discs,  
large homolog 1 (Drosophila)) is also known as synapse-associated protein  
97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The  
gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783  
has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a  
novel gene with unknown function, however, being a zinc finger protein,  
it likely to be a transcription factor. The gene DPf3 (D4, zinc and  
double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079  
and 2810403H03R1K. DPf3 is a Rho family guanine-nucleotide exchange  
factor. DPf3 has been mapped to chromosomal position 14q24.3-q31.1. The  
gene CENPC1 (centromere protein C1) is also known as Centromere  
autoantigen C1. CENPC1 has been mapped to chromosomal position 4q12-  
q13.3. CENPC1 is a centromere autoantigen and a component of the inner  
kinetochore plate. The CENPC1 protein is required for maintaining proper  
kinetochore size and a timely transition to anaphase. The method is  
useful for identifying a subject at risk of breast cancer, for early



CC diagnosis, prevention and treatment of breast cancer, to analyze and  
 CC predict a response to a breast cancer treatment, and in clinical drug  
 CC trials. The present sequence was used in an example from the invention.  
 XX  
 SQ Sequence 18 BP; 1 A; 8 C; 0 G; 9 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 66 GGGAGAGAAAGAGAGA 81  
 Db 17 GTGAGAGAAAGAGAGA 2  
 RESULT 566  
 ADP46381/c  
 ID ADP46381 standard; DNA; 18 BP.  
 XX  
 AC ADP46381;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Extend primer 10 used to genotype human NUMA1/FLJ20625/LOC220074 SNP.  
 XX  
 KW breast cancer; cytostatic; gene therapy; human; ss; primer; PCR; SNP;  
 KW single nucleotide polymorphism; NUMA1; FLJ20625; LOC220074;  
 KW chromosome 11q13.3; probe.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004047623-A2.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 25-NOV-2003; 2003WO-US037948.  
 PR 25-NOV-2002; 2002US-0429136P.  
 PR 24-JUL-2003; 2003US-0490234P.  
 XX  
 PA (SEQU-) SEQUENOM INC.  
 XX  
 PI Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;  
 XX  
 DR WPI; 2004-441051/41.  
 XX  
 PT Identifying a subject at risk of breast cancer by detecting the presence  
 PT of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUMA1 or GALE  
 PT regions which are associated with breast cancer in a nucleic acid sample  
 PT from a subject.  
 XX  
 PS Example 7; Page 106; 289pp; English.  
 XX  
 CC The invention relates to a novel method for identifying a subject at risk  
 CC of breast cancer comprising detecting the presence or absence of one or  
 CC more polymorphic variations associated with breast cancer in a nucleic  
 CC acid sample from a subject. The method of the invention has cytostatic  
 CC applications and may be useful for identifying a subject at risk of  
 CC breast cancer, for early diagnosis, prevention and treatment of breast  
 CC cancer, possibly via gene therapy, as well as to analyze and predict a  
 CC response to a breast cancer treatment and in clinical drug trials. The  
 CC current sequence is that of an Extend primer (also described as probe) of  
 CC the invention which was used to genotype human NUMA1/FLJ20625/LOC220074  
 CC region gDNA. FLJ20625 and LOC220074 have been mapped to chromosomal  
 CC position 11q13.3.  
 XX  
 SQ Sequence 18 BP; 0 A; 5 C; 2 G; 11 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 927 GGAGAGAAAAAACA 942

Db 17 GGGGAAAAAACA 2  
 RESULT 567  
 ADS90062  
 ID ADS90062 standard; DNA; 18 BP.  
 XX  
 AC ADS90062;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Oligonucleotide of the invention SEQ ID NO:1078.  
 XX  
 KW ss; cell proliferative disorder; breast; methylation; cytostatic;  
 KW gene therapy; single nucleotide polymorphism; SNP.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2004035803-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PF 01-OCT-2003; 2003WO-EP010881.  
 XX  
 PR 01-OCT-2002; 2002DE-01045779.  
 PR 07-JAN-2003; 2003DE-01000096.  
 PR 17-APR-2003; 2003DE-01017955.  
 XX  
 PA (EPTG-) EPIGENOMICS AG.  
 XX  
 PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;  
 PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;  
 XX  
 DR WPI; 2004-348468/32.  
 XX  
 PT Predicting responsiveness of a subject with breast cell proliferative  
 PT disorder, useful for treating or differentiating breast cell  
 PT proliferative disorders comprises analyzing methylation pattern of a  
 PT genomic DNA from the subject.  
 XX  
 PS Disclosure; SEQ ID NO 1078; 104pp; English.  
 XX  
 CC The invention relates to a novel method for predicting the responsiveness  
 CC of a subject with a cell proliferative disorder of the breast tissues to  
 CC a therapy comprising analysing the methylation pattern of a target  
 CC nucleic acid by contacting at least one of the target nucleic acids in a  
 CC biological sample obtained from the subject prior to or during treatment.  
 CC The method of the invention has cytostatic activity, and may have a use  
 CC in gene therapy. The set of oligonucleotides comprising at least two of  
 CC the oligomers are useful for detecting the cytosine methylation state  
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The  
 CC methods, nucleic acid, oligonucleotide, and kit are useful for the  
 CC treatment, characterisation, classification and/or differentiation, of  
 CC breast cell proliferative disorders. The method is also useful for  
 CC predicting the responsiveness of a subject with a cell proliferative  
 CC disorder of the breast tissues to a therapy. The present sequence is used  
 CC in the exemplification of the invention.  
 XX  
 SQ Sequence 18 BP; 1 A; 0 C; 8 G; 9 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.4; DB 1; Length 18;  
 Best Local Similarity 93.8%; Pred. No. 3e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4130 AGTTTGGTTGAGTTTT 4145  
 Db 3 AGTTTGGTTGAGTTTT 18  
 RESULT 568  
 ADR78534/c  
 ID ADR78534 standard; DNA; 18 BP.

XX ADR78534;  
XX  
XX 16-DEC-2004 (first entry)  
XX  
XX Human apolipoprotein B (ApoB) oligonucleotide seqid 3019.  
XX  
XX antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;  
XX cytosolic; anticonvulsant; nootropic; muscular; anti-HIV;  
XX RNA interference; RNA; antisense technology; lipid metabolism;  
XX cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
XX coronary artery disease; CAD; coronary heart disease; CHD;  
XX atherosclerosis; hepatic glucose production;  
XX glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
XX colon cancer; lung cancer; neurological disease; Huntington disease;  
XX spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2004080406-A2.  
XX  
XX 23-SEP-2004.  
XX  
XX 08-MAR-2004; 2004WO-US007070.  
XX  
XX 07-MAR-2003; 2003US-0452682P.  
XX PR 12-MAR-2003; 2003US-0454265P.  
XX PR 13-MAR-2003; 2003US-0454962P.  
XX PR 13-MAR-2003; 2003US-0455050P.  
XX PR 14-APR-2003; 2003US-0462894P.  
XX PR 17-APR-2003; 2003US-0463772P.  
XX PR 25-APR-2003; 2003US-0465665P.  
XX PR 25-APR-2003; 2003US-0465802P.  
XX PR 09-MAY-2003; 2003US-0469612P.  
XX PR 08-AUG-2003; 2003US-0493986P.  
XX PR 11-AUG-2003; 2003US-0494597P.  
XX PR 26-SEP-2003; 2003US-0506341P.  
XX PR 09-OCT-2003; 2003US-0510246P.  
XX PR 10-OCT-2003; 2003US-0510318P.  
XX PR 07-NOV-2003; 2003US-0518453P.  
XX  
XX (ALNY-) ALNYLAM PHARM.  
XX  
XX Manoharan M, Bumcrot D;  
XX WPI; 2004-677362/66.  
XX  
XX Interference RNA agent useful for treating dyslipidemias, coronary artery  
XX disease, diabetes, cancer or neurological disease, comprises sense  
XX sequence and antisense sequence which has specific modifications.  
XX  
XX Example 5; SEQ ID NO 3019; 378pp; English.  
XX  
XX The invention describes a RNA interference (iRNA) agent (I) comprising a  
XX sense sequence and an antisense sequence, where the sense sequences have  
XX one or more asymmetrical 2'-O alkyl modifications, the antisense  
XX sequences have one or more asymmetrical phosphorothioate modifications  
XX and the antisense sequence targets a human gene sequence. Also described  
XX are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100  
XX levels or glucose-6-phosphatase levels in a subject; producing (I);  
XX stabilising (I), involves selecting a sequence with activity and  
XX introducing one or more asymmetrical modification in the sequence, where  
XX the modification decreases nuclease sensitivity while not decreasing its  
XX activity; a kit comprising (I) and instruction for its use; and a device  
XX that can be dispense or administer a composition comprising (I). (I) is  
XX useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)  
XX is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.  
XX The subject is suffering from a disorder characterised by elevated or  
XX otherwise unwanted expression of apoB-100, elevated or otherwise unwanted  
XX levels of cholesterol, and/or dysregulation of lipid metabolism. The  
XX disorder is chosen from the HDL/LDL cholesterol imbalance,  
XX dyslipidaemias, hypercholesterolaemia, statin-resistant  
XX hypercholesterolaemia, coronary artery disease (CAD), coronary heart

CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
CC inhibit hepatic glucose production or for treating glucose-metabolism-  
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
CC lung cancer), neurological disease (e.g., Huntington disease or  
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that  
CC can be used to control ApoB gene expression.  
XX  
XX SQ Sequence 18 BP; 4 A; 6 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 0.3%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3362 GAAGTGGCTGTTGATC 3377  
DB 16 GAAGCGGCTGTTGATC 1  
RESULT 569  
ABZ88813/C  
ID ABZ88813 standard; DNA; 20 BP.  
XX  
XX AC ABZ88813;  
XX  
XX DT 17-OCT-2003 (first entry)  
XX  
XX DE Human oligonucleotide sequence.  
XX  
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200285308-A2.  
XX  
XX PD 31-OCT-2002.  
XX  
XX PF 23-APR-2002; 2002WO-US013135.  
XX  
XX PR 24-APR-2001; 2001US-0286137P.  
XX  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shahabuddin S;  
XX  
XX DR WPI; 2003-229219/22.  
XX  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.  
XX  
XX PS Disclosure; SEQ ID NO 4055; 872pp; English.  
XX  
XX CC The invention relates to a novel pharmaceutical composition, which has a  
XX first active agent comprising an oligonucleotide antisense to the  
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX junctions of genes encoding a polypeptide associated with lung and/or  
XX nasal airway dysfunction and a second active agent comprising an  
XX antiinflammatory steroid and ubiquinone. A composition of the invention  
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX immunosuppressive, and cytostatic activity. The composition may have a  
XX use in antisense gene therapy. The composition is useful for treating or  
XX preventing a respiratory, lung or malignant disease or condition, also  
XX for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3264 TTTTTCCTTTTAAATT 3282  
 Db 20 TTTTTCCTTTTAAATT 2  
 RESULT 570  
 ABD25043/C  
 ID ABD25043 standard; DNA; 20 BP.  
 XX AC  
 XX ABD25043;  
 XX  
 XX 29-JUL-2004 (first entry)  
 XX  
 XX A1128305-derived oligonucleotide SEQ ID 4055.  
 XX  
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200285309-A2.  
 XX  
 XX 31-OCT-2002.  
 XX  
 XX 23-APR-2002; 2002WO-US013143.  
 XX  
 XX 24-APR-2001; 2001US-0286036P.  
 XX  
 XX (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 XX WPI; 2003-093058/08.  
 XX  
 XX Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 XX Claim 15; SEQ ID NO 4055; 763pp; English.  
 XX  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)

CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer.  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 XX Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 14.2; DB 1; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3264 TTTTTCCTTTTAAATT 3282  
 Db 20 TTTTTCCTTTTAAATT 2  
 RESULT 571  
 ABQ99687/C  
 ID ABQ99687 standard; DNA; 17 BP.  
 XX AC  
 XX ABQ99687;  
 XX  
 XX 08-NOV-2002 (first entry)  
 XX  
 XX Murine Ikbkap exon 27 acceptor site.  
 XX  
 XX Murine; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; ds;  
 KW Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening.  
 XX  
 XX Mus sp.  
 XX  
 XX WO200259381-A2.  
 XX  
 XX 01-AUG-2002.  
 XX  
 XX 07-JAN-2002; 2002WO-US000473.  
 XX  
 XX 06-JAN-2001; 2001US-0260080P.  
 XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 XX  
 XX Slaugenhaupt S, Gusella JF;  
 PI  
 XX WPI; 2002-674806/72.  
 XX  
 XX New IKBKAP genes with mutations, useful for identifying a subject with  
 PT familial dysautonomia (FD), or for rapid carrier screening in the  
 PT Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or  
 PT prenatal diagnosis.  
 XX  
 XX Disclosure; Fig 11; 109pp; English.  
 XX  
 XX The present invention relates to methods and compositions useful for  
 CC detecting mutations which cause Familial Dysautonomia (FD, Riley-Day  
 CC syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OMIM  
 CC 223900). It was found that mutations in the IKBKAP gene (see ABQ05055)  
 CC are associated with FD. The mutation associated with the major haplotype

CC of FD, FD1 mutation, is a base pair (bp) mutation, where the thymine  
 CC nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced  
 CC with a cytosine. This results in skipping of exon 20 in the mRNA from FD  
 CC patients, although they continue to express varying levels of wild-type  
 CC message in a tissue-specific manner. The mutation associated with the  
 CC minor haplotype, FD2 mutation, is a bp mutation, where the guanine  
 CC nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine.  
 CC This bp mutation causes an arginine to proline missense mutation (R696P)  
 CC in the IKBKAP protein, which is predicted to disrupt a potential  
 CC phosphorylation site. The IKBKAP nucleic acid sequences are useful for  
 CC identifying a subject with FD and for rapid carrier screening. The IKBKAP  
 CC gene maps to chromosome 9q31. A mouse model of FD was created in an  
 CC example from the invention. Expression of murine Ikbkap was examined  
 CC using both mouse embryo and adult mouse multiple tissue Northern blots.  
 CC The blots were probed with a 1045bp PCR fragment that contains exons 2  
 CC through 11, which was generated using PCR primers ABQ80563-ABQ80564.  
 CC ABQ99662-ABQ99733 are the murine Ikbkap exon and intron boundaries  
 XX  
 SQ Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.3%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2801 TGAATAAAAAAAAAA 2814  
 DB 14 TGAATAAAAAAAAAA 1

RESULT 572  
 ID ADB40890  
 AC ADB40890 standard; DNA; 17 BP.  
 AC ADB40890;  
 DT 18-DEC-2003 (revised)  
 DT 04-DEC-2003 (first entry)  
 XX Tumour suppression/reversion associated nucleotide #1213.  
 XX cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;  
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.  
 XX Homo sapiens.  
 XX WO2003040369-A2.  
 XX 15-MAY-2003.  
 XX 17-SEP-2002; 2002WO-IB004219.  
 XX 17-SEP-2001; 2001FR-00011981.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 XX Telerman A, Amson R, Tuijnder M;  
 XX WPI; 2003-441574/41.  
 XX New nucleic acid encoding human prostate membrane-specific antigen,  
 PT useful e.g. for treatment of tumors and viral infection, also related  
 PT polypeptide and antibodies.  
 XX Disclosure; Page 173; 771pp; French.  
 XX The invention relates to the isolation of 6327 nucleotide sequences,  
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
 CC sequence having at least 80% identity, after optimal alignment, with the  
 CC nucleotides, a sequence that hybridizes under stringent conditions with  
 CC the nucleotides, or the complement, or corresponding RNA, of the  
 CC nucleotides. The nucleotides are used as probes or primers for detecting,

CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
 CC sense and antisense sequences, of nucleotides involved in tumour  
 CC suppression or reversion, apoptosis and or viral resistance, to produce  
 CC recombinant polypeptides, and to prepare transgenic animals, as  
 CC experimental models. The nucleotides (also vectors containing them and  
 CC cells containing the vectors), the encoded polypeptides and antibodies  
 CC (Ab) against the polypeptide are useful for prevention and/or treatment  
 CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis  
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.  
 XX

SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.3%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2742 ATCTTTT TTTT 2755  
 DB 2 ATCTTTT TTTT 15

RESULT 573  
 ADI51580  
 ID ADI51580 standard; DNA; 17 BP.  
 XX  
 AC ADI51580;  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Human tumour suppression/reversion-related DNA sequence SeqID4083.  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytostatic; virucide; neuroprotective; nontropic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX Homo sapiens.  
 XX WO2003025177-A2.  
 XX 27-WAR-2003.  
 XX 17-SEP-2002; 2002WO-IB004523.  
 XX 17-SEP-2001; 2001FR-00011980.  
 XX (MOLE-) MOLECULAR ENGINES LAB.  
 XX Telerman A, Amson R, Tuijnder M;  
 XX WPI; 2003-313354/30.  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX Disclosure; SEQ ID NO 4083; 30pp; French.  
 XX This invention relates to novel isolated nucleic acid sequences involved  
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis  
 CC and/or resistance to viruses. The invention may be useful for the  
 CC development of compounds with a cytostatic, virucide, neuroprotective,  
 CC nontropic or neuroleptic activity. The DNA sequences may be useful as  
 CC probes and primers for detecting, identifying, quantifying and/or  
 CC amplifying nucleic acid, for example as one component of a gene chip, in  
 CC vitro as antisense reagents and for production of recombinant  
 CC polypeptides. The invention may therefore be useful for preparation of  
 CC pharmaceuticals for prevention and/or treatment of viral diseases that



Db 1 UUUUUUUUUUUUAAAG 17

RESULT 576  
ADL49409

ID AAX18370 standard; DNA; 17 BP.  
AC AAX18370;  
XX  
XX  
XX 11-MAY-1999 (first entry) `

XX RT-PCR primer of the invention SEQ ID 11.  
DE  
XX  
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
XX  
XX Synthetic.  
XX  
XX JF11032765-A.  
XX  
XX 09-FEB-1999.  
XX  
XX 18-JUL-1997; 97JP-00208312.  
XX  
XX 18-JUL-1997; 97JP-00208312.  
XX (TAKI ) TAKARA SHUZO CO LTD.  
XX WPI; 1999-183822/16.  
XX  
XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
XX  
XX Disclosure; Page 11; 19pp; Japanese.  
XX  
XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences  
XX  
XX Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3264 TTTTTCCTTTTCCCTTTTAA 3280  
Db 1 TTTTTCCTTTTCCCTTTTAA 17

RESULT 577  
ADL49409

ID ADL49409 standard; RNA; 17 BP.  
XX  
XX ADL49409;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX Human PKR substrate sequence #523.  
XX  
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;  
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
KW protein kinase PKR; cerebrovascular accident;  
KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
XX substrate; ds.  
XX  
XX Unidentified.  
XX  
XX WO200281628-A2.  
XX  
XX 17-OCT-2002.  
XX  
XX 03-APR-2002; 2002WO-US010512.  
XX  
XX 05-APR-2001; 2001US-00827395.  
XX  
XX 29-MAY-2001; 2001US-0294412P.  
XX  
XX 28-AUG-2001; 2001US-0315315P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Blatt L, Chowrira B, Haeberli P, Mcswiggen J, Fosnaugh K;  
XX WPI; 2003-058513/05.  
XX  
XX Novel enzymatic nucleic acid that down-regulates expression of neurite growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or protein kinase PKR genes, for treating cancer and inflammatory disease.  
XX  
XX Claim 59; SEQ ID NO 2942; 317pp; English.  
XX  
XX The invention comprises nucleic acids (e.g. antisense oligonucleotides) that down regulate the expression or inhibit the function of a receptor for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR), IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the invention are useful for treating: cerebrovascular accident, central nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma, lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis, restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The nucleic acids of the invention are also useful for down-regulating the expression of a target gene and as a diagnostic tool to examine genetic drifts and mutations within diseased cells or to detect the presence of a target RNA in a cell. The present RNA sequence represents a human PKR substrate sequence.

QY 2741 CATCTTTTTCCTTTTAA 2757  
Db 1 CUUUUUUUUUUUUUA 17

RESULT 578  
ADP86176/c

ID ADP86176 standard; DNA; 17 BP.  
XX  
XX ADP86176;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX CpG immunostimulatory oligonucleotide #47.  
XX  
XX CpG immunostimulatory oligonucleotide; immune response; asthma;  
KW viral infection; bacterial infection; cancer; lymphoma;  
KW intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;  
KW carcinoma; sarcoma; gene therapy; phosphorothioate; ss.

OS Unidentified.  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 XX  
 XX WO2004053104-A2.  
 XX  
 XX PD 24-JUN-2004.  
 XX  
 XX PF 11-DEC-2003; 2003WO-US039775.  
 XX  
 XX PR 11-DEC-2002; 2002US-0432409P.  
 XX PR 25-SEP-2003; 2003US-0506108P.  
 XX  
 XX PA (COLE-) COLEY PHARM GROUP INC.  
 XX PA (COLE-) COLEY PHARM GMBH.  
 XX  
 XX PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;  
 XX  
 XX DR WPI; 2004-487902/46.  
 XX  
 XX PT New oligonucleotides, useful for treating allergy or asthma, viral and  
 PT bacterial infections, and cancer, e.g. biliary tract cancer, breast  
 PT cancer, cervical cancer.  
 XX  
 XX PS Example; SEQ ID NO 47; 104pp; English.

XX  
 CC The invention relates to a class of CpG immunostimulatory  
 CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that  
 CC are useful for stimulating an immune response. Oligonucleotides and  
 CC compositions of the invention are useful for treating allergy or asthma,  
 CC viral and bacterial infections and cancer e.g. biliary tract cancer,  
 CC breast cancer, cervical cancer, choriocarcinoma, colon cancer,  
 CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,  
 CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,  
 CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,  
 CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain  
 CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,  
 CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,  
 CC testicular cancer, as well as other carcinomas and sarcomas. The  
 CC invention is also useful in gene therapy. The present sequence is a CpG  
 CC immunostimulatory oligonucleotide.  
 XX  
 XX SQ Sequence 17 BP; 11 A; 1 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 3.2e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1032 TTTTCTTTTAAAGGA 1048  
 |||||  
 DB 17 TTTTCTTTTAAACGA 1

RESULT 579  
 ADL49414  
 ID ADL49414 standard; RNA; 17 BP.  
 XX  
 XX AC ADL49414;  
 XX  
 XX DT 20-MAY-2004 (first entry)  
 XX  
 XX DE Human PKR substrate sequence #528.  
 XX  
 XX KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
 KW prostaglandin D2 receptor; PTGDR; ikappaB kinase; IKK;  
 KW protein kinase PKR; cerebrovascular accident;  
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;

KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
 KW substrate; ds.  
 XX Unidentified.  
 OS  
 XX WO200281628-A2.  
 XX  
 XX PD 17-OCT-2002.  
 XX  
 XX PF 03-APR-2002; 2002WO-US010512.  
 XX  
 XX PR 05-APR-2001; 2001US-00827395.  
 XX PR 29-MAY-2001; 2001US-0294412P.  
 XX PR 28-AUG-2001; 2001US-0315315P.  
 XX  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;  
 XX WPI; 2003-058513/05.  
 XX  
 XX DR Novel enzymatic nucleic acid that down-regulates expression of neurite  
 XX growth inhibitor receptor, prostaglandin D2 receptor, ikappaB kinase or  
 XX protein kinase PKR genes, for treating cancer and inflammatory disease.  
 XX  
 XX PS Claim 59; SEQ ID NO 2947; 317pp; English.

XX  
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
 CC that down regulate the expression or inhibit the function of a receptor  
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
 CC ikappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
 CC invention are useful for treating: cerebrovascular accident, central  
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
 CC nucleic acids of the invention are also useful for down-regulating the  
 CC expression of a target gene and as a diagnostic tool to examine genetic  
 CC drifts and mutations within diseased cells or to detect the presence of a  
 CC target RNA in a cell. The present RNA sequence represents a human PKR  
 CC substrate sequence.

XX SQ Sequence 17 BP; 5 A; 1 C; 1 G; 0 T; 10 U; 0 Other;

Query Match 0.3%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 29.4%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 2746 TTTTCTTTTAAAGGAA 2762  
 |||||  
 DB 1 UUUUUUUUUAAAGACA 17

Search completed: February 25, 2005, 09:48:43  
 Job time : 28 secs

